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**P- 2023/25343**

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
**DIRECCIÓN DE NUEVAS CREACIONES**
E. S. D.

Re: Expediente No. **NC2023/0011606**
Solicitud de patente a nombre de **MAVERICK THERAPEUTICS, INC.**

Yo, CAROLINA DAZA MONTALVO identificada como aparece al pie de mi firma, domiciliada en la Carrera 11 No. 86-53, obrando como apoderada de la sociedad MAVERICK THERAPEUTICS, INC., domiciliada en California, Estados Unidos de América, en respuesta al Oficio No. **16219** notificado electrónicamente el 6 de octubre del 2023, relacionado con el Artículo 17 del Código de Procedimiento Administrativo y Contencioso Administrativo, mediante el cual su despacho requiere al solicitante *completar* la solicitud de divisional, atentamente me permito manifestar la siguiente información:

1. **Caso particular**

Su despacho indica que el capítulo reivindicatorio de la solicitud divisional con radicado No. NC2023/0011606 el 31 de agosto de 2023 reivindica materia contenida en el capítulo reivindicatorio de la solicitud parental No. NC2020/0004288, radicado el 31 de mayo de 2023 y que fue concedido en la Resolución No. 44137

En particular, su despacho indica que las reivindicaciones 1 a 10 de la solicitud divisional se refieren, al igual que la solicitud parental (NC2020/0004288), a una proteína que comprende de N- a C- terminal:

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a) un primer dominio de unión a antígeno de dominio único (sdABD) que se une a un antígeno objetivo de tumor humano (TTA) (sdABD-TTA);

b) un primer enlazador de dominio;

c) un dominio Fv restringido que comprende:
   i. un primer dominio pesado variable que comprende un vhCDR1, vhCDR2 y vhCDR3;
   ii. un enlazador no escindible restringido (CNCL);
   iii. un primer dominio ligero variable que comprende vlCDR1, vlCDR2 y vlCDR3;

d) un segundo enlazador de dominio;

e) un segundo sdABD-TTA;

f) un enlazador escindible (CL);

g) un pseudo dominio Fv restringido que comprende:
   i. un primer pseudo dominio variable ligero;
   ii. un enlazador no escindible (NCL);

h) un primer pseudo dominio variable pesado;

i) un tercer sdABD que se une a la albúmina sérica humana;

En donde además dicha proteína:

- Tiene la capacidad de unirse a CD3 humano,
- Comprende un Fv inactivo producto de la asociación intramolecular del primer dominio y pseudo dominio,
- Además, dicho primer y segundo TTA es EGFR,
- Dichos primer y segundo sdABD-TTA se seleccionan del grupo que consiste en la SEQ IDNO: 1, SEQ IDNO: 5, SEQ IDNO: 9 o SEQ ID NO: 13 y
- El dominio de extensión de vida media tiene la SEQ ID NO: 45.

Por lo tanto, su despacho solicita modificar el capítulo reivindicatorio de la solicitud divisional de modo que no exista materia superpuesta con la de la solicitud parental.

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Finalmente, el examinador señala que es necesario el pago por reivindicaciones adicionales, a partir de la undécima, de manera que sea posible estudiar el capítulo reivindicatorio completo en el momento procedimental oportuno.

En respuesta a dichas observaciones, se presentan las siguientes aclaraciones:

## 2. Modificación al pliego reivindicatorio de la solicitud parental

Con fundamento en la facultad que confiere el Artículo 34 de la Decisión 486 a los solicitantes para modificar la solicitud de patente en cualquier momento del trámite y en atención a las observaciones de su despacho, presento junto con este memorial un nuevo pliego reivindicatorio que consta de diecinueve (19) reivindicaciones y que reemplaza completamente el pliego presentado el 31 de agosto de 2023.

Las modificaciones realizadas se detallan a continuación:

**2.1** Se modificó la reivindicación independiente 1 de manera que ahora:

2.1.1 Define las secuencias de aminoácidos especificas SEQ ID NO: 29 o 33, las cuales fueron incluidas para caracterizar el primer dominio de unión a antígeno de dominio único (sdABD) que se une a un antígeno objetivo de tumor humano (TTA) (sdABD-TTA). Dicha modificación se sustenta en el párrafo [0013] de la página 4 de la descripción.

2.1.2 el subpárrafo c)-ii) no hace referencia a que el enlazador restringido es no-escindible.

2.1.3 En los subpárrafos c-i), c-iii), g-i) y g-iii) se eliminó la referencia a un *primer* dominio pesado, *primer* dominio ligero variable o un *primer* pseudo dominio variable ligero.

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**2.2** Se modificó la reivindicación 2 de manera que ahora sea dependiente de la reivindicación 1 y reclame la característica eliminada de dicha reivindicación que corresponde a que el enlazador no escindible restringido (CNCL).

**2.3** Se incluyó la nueva reivindicación 3 de manera que se contemple que el enlazador restringido también pueda ser un enlazador escindible restringido (CCL). Dicha modificación se sustenta en el párrafo [0088] de la página 16 de la descripción.

**2.4** Se eliminó el término "primer" de las antiguas reivindicaciones 3 a 7 (nuevas reivindicaciones 4 a 6) de la referencia los dominios de la proteína que busca caracterizar.

**2.5** Se incluyó la nueva reivindicación 8, en donde se reclaman las secuencias características de las CDRs de cadena pesada y ligera. Dicha modificación se sustenta en listado de secuencias.

**2.6** Se incluyó la nueva reivindicación 9 en donde se reclaman las secuencias de aminoácidos a los dominios variables de la cadena pesada y ligera. Dicha modificación se sustenta en el párrafo [0205] de la página 41 de la descripción.

**2.7** Se incluyó la nueva reivindicación 10 en donde se reclaman las secuencias de aminoácidos de los dominios de extensión de vida media. Dicha modificación se sustenta en el párrafo [0229] de la página 44 de la descripción y en el listado de secuencias.

**2.8** Se eliminaron las reivindicaciones 7 a 11 y 18 a 49 y se reajustó la numeración del documento.

**2.9** Se modificó la reivindicación 13 de manera que se incluyan las secuencias con su respectivo SEQ ID NO del grupo de proteínas incluidas en la caracterización.

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**2.10** Se incluyó la nueva reivindicación 13, con el fin de reclamar la secuencia de aminoácidos con su respectivo SEQ ID NO de la proteína Pro225. Dicha modificación se sustenta en el listado de secuencias de la descripción y en el párrafo [0250] de la página 47 de la descripción.

**2.11** Se incluyó la nueva reivindicación 14 con el fin de reclamar la secuencia de aminoácidos con su respectivo SEQ ID NO de la proteína Pro226 Dicha modificación se sustenta en el listado de secuencias de la descripción y en el párrafo [0250] de la página 47 de la descripción.

**2.12** Se incluyó la nueva reivindicación 15, con el fin de reclamar la secuencia de aminoácidos con su respectivo SEQ ID NO de la proteína Pro495. Dicha modificación se sustenta en el listado de secuencias de la descripción y en el párrafo [0250] de la página 47 de la descripción.

Al respecto, me permito señalar que dichas modificaciones no amplían de ninguna manera la materia objeto de la solicitud, se realizan con el fin de definir la materia reclamada de forma clara, y buscan ayudar a superar las objeciones planteadas por su Despacho.

## 3. Aclaraciones con respecto a las objeciones del señor examinador

Ahora bien, en relación las objeciones del examinador, me permito resaltar que se ha modificado el capítulo reivindicatorio de manera que el alcance de esta solicitud divisional sea redireccionado a modalidades no contempladas en la solicitud parental. En ese sentido, se incluyó dentro de las características técnicas esenciales las secuencias de aminoácidos SEQ ID NO: 29 o 33 con respecto al primer dominio de unión a antígeno de dominio único (sdABD) que se une a un antígeno objetivo de tumor humano (TTA) sdABD-TTA. Dichas secuencias no se mencionan en las reivindicaciones concedidas para la solicitud parental.

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Además, en el nuevo capítulo reivindicatorio se contemplan estructuras de la proteína SEQ ID NO:147 (Pro225), SEQ ID NO:148 (Pro226), SEQ ID NO:173 (Pro359), SEQ ID NO:257 (Pro373), SEQ ID NO:258 (Pro374), SEQ ID NO:181 (Pro479), SEQ ID NO:182 (Pro480), and SEQ ID NO:183 (Pro495), con particular atención en la Pro225, Pro226 y Pro495, las cuales son estructuras de la proteína no contempladas en la solicitud parental. En ese sentido, la solicitud divisional se refiere a proteínas que presentan estructuras distintas a las que se encuentran al alcance de la solicitud parental, por lo que es posible inferir que no solo el alcance estructural sino el efecto técnico presenta un alcance que no se sobrelapa con el de la proteína de la solicitud parental.

En consecuencia, el alcance de la presente solicitud es diferente a la materia que ha sido concedida previamente para la solicitud parental, y, por lo tanto, amablemente solicito que se proceda a aceptar la presente solicitud y continuar con el trámite pertinente.

Así, en vista de las modificaciones realizadas al pliego reivindicatorio y las aclaraciones aquí presentadas, es posible manifestar que la materia reclamada en el nuevo capítulo reivindicatorio no corresponde con la materia descrita y protegida por la solicitud parental de esta familia, de manera tal que el capítulo reivindicatorio de la presente solicitud fraccionaria *no abarca la misma materia* que se otorgó en la solicitud anterior.

Adicionalmente, junto a este memorial se presenta nuevamente las Figuras y el listado de secuencias radicados junto a la presentación de la solicitud dado que no se encuentran visibles en la plataforma.

## 4. Pago de tasas

Considerando que el presente memorial se presenta junto con modificaciones a las reivindicaciones, se anexa el comprobante de pago correspondiente a la tasa de

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modificación a las reivindicaciones, según lo establecido en la Resolución No. **59669** de 2020.

Ahora, en relación con el número de reivindicaciones, atentamente me permito resaltar que junto a la presente respuesta se realiza el pago de la tasa por concepto de 9 reivindicaciones adicionales, de manera que pueda ser estudiado por su despacho.

## 5. Conclusiones

Considerando las modificaciones introducidas en esta oportunidad, puede concluirse que:

i. Las modificaciones aquí presentadas no amplían de ninguna manera la materia objeto de la solicitud original, por lo que es posible afirmar que el nuevo pliego reivindicatorio se ajusta a las disposiciones del Artículo 34 de la Decisión 486/00;

ii. La solicitud de divisional del expediente de la referencia cumple con los requisitos establecidos en la Decisión 486 y en el Capítulo Primero, Título X de la Circular Única dado que (a) no implica una ampliación de la protección que corresponde a la divulgación contenida en la solicitud inicial; (b) el alcance de la invención reivindicada ***no abarca la misma materia*** que se reivindica en la solicitud parental; (c) la memoria descriptiva es igual a la memoria descriptiva de la solicitud parental e incluye las figuras o el listado de secuencias de la solicitud parental; (d) el formulario de la presente solicitud fraccionaria fue debidamente diligenciado y acompañado de los documentos necesarios para formar la solicitud fraccionaria y (e) se acreditó el pago de las tasas pertinentes.

Así, respetuosamente se solicita aceptar la solicitud divisional y examinar la novedad, el nivel inventivo y la aplicación industrial para la invención titulada " PROTEÍNAS DE UNIÓN CONDICIONALMENTE ACTIVADAS RESTRINGIDAS" a nombre de MAVERICK

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THERAPEUTICS, INC., y si los cumpliese, pedir a la Superintendencia de Industria y Comercio conceder el privilegio de patente; o si el señor examinador considera que subsisten razones para no aceptar la solicitud divisional, rogamos **comunicarnos** los debidos motivos y razones que sustenten su objeción con el fin de que nuestro mandante tenga la posibilidad completar la solicitud con base en la interpretación del 42 del Código de Procedimiento Administrativo y de lo Contencioso Administrativo que señala que: *"Habiéndose dado oportunidad a los interesados para expresar sus opiniones, y con base en las pruebas e informes disponibles, se tomará la decisión, que será motivada. La decisión resolverá todas las peticiones que hayan sido oportunamente planteadas dentro de la actuación por el peticionario y por los terceros reconocidos",* (el subrayado es nuestro).

En consecuencia, solicitamos a ese despacho pronunciarse en relación con todos los argumentos presentados en este memorial dando estricta aplicación al principio del debido proceso consagrado en el artículo 29 de la Constitución Nacional.

## 6. Anexos

- Nuevo pliego reivindicatorio conformado por diecinueve (19) reivindicaciones.

- Comprobante de pago por concepto de modificación a las reivindicaciones.

- Comprobante de pago por concepto de 9 reivindicaciones adicionales.

- Listado de Secuencias de la divisional.

- Figuras de la divisional.

Señora Directora,

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P- 2023/25343
Reivindicación Modificadas en respuesta a AO 16219
3 de noviembre de 2023

## REIVINDICACIONES

1. Una proteína que comprende, de N- a C-terminal:

a) un primer dominio de unión a antígeno de dominio único (sdABD) que se une a un antígeno objetivo de tumor humano (TTA) (sdABD-TTA) que comprende la secuencia de aminoácidos con SEQ ID NOs: 29 o 33;

b) un primer enlazador de dominio;

c) un dominio Fv restringido que comprende:

i) un dominio pesado variable que comprende un vhCDR1, vhCDR2 y vhCDR3;

ii) un enlazador restringido; y

iii) un dominio ligero variable que comprende vlCDR1, vlCDR2 y vlCDR3;

d) un segundo enlazador de dominio;

e) un segundo sdABD-TTA que comprende la secuencia de aminoácidos de SEQ ID NOs: 29 o 33;

f) un enlazador escindible (CL);

g) un pseudo dominio Fv restringido que comprende:

i) un pseudo dominio variable ligero;

ii) un enlazador no escindible (NCL); y

iii) un pseudo dominio variable pesado;

h) un tercer enlazador de dominio; y

i) un tercer sdABD que se une a la albúmina sérica humana;

en donde dicho dominio pesado variable y dicho dominio ligero variable son capaces de unir CD3 humano pero dicho dominio Fv restringido no se une a CD3; en donde dicho dominio pesado variable y dicho pseudo dominio ligero variable se asocian intramolecularmente para formar un Fv inactivo; y en el que dicho primer dominio ligero variable y dicho dominio pesado pseudo variable se asocian intramolecularmente para formar un Fv inactivo.

2. La proteína de conformidad con la reivindicación 1, en donde el enlazador restringido es un enlazador no escindible restringido (CNCL).

3. La proteína de la reivindicación 1, en donde el enlazador restringido es un enlazador escindible restringido (CCL).

4. Una proteína de conformidad con cualquiera de las reivindicaciones 1 a 3, caracterizada porque dicho dominio pesado variable es N-terminal a dicho dominio ligero variable y dicho pseudo dominio variable ligero es N-terminal a dicho pseudo dominio pesado variable.

5. Una proteína de conformidad con cualquiera de las reivindicaciones 1 a 3, caracterizada porque dicho dominio pesado variable es N-terminal a dicho dominio ligero variable y dicho pseudo dominio pesado variable es N-terminal a dicho pseudo dominio ligero variable.

6. Una proteína de conformidad con cualquiera de las reivindicaciones 1 a 3, caracterizada porque dicho dominio ligero variable es N-terminal a dicho dominio pesado variable y dicho pseudo dominio variable ligero es N-terminal a dicho pseudo dominio pesado variable.

7. Una proteína de conformidad con cualquiera de las reivindicaciones 1 a 3, caracterizada porque dicho dominio ligero variable es N-terminal a dicho dominio pesado variable y dicho pseudo dominio pesado variable es N-terminal a dicho pseudo dominio ligero variable.

8. Una proteína según cualquiera de las reivindicaciones 1, en la que:

la vhCDR1 del dominio pesado variable comprende la secuencia de aminoácidos de SEQ ID NO:62;

la vhCDR2 del dominio pesado variable comprende la secuencia de aminoácidos de SEQ ID NO:63;

la vhCDR3 del dominio pesado variable comprende la secuencia de aminoácidos de SEQ ID NO:64;

la vlCDR1 del dominio ligero variable comprende la secuencia de aminoácidos de SEQ ID

NO:50;

la vlCDR2 del dominio ligero variable comprende la secuencia de aminoácidos de SEQ ID NO:51; y

el vlCDR3 del dominio ligero variable comprende la secuencia de aminoácidos de SEQ ID NO:52.

9. Una proteína según cualquiera de las reivindicaciones 1-8, en la que:

el dominio pesado variable comprende la secuencia de aminoácidos de SEQ ID NO:61; y

el dominio ligero variable comprende la secuencia de aminoácidos de SEQ ID NO:49.

10. La proteína de conformidad con las reivindicaciones 1 a 9, caracterizada porque dicho dominio de extensión de vida media tiene la SEQ ID NO: 45 o SEQ ID NO: 142.

11. La proteína de conformidad con las reivindicaciones 1 a 10, caracterizada porque dicho enlazador escindible se escinde por una proteasa humana seleccionada del grupo que consiste en MMP2, MMP9, Meprin A, Meprin B, catepsina S, catepsina K, catespina L, GranzimaB, uPA, Kallekriein7, matriptasa y trombina.

12. La proteína de conformidad con la reivindicación 1, caracterizada porque comprende una proteína seleccionada del grupo que consiste en SEQ ID NO:147 (Pro225), SEQ ID NO:148 (Pro226), SEQ ID NO:173 (Pro359), SEQ ID NO:257 (Pro373), SEQ ID NO:258 (Pro374), SEQ ID NO:181 (Pro479), SEQ ID NO:182 (Pro480), y SEQ ID NO:183 (Pro495).

13. El polipéptido de la reivindicación 1, que comprende la secuencia de aminoácidos de SEQ ID NO:147 (Pro225).

14. El polipéptido de la reivindicación 1, que comprende la secuencia de aminoácidos de SEQ ID NO:148 (Pro226).

15. El polipéptido de la reivindicación 1, que comprende la secuencia de aminoácidos de SEQ ID NO:183 (Pro495).

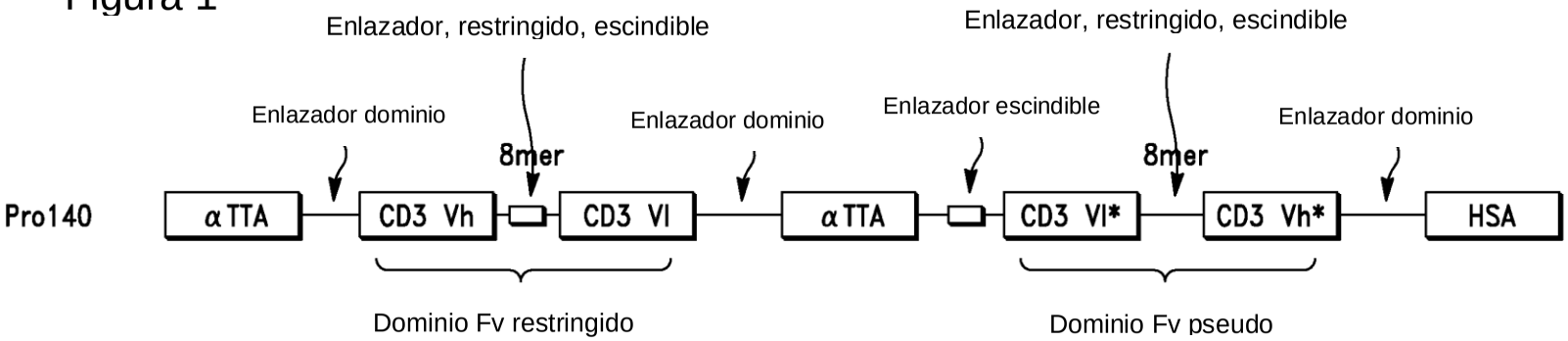
16. Un ácido nucleico que codifica una proteína de conformidad con cualquiera de las reivindicaciones 1 a 15.

17. Un vector de expresión que comprende el ácido nucleico de la reivindicación 16.

18. Una célula huésped que comprende el vector de expresión de la reivindicación 17.

19. Un método para preparar una proteína que comprende cultivar la célula huésped de la reivindicación 18 en condiciones en las que dicha proteína se expresa y recupera dicha proteína.

Figura 1


Enlazador, restringido, escindible
Enlazador, restringido, escindible
Enlazador dominio
Enlazador dominio
Enlazador escindible
Enlazador dominio
8mer
8mer
Pro140
αTTA
CD3 Vh
CD3 Vl
αTTA
CD3 Vl*
CD3 Vh*
HSA
Dominio Fv restringido
Dominio Fv pseudo

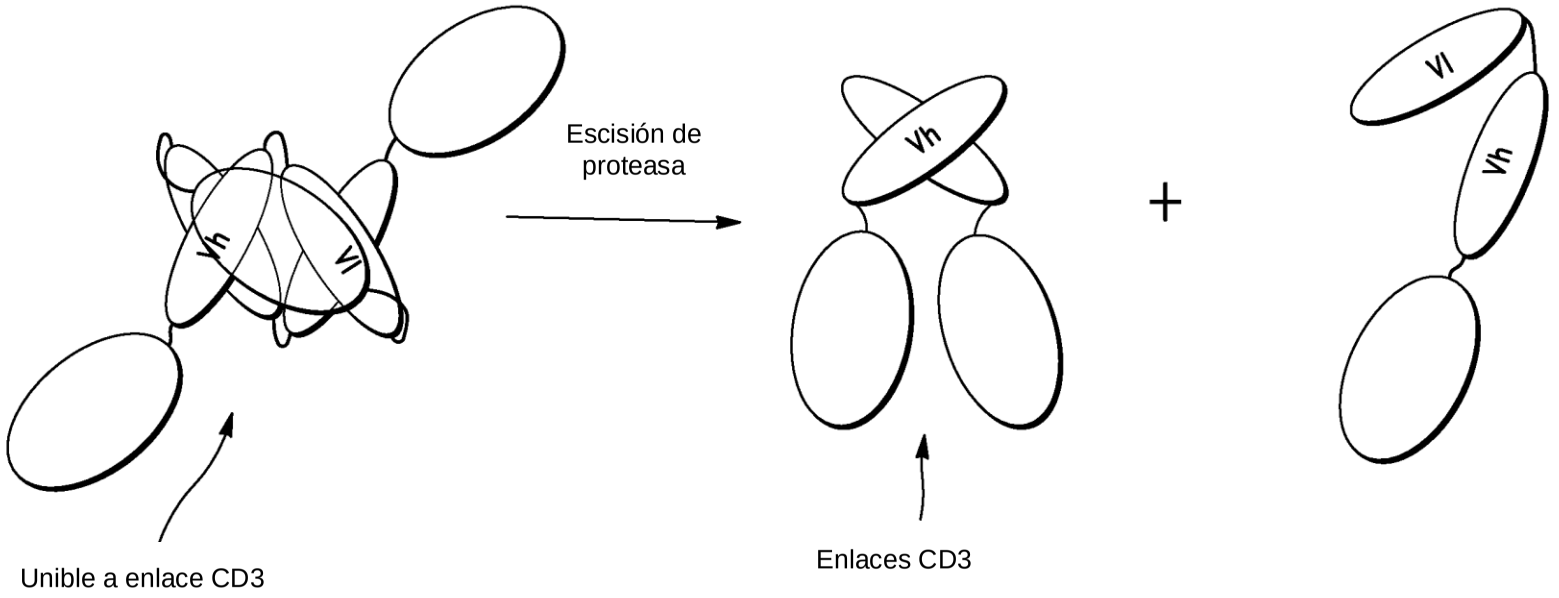

Vh
Vl
Escisión de proteasa
Vh
+
Vl
Vh
Unible a enlace CD3
Enlaces CD3

Figura 2

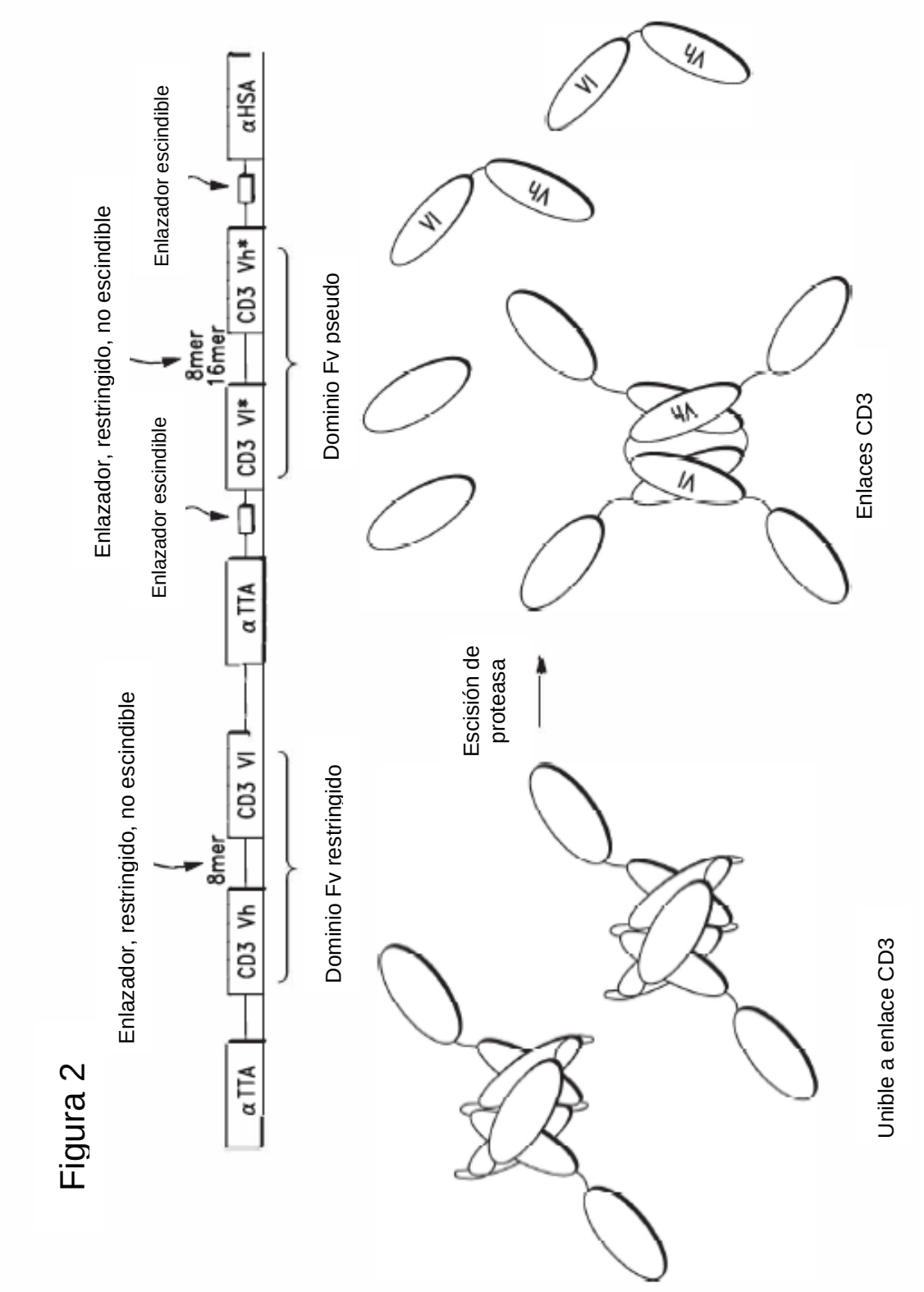
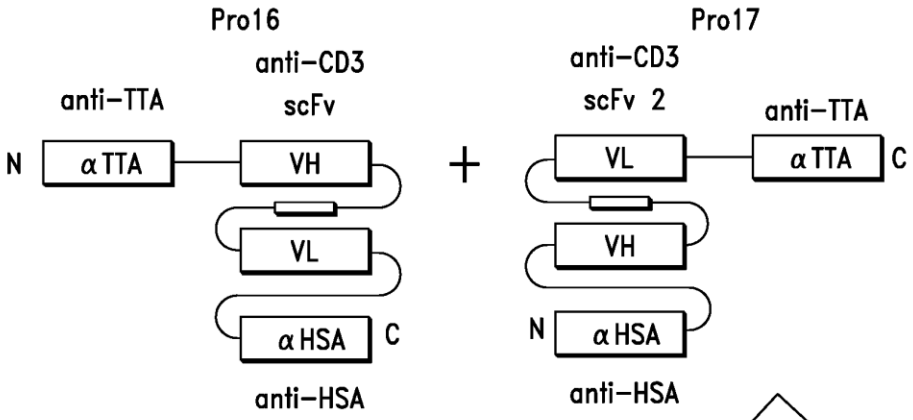

Enlazador, restringido, no escindible
Enlazador escindible
Enlazador escindible
Enlazador, restringido, no escindible
8mer
16mer
8mer
αTTA
CD3 Vh
CD3 Vl
αTTA
CD3 Vl*
CD3 Vh*
αHSA
Dominio Fv restringido
Dominio Fv pseudo
Escisión de proteasa
Enlaces CD3
Unible a enlace CD3

Figura 3A

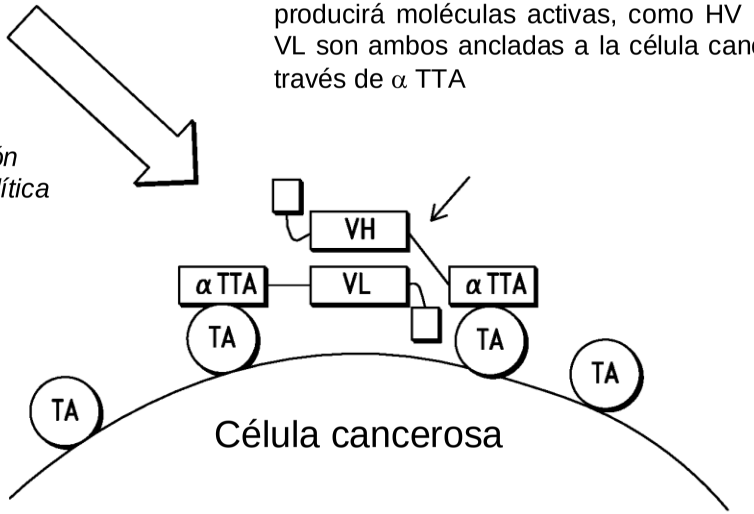



Moléculas escindidas:

- Unir a antígeno de tumor
- No unir a CD3
- No activo en ensayo TDCC

Post escisión, la mezcla de Pro16 y Pro17 producirá moléculas activas, como HV intacto y VL son ambos ancladas a la célula cancerosa a través de α TTA

*Escisión proteolítica*




Sitio de escisión de proteasa

Figura 3B

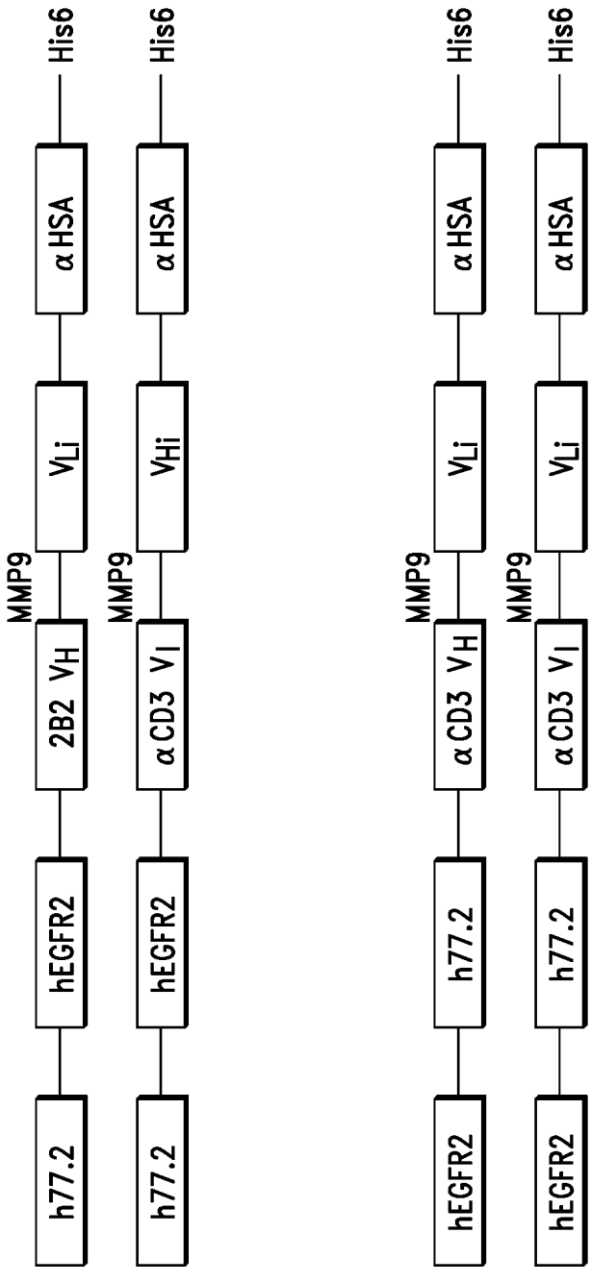
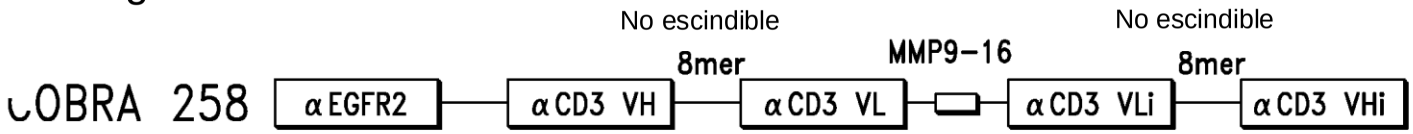
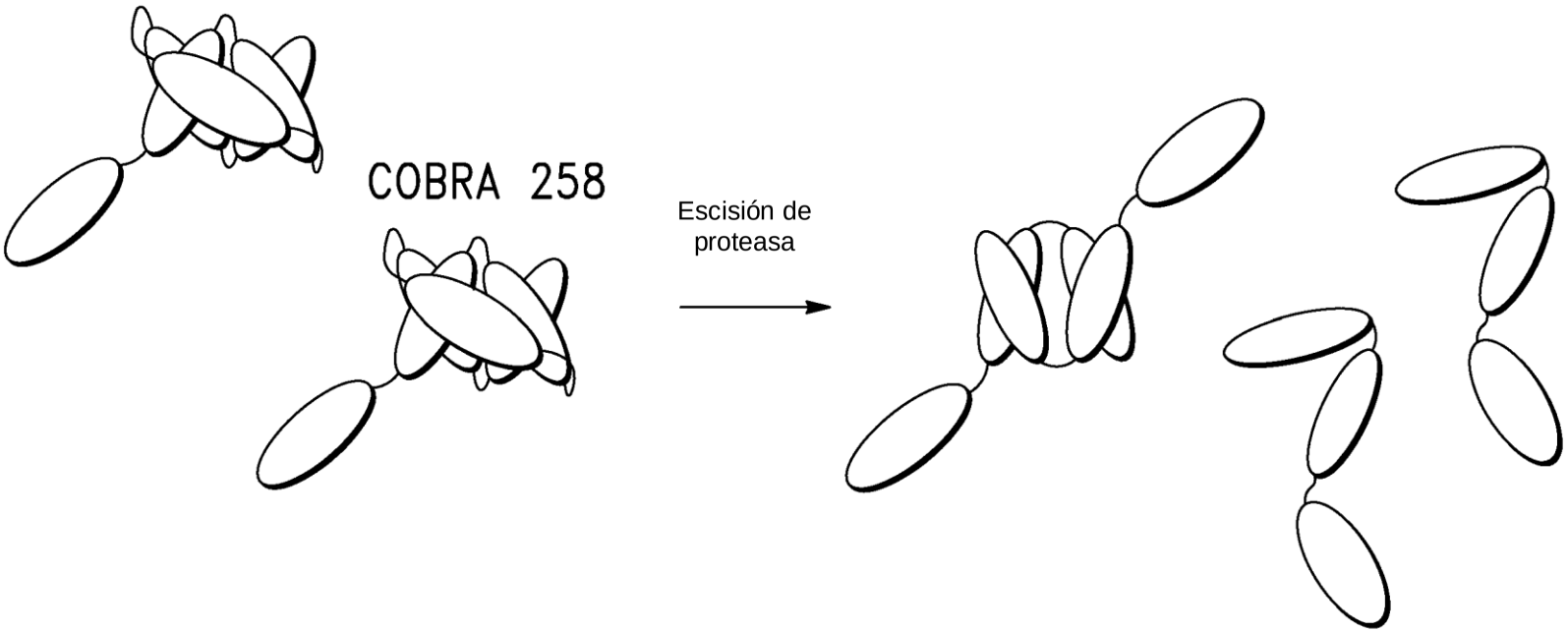

Pro448
h77.2
hEGFR2
2B2 VH
MMP9
VLi
αHSA
His6
Pro450
h77.2
hEGFR2
αCD3 VI
MMP9
VHi
αHSA
His6
Pro449
hEGFR2
h77.2
αCD3 VH
MMP9
VLi
αHSA
His6
Pro451
hEGFR2
h77.2
αCD3 VI
MMP9
VLi
αHSA
His6

Figura 4


No escindible
8mer
MMP9-16
No escindible
8mer
COBRA 258
αEGFR2
αCD3 VH
αCD3 VL
αCD3 VLi
αCD3 VHi


COBRA 258
Escisión de proteasa

# Figura 5A

**sdAbs direccionada**

**αEGFR1**

EVQLVESGGGLVQAGGSLRLSCAAS**GRTFSSYAMG**WFRQAPGKEREFVVA**INWSSGSTYYADS VKG**RFTISRDNAKNTMYLQMNSLKPEDTAVYYCAA**GYQINSGNYNFKDYEYDY**WGQGTQVTVS S (SEQ ID NO:1)

sdCDR1 **GRTFSSYAMG** (SEQ ID NO:2)

sdCDR2 **INWSSGSTYYADSVKG** (SEQ ID NO:3)

sdCDR3 **GYQINSGNYNFKDYEYDY** (SEQ ID NO:4)

**αEGFR2**

QVKLEESGGGSVQTGGSLRLTCAAS**GRTSRSYGMG**WFRQAPGKEREFVS**GISWRGDSTGYAD SVKG**RFTISRDNAKNTVDLQMNSLKPEDTAIYYCAA**AAGSAWYGTLYEYDY**WGQGTQVTVSS (SEQ ID NO:5)

sdCDR1 **GRTSRSYGMG** (SEQ ID NO:6)

sdCDR2 **GISWRGDSTGYADSVKG** (SEQ ID NO:7)

sdCDR3 **AAGSAWYGTLYEYDY** (SEQ ID NO:8)

**hαEGFR1**

EVQLVESGGGLVQPGGSLRLSCAAS**GRTFSSYAMG**WFRQAPGKEREFVVA**INWSSGSTYYADS VKG**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAA**GYQINSGNYNFKDYEYDY**WGQGTLVTVSS (SEQ ID NO:9)

sdCDR1 **GRTFSSYAMG** (SEQ ID NO:10)

sdCDR2 **INWSSGSTYYADSVKG** (SEQ ID NO:11)

sdCDR3 **GYQINSGNYNFKDYEYDY** (SEQ ID NO:12)

**hαEGFR2**

QVKLVESGGGVVRPGGSLTLSCAAS**GRTSRSYGMG**WFRQAPGKEREFVS**GISWRGDSTGYAD SVKG**RFTISRDNAKNSLYLQMNSLRAEDTALYYCAA**AAGSAWYGTLYEYDY**WGQGTLVTVSS (SEQ ID NO:13)

sdCDR1 **GRTSRSYGMG** (SEQ ID NO:14)

sdCDR2 **GISWRGDSTGYADSVKG** (SEQ ID NO:15)

sdCDR3 **AAGSAWYGTLYEYDY** (SEQ ID NO:16)

# Figura 5B

**sdAbs direccionada - Continuación**

**αFOLR1 h77-2**

QVQLVESGGGLVQPGGSLRLSCAAS**GFTVSNSVMA**WYRQTPGNEREFVA**IINSIGITNYADSVK G**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNR**NFDRIY**WGQGTLVTVSS (SEQ ID NO:17)

sdCDR1 **GFTVSNSVMA** (SEQ ID NO:18)

sdCDR2 **IINSIGITNYADSVKG** (SEQ ID NO:19)

sdCDR3 **NFDRIY** (SEQ ID NO:20)

**αFOLR1 h59.3**

QVQLVESGGGLVQPGGSLRLSCAAP**GNTFSISAMG**WYRQAPGKQREWVA**VTHSDYSTNYADS VKG**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCKH**YGIDY**WGQGTLVTVSS (SEQ ID NO:21)

sdCDR1 **GNTFSISAMG** (SEQ ID NO:22)

sdCDR2 **VTHSDYSTNYADSVKG** (SEQ ID NO:23)

sdCDR3 **YGIDY** (SEQ ID NO:24)

**αFOLR1 h22-4**

QVQLVESGGGLVQPGGSLRLSCEAS**GTTFSRDVMG**WYRQAPGKQRELVA**IISRGGSTNYADSV KG**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNA**NTATWGRVF**WGQGTLVTVSS (SEQ ID NO:25)

sdCDR1 **GTTFSRDVMG** (SEQ ID NO:26)

sdCDR2 **IISRGGSTNYADSVKG** (SEQ ID NO:27)

sdCDR3 **NTATWGRVF** (SEQ ID NO:28)

**αB7H3 hF7**

QVQLQESGGGLVQPGGSLRLSCAPS**RRTFHTYHMG**WFRQAPGKEREFVA**VINWSGGSTVYAD SVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAA**GGATTQRATEASYDY**WGQGTLVTVSS (SEQ ID NO:29)

sdCDR1 **RRTFHTYHMG** (SEQ ID NO:30)

sdCDR2 **VINWSGGSTVYADSVKG** (SEQ ID NO:31)

sdCDR3 **GGATTQRATEASYDY** (SEQ ID NO:32)

# Figura 5C

**sdAbs direccionada - Continuación**

**αB7H3 hF12**

QVQLQESGGGLVQPGGSLRLSCEAS**PRTFSTYSMA**WFRQAPGKERSFVA**AINWSGGNTSYAD SVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAA**GGVLAHHNYEYDY**WGQGTLVTVSS (SEQ ID NO:33)

sdCDR1 **PRTFSTYSMA** (SEQ ID NO:34)

sdCDR2 **AINWSGGNTSYADSVKG** (SEQ ID NO:35)

sdCDR3 **GGVLAHHNYEYDY** (SEQ ID NO:36)

**αEpCAM h13**

QVQLVESGGGLVQPGGSLTLSCAAS**GTGSIFSINLMG**WYRQAPGKQRELVA**RITSGDSTVYADS VKG**RFTISRDNSKNTLYLQMNSLRPEDTAVYYCNL**LLRSSPGATTPY**WGQGTLVTVSS (SEQ ID NO:37)

sdCDR1 **GTGSIFSINLMG** (SEQ ID NO:38)

sdCDR2 **RITSGDSTVYADSVKG** (SEQ ID NO:39)

sdCDR3 **LLRSSPGATTPY** (SEQ ID NO:40)

**αEpCAM h23**

QVQLVESGGGLVQPGGSLTLSCVIS**GSFSALWAMR**WYRQAPGQQRELVA**SSRGGTTSYADSV KG**RFTISRDNSKNTLYLQMNSLRPEDTAVYYCNA**IDGHLAY**WGQGTLVTVSS (SEQ ID NO:41)

sdCDR1 **GSFSALWAMR** (SEQ ID NO:42)

sdCDR2 **SSRGGTTSYADSVKG** (SEQ ID NO:43)

sdCDR3 **IDGHLAY** (SEQ ID NO:44)

**αHSA half-life extension domain**

EVQLVESGGGLVQPGNSLRLSCAAS**GFTFSKFGMS**WVRQAPGKGLEWVS**SISGSGRDTLYAES VKG**RFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI**GGSLSV**SSQGTLVTVSS (SEQ ID NO:45)

sdCDR1 **GFTFSKFGMS** (SEQ ID NO:46)

sdCDR2 **SISGSGRDTLYAESVKG** (SEQ ID NO:47)

sdCDR3 **GGSLSV** (SEQ ID NO:48)

EVQLVESGGGLVQPGNSLRLSCAAS**GFTFSKFGMS**WVRQAPGKGLEWVS**SISGSGRDTLYAES VKG**RFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI**GGSLSV**SSQGTLVTVSS/HHHHHH (SEQ ID NO:142)

# Figura 5D

**Dominios αCD3 scFv**

**αCD3 $V_L$**

QTVVTQEPSLTVSPGGTVTLTC**ASSTGAVTSGNYPN**WVQQKPGQAPRGLIG**GTKFLVP**GTPARF SGSLLGGKAALTLSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL (SEQ ID NO:49)

aVLCDR1 **ASSTGAVTSGNYPN** (SEQ ID NO:50)

aVLsdCDR2 **GTKFLVP** (SEQ ID NO:51)

aVLsdCDR3 **TLWYSNRWV** (SEQ ID NO:52)

**αCD3 $V_{Li}$**

QTVVTQEPSLTVSPGGTVTLTC**GSSTGAVTSGNYPN**WVQQKPGQAPRGLIG**DYKDDDDK**GTPA RFSGSLLGGKAALTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL (SEQ ID NO:53)

iVLCDR1 **GSSTGAVTSGNYPN** (SEQ ID NO:54)

iVLsdCDR2 **DYKDDDDK** (SEQ ID NO:55)

iVLsdCDR3 **VLWYSNRWV** (SEQ ID NO:56)

**αCD3 $V_{Li2}$**

QTVVTQEPSLTVSPGGTVTLTC**GSSTGAVTSGNYPN**WVQQKPGQAPRGLIG**GTKDDAP**GTPAR FSGSLLGGKAALTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL (SEQ ID NO:57)

iVLCDR1 **GSSTGAVTSGNYPN** (SEQ ID NO:58)

iVLsdCDR2 **GTKDDAP** (SEQ ID NO:59)

iVLsdCDR3 **VLWYSNRWV** (SEQ ID NO:60)

**αCD3 $V_H$**

EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGKGLEWVA**RIRSKYNNYATYYA DQVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTLVTVSS (SEQ ID NO:61)

aVHCDR1 **GFTFNKYAIN** (SEQ ID NO:62)

aVHsdCDR2 **RIRSKYNNYATYYADQVKD** (SEQ ID NO:63)

aVHsdCDR3 **HANFGNSYISYWAY** (SEQ ID NO:64)

# Figura 5E

**Dominios αCD3 scFv - Continuación**

**αCD3 $V_{Hi}$**

EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAMN**WVRQAPGKGLEWVA**RIRSKYDYKDDDD KADSVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGTLVTVSS (SEQ ID NO:65)

iVHsdCDR1 **GFTFNKYAMN** (SEQ ID NO:66)

iVHsdCDR2 **RIRSKYDYKDDDDKADSVKD** (SEQ ID NO:67)

iVHsdCDR3 **HGNFGNSYISYWAY** (SEQ ID NO:68)

**αCD3 $V_{Hi2}$**

EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKHAMN**WVRQAPGKGLEWVA**RIRSKYNNYATAY ADSVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGTLVTVSS (SEQ ID NO:69)

iVHsdCDR1 **GFTFNKHAMN** (SEQ ID NO:70)

iVHsdCDR2 **RIRSKYNNYATAYADSVKD** (SEQ ID NO:71)

iVHsdCDR3 **HGNFGNSYISYWAY** (SEQ ID NO:72)

**Enlazadores αCD3 scFv**

**Normal/No escindible**

GGGGSGGGGSGGGGS (SEQ ID NO:73)

**Restringida**

GGGSGGGS (SEQ ID NO:74)

# Figura 5F

**Enlazadores escindibles (Sitio de reconocimiento en negritas, sitio de escisión - *I*)**

**MMP 2/9**

**GPAG/MKGL** (SEQ ID NO:75)

SGGP**GPAG/MKGL**PGS (SEQ ID NO:76)

SGGGP**GPAG/MKGL**PGGS (SEQ ID NO:77)

**Meprina A/B**

GGGG**KKLA/DEPE**GGGS (SEQ ID NO:78)

**KKLA/DEPE** (SEQ ID NO:79)

**Meprina A/B (Variante, alta eficiencia)**

GGG**KFLA/DEPE**GG (SEQ ID NO:80)

**Catepsina S, K, L**

SGGG**ARLQ/SAAP**GGGS (SEQ ID NO:81)

**ARLQ/SAAP** (SEQ ID NO:82)

**Meprina/Granzima B**

SGGG**GVYADSLEDG**GGGS (SEQ ID NO:83)

**GVYADSLEDG** (SEQ ID NO:84)

**Matriptasa/uPA (MS)**

GGGS**LSGR/SDNH**GGGS (SEQ ID NO:85)

G**LSGR/SDNHG** (SEQ ID NO:86)

**Matriptasa (MV)**

SGGG**SFTR/QARVV**GGGS (SEQ ID NO:87)

**SFTR/QARVV** (SEQ ID NO:88)

**Catepsina S/MMP9/Meprina A**

**ARLQ/SAAPAG/LKGA** (SEQ ID NO:89)

**MMP9 (Variante, alta eficiencia)**

GGP**GPAG/MHGL**PG (SEQ ID NO:90)

**MMP9 (Variante, baja eficiencia)**

GGP**GPAG/MEGL**PG (SEQ ID NO:91)

# Figura 5G

**Enlazadores escindibles (Sitio de reconocimiento en negritas, sitio de escisión - *I)* - continuación**

**Trombina 1**

GGGG**LVPR/GSL**GGGGS (SEQ ID NO:92)

**Trombina 2**

SSGG**GMPR/SFR**GGGS (SEQ ID NO:93)

**Enteroquinasa/bandera**

GGGG**DYKDDDDK**/GGGS (SEQ ID NO:94)

**KLK7-6**

SGGG**QNPY/SAGR**GGGS (SEQ ID NO:95)

**KLK7-13**

SGGG**QNPY/SAGG**GSGG (SEQ ID NO:96)

**KLK7-11**

SGGG**RNVY/SAGG**GSGG (SEQ ID NO:97)

**KLK7-10**

SGGG**QNTW/SAGK**GGGS (SEQ ID NO:98)

**uPA**

GGGS**HTGR/SAYF**GGGS (SEQ ID NO:99)

**MMP9-2**

SGGPGPAG/LKGAPGS (SEQ ID NO:184)

Figura 6A

| Proteasa | Secuencia de dominio de escisión | Seq id no: |
|---|---|---|
| MMP7 | KRALGLPG | 100 |
| MMP7 | $(DE)_8$RPLALWRS$(DR)_8$ | 101 |
| MMP9 | PR(S/T)(L/I)(S/T) | 102 |
| MMP9 | LEATA | 103 |
| MMP11 | GGAANLVRGG | 104 |
| MMP14 | SGRIGFLRTA | 105 |
| MMP | PLGLAG | 106 |
| MMP | PLGLAX | 107 |
| MMP | PLGC(ME)AG | 108 |
| MMP | ESPAYYTA | 109 |
| MMP | RLQLKL | 110 |
| MMP | RLQLKAC | 111 |
| MMP2, MMP9, MMP14 | EP(CIT)G(HOF)YL | 112 |
| Urokinase plasminogen activator (upa) | SGRSA | 113 |
| Activador de uroquinasa plasminógeno (upa) | DAFK | 114 |
| Activador de uroquinasa plasminógeno (upa) | GGGRR | 115 |
| Enzima lisosomal | GFLG | 116 |
| Enzima lisosomal | ALAL | 117 |
| Enzima lisosomal | FK | 118 |
| Catepsina B | NLL | 119 |
| Catepsina D | PIC(ET)FF | 120 |
| Catepsina K | GGPRGLPG | 121 |
| Antígeno específico de próstata | HSSKLQ | 122 |
| Antígeno específico de próstata | HSSKLQL | 123 |
| Antígeno específico de próstata | HSSKLQEDA | 124 |
| Proteasa de virus de herpes simple | LVLASSSFGY | 125 |
| Proteasa Hiv | GVSQNYPIVG | 126 |
| Proteasa Cmv | GVVQASCRLA | 127 |

Figura 6B

| Proteasa | Secuencia de dominio de escisión | Seq id no: |
|---|---|---|
| Trombina | F(PIP)RS | 128 |
| Trombina | DPRSFL | 129 |
| Trombina | PPRSFL | 130 |
| Caspasa-3 | DEVD | 131 |
| Caspasa-3 | DEVDP | 132 |
| Caspasa-3 | KGSGDVEG | 133 |
| Enzima que convierte Interleucina 1β | GWEHDG | 134 |
| Enteroquinasa | EDDDDKA | 135 |
| Fap | KQEQNPGST | 136 |
| Kalikreina 2 | GKAFRR | 137 |
| Plasmina | DAFK | 138 |
| Plasmina | DVLK | 139 |
| Plasmina | DAFK | 140 |
| Superior | ALLLALL | 141 |

Unión de Pro6 digerido con EK a OVCAR-8,
detectado con A488-cyCD3::Flag::hFC

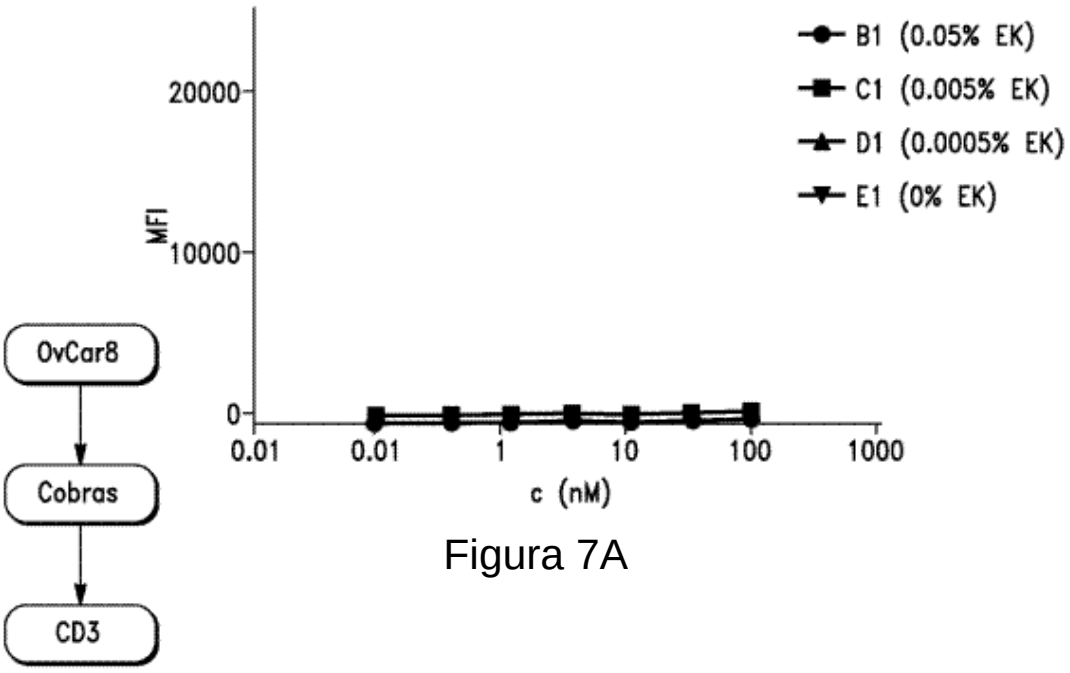



Figura 7A

Unión de Pro7 digerido con EK a OVCAR-8,
detectado con A488-cyCD3::Flag::hFC

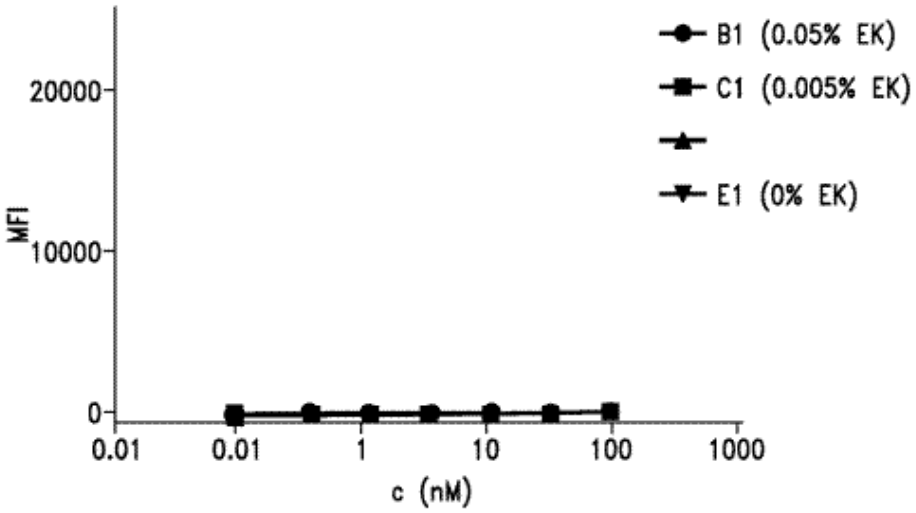



Figura 7B

Unión de Pro6+7 digerido con EK a OVCAR-8,
detectado con A488-cyCD3::Flag::hFC

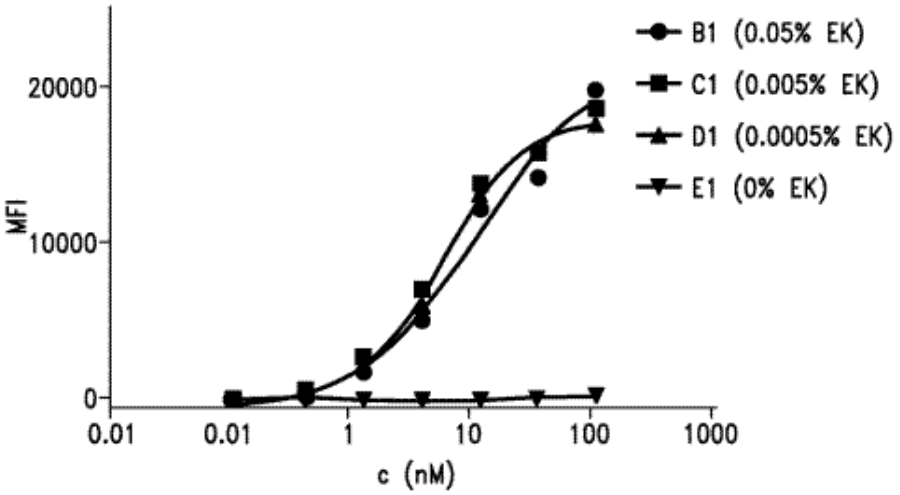



Figura 7C

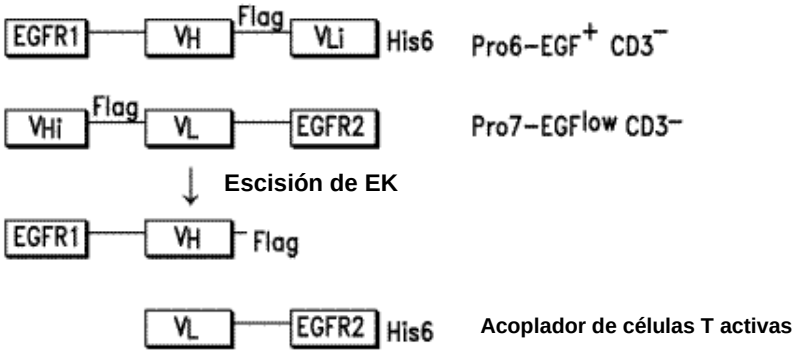



Figura 7D

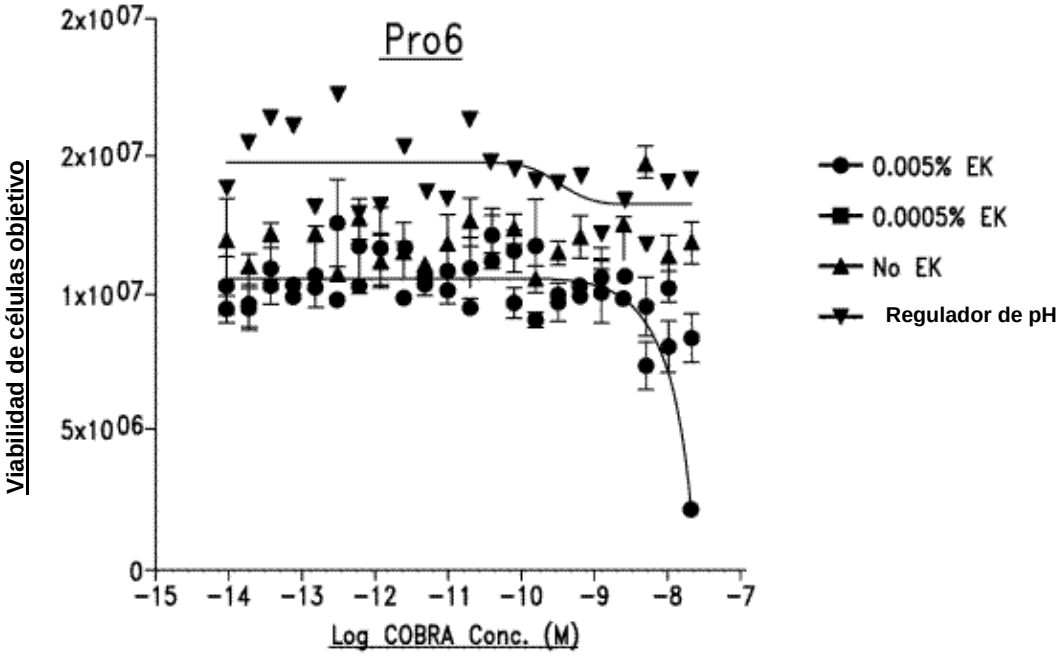



Figura 8A

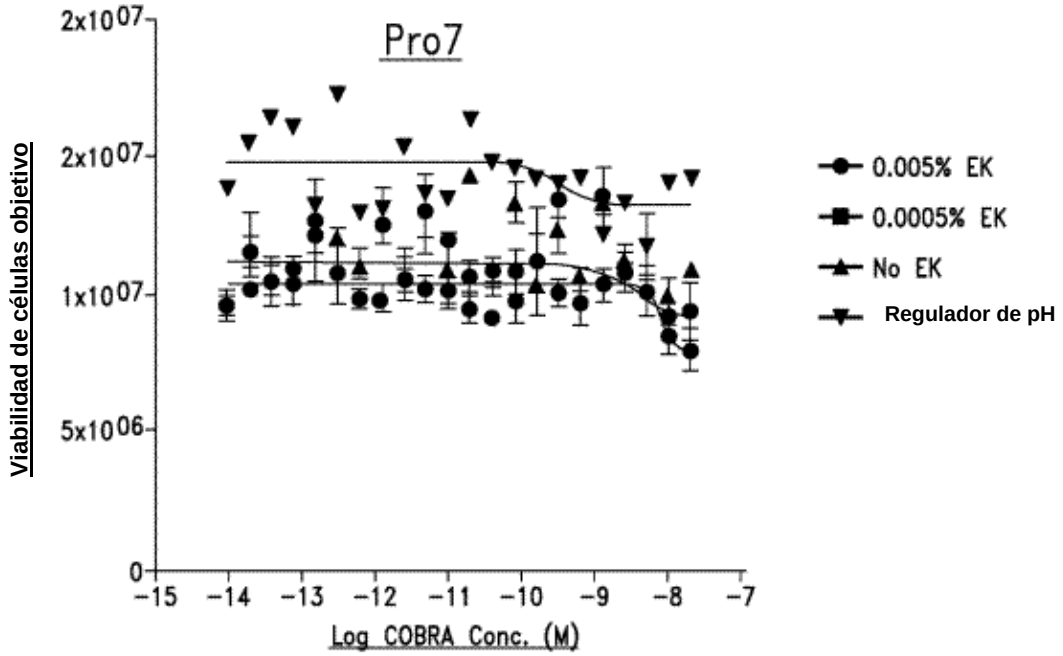



Figura 8B

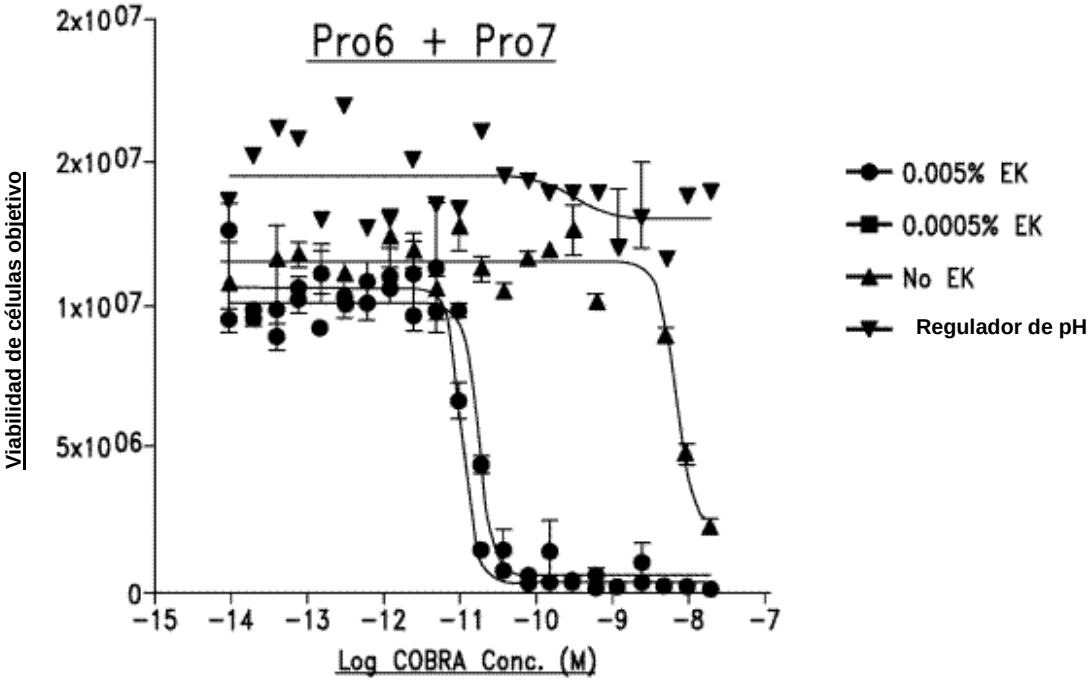



Figura 8C

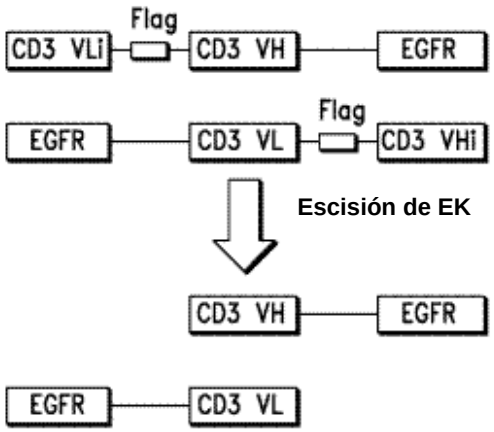



Figura 8D

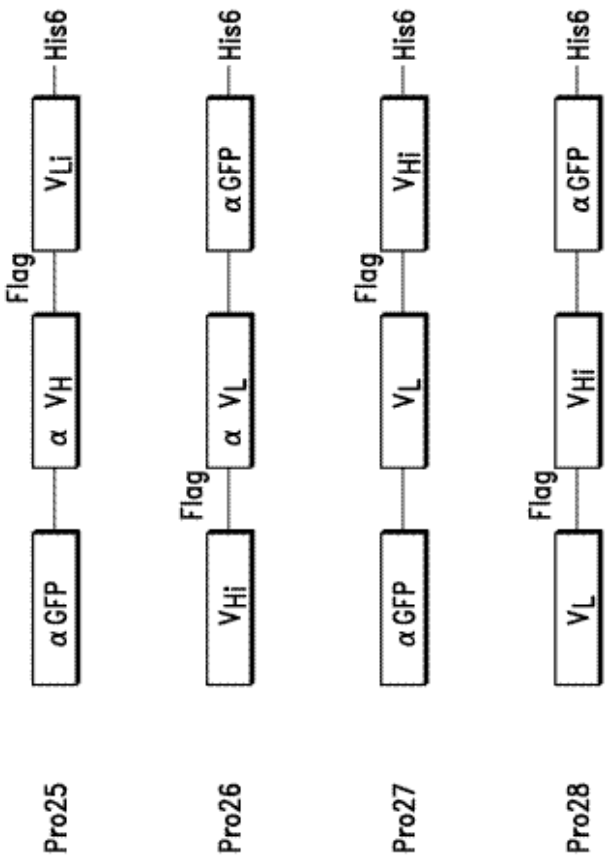

Pro25
αGFP
Flag
α VH
VLi
His6
Pro26
VHi
Flag
α VL
αGFP
His6
Pro27
αGFP
Flag
VL
VHi
His6
Pro28
VL
Flag
VHi
αGFP
His6

Figura 9

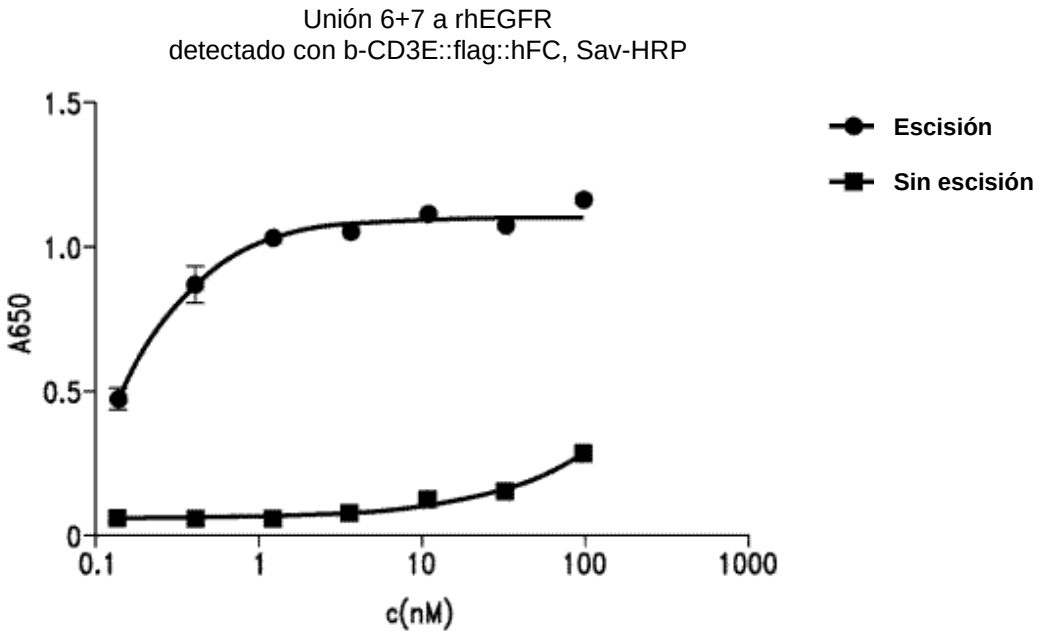



Figura 10A

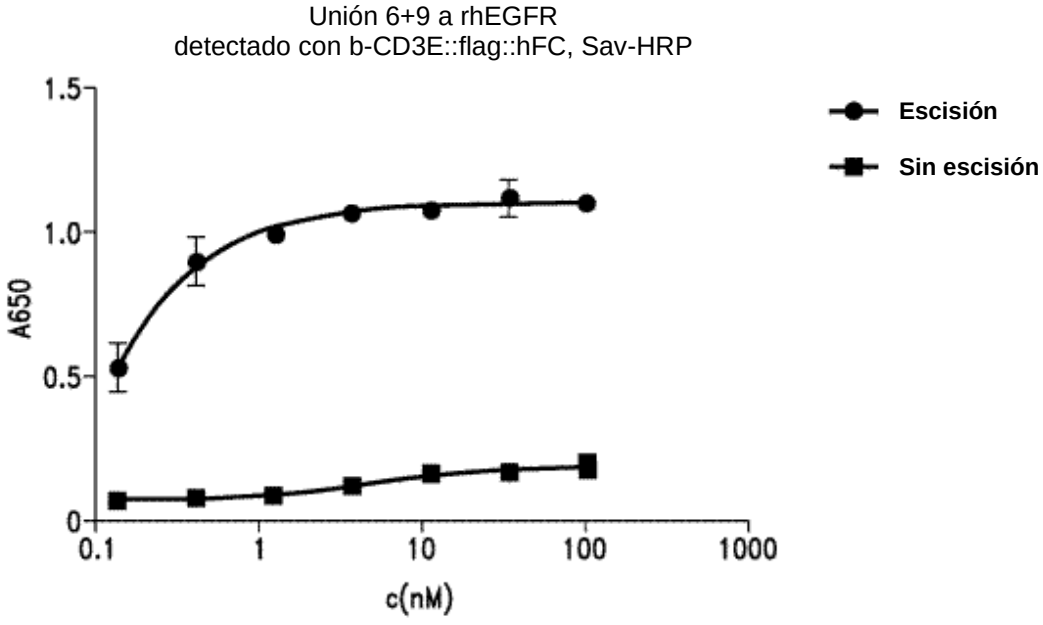



Figura 10B

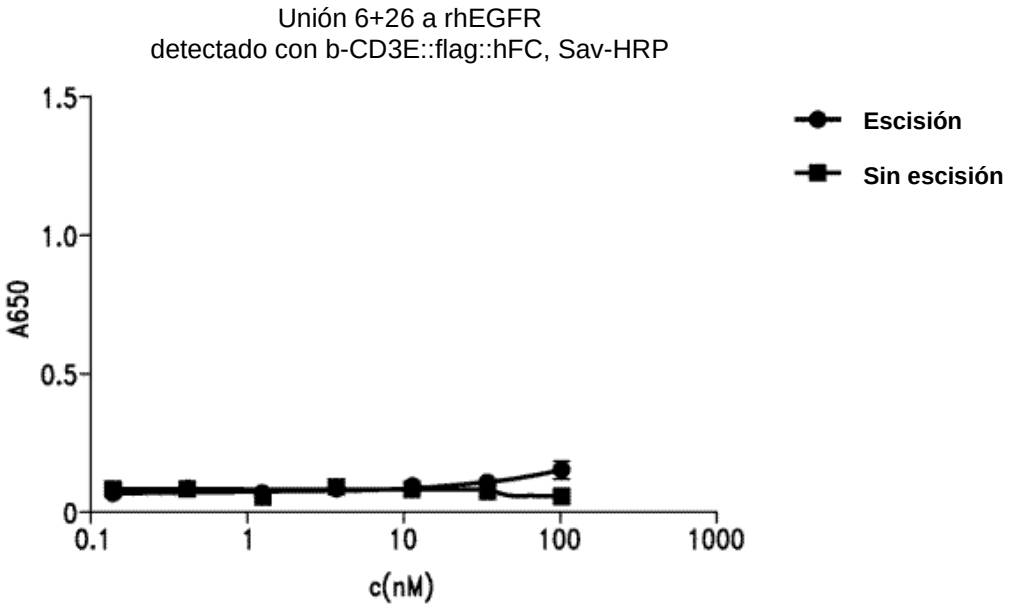



Figura 10C

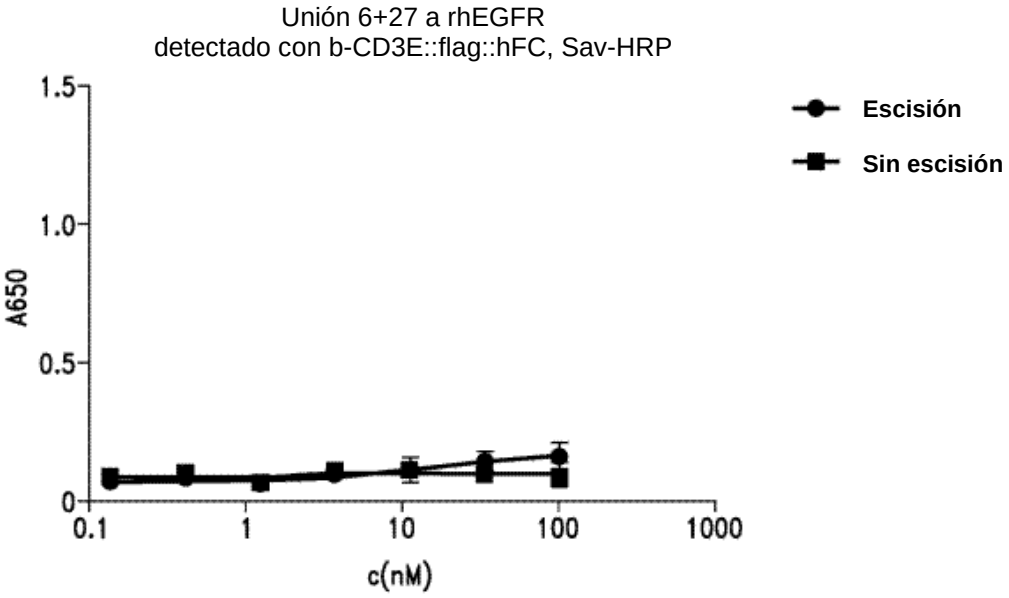



Figura 10D

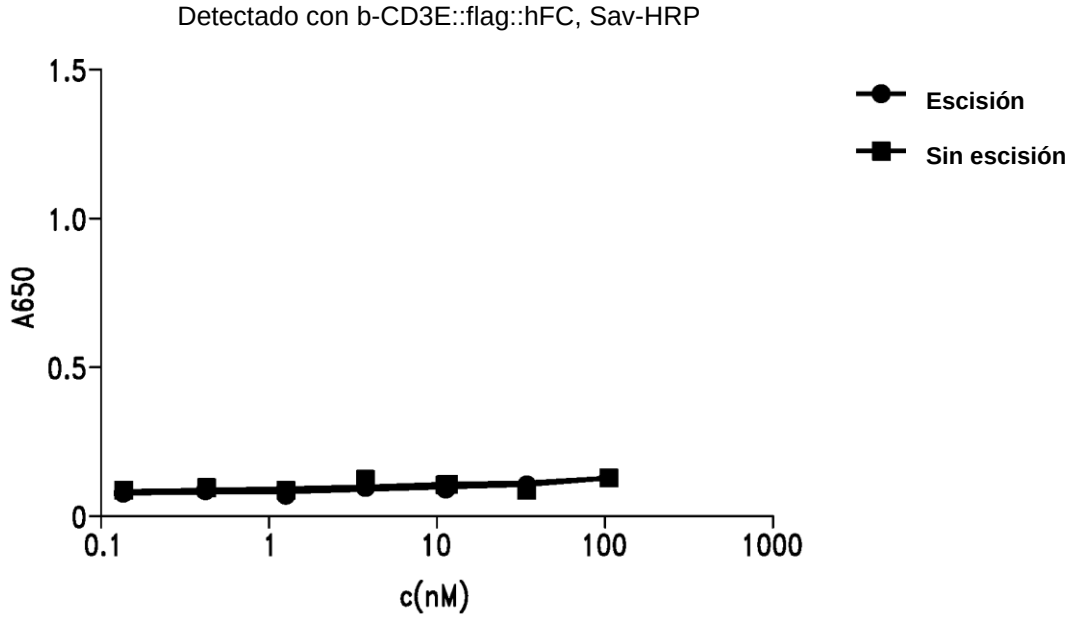



Figura 10E

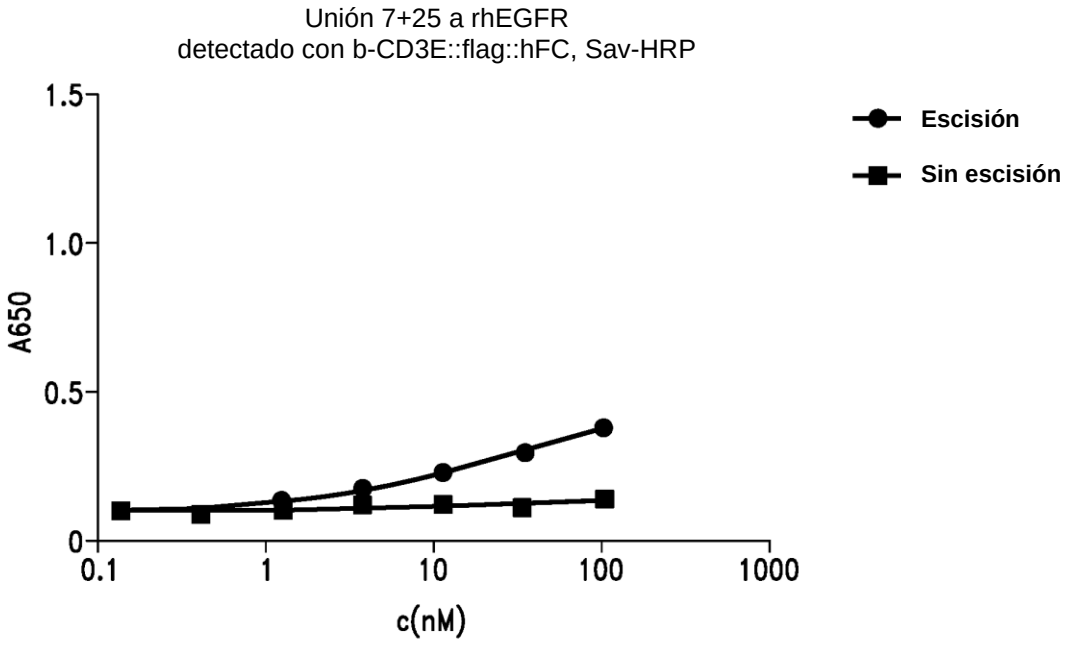
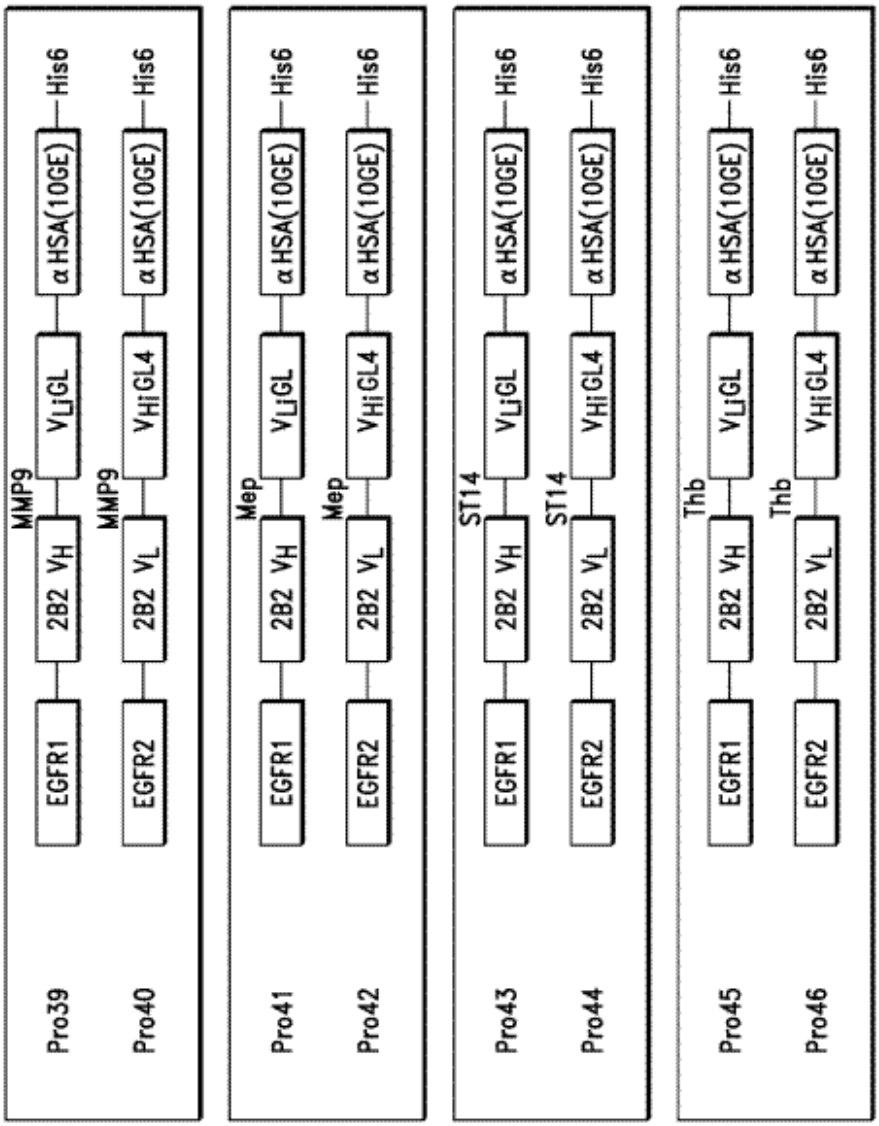



Figura 10F

Figura 11


Pro39
EGFR1
2B2 VH
MMP9
VLiGL
αHSA(10GE)
His6
Pro40
EGFR2
2B2 VL
MMP9
VHiGL4
αHSA(10GE)
His6
Pro41
EGFR1
2B2 VH
Mep
VLiGL
αHSA(10GE)
His6
Pro42
EGFR2
2B2 VL
Mep
VHiGL4
αHSA(10GE)
His6
Pro43
EGFR1
2B2 VH
ST14
VLiGL
αHSA(10GE)
His6
Pro44
EGFR2
2B2 VL
ST14
VHiGL4
αHSA(10GE)
His6
Pro45
EGFR1
2B2 VH
Thb
VLiGL
αHSA(10GE)
His6
Pro46
EGFR2
2B2 VL
Thb
VHiGL4
αHSA(10GE)
His6

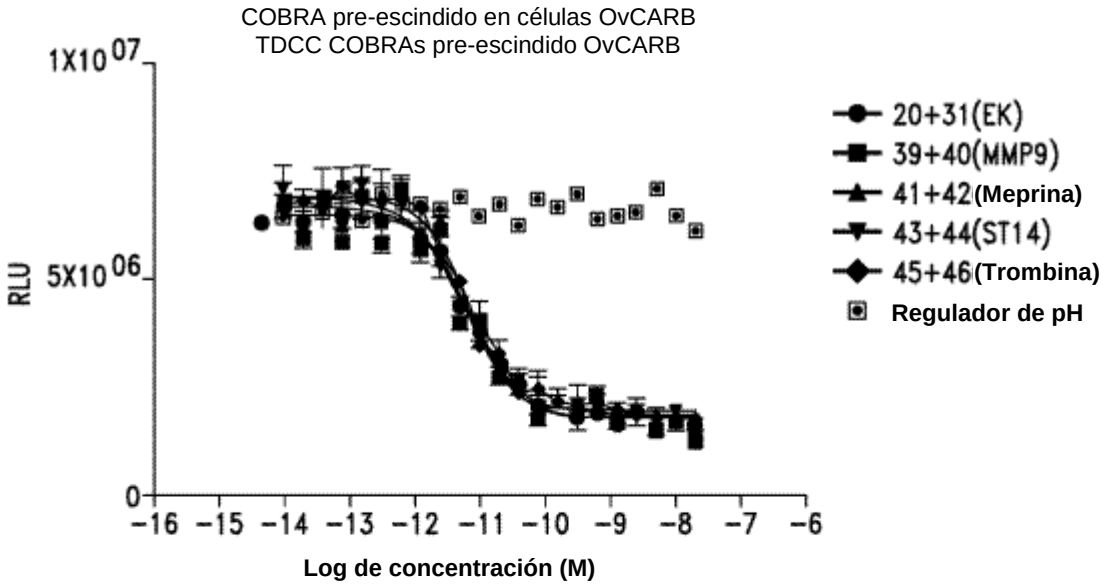



Figura 12A

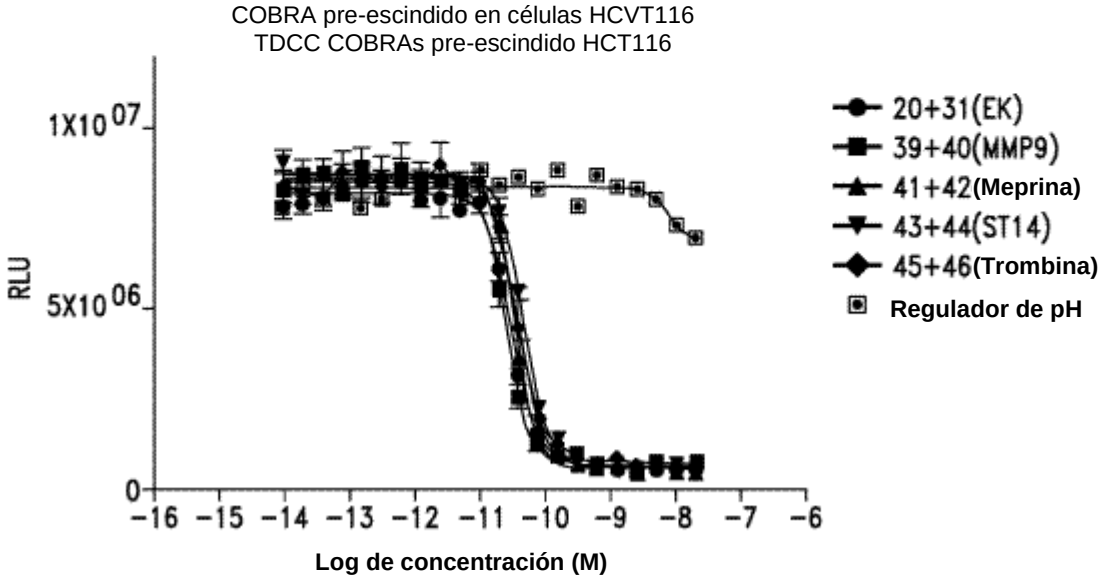



Figura 12B

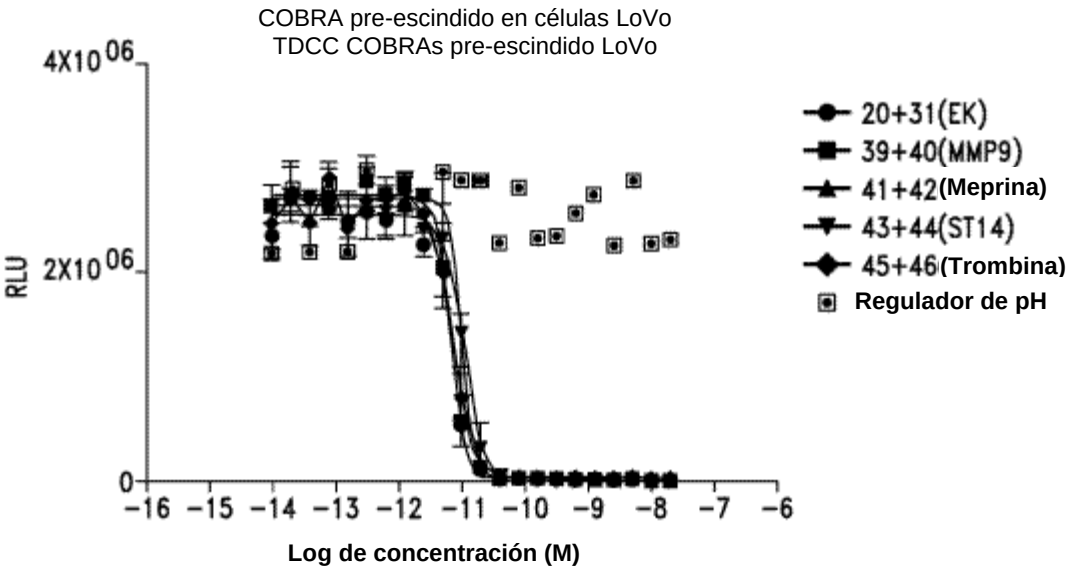
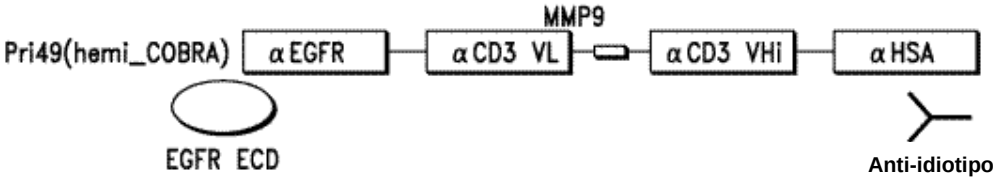

COBRA pre-escindido en células LoVo
TDCC COBRAs pre-escindido LoVo
4X10 06
2X10 06
0
RLU
−16 −15 −14 −13 −12 −11 −10 −9 −8 −7 −6
Log de concentración (M)
20+31(EK)
39+40(MMP9)
41+42(Meprina)
43+44(ST14)
45+46(Trombina)
Regulador de pH

Figura 12C




**Dosificada 0.5 mg/kg**
**Dosis única IV**
**Ratones NSG**

Figura 13A

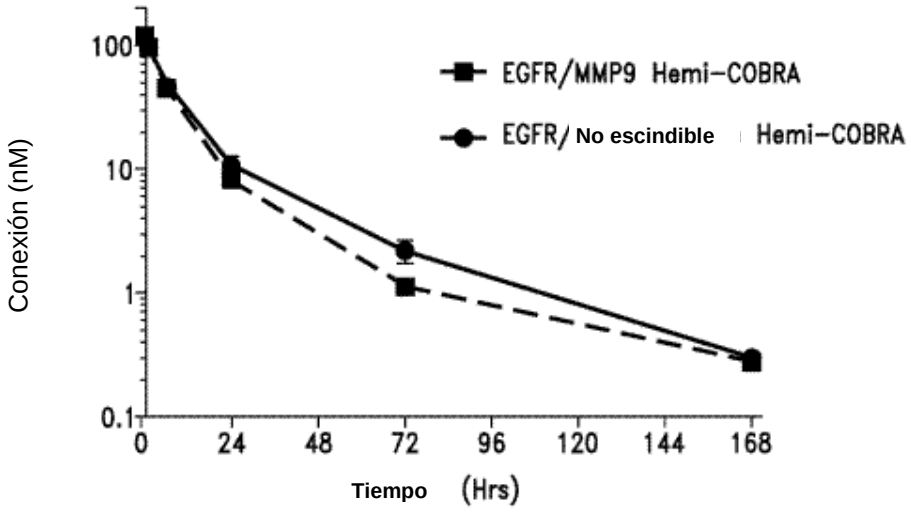



Figura 13B

Figura 14

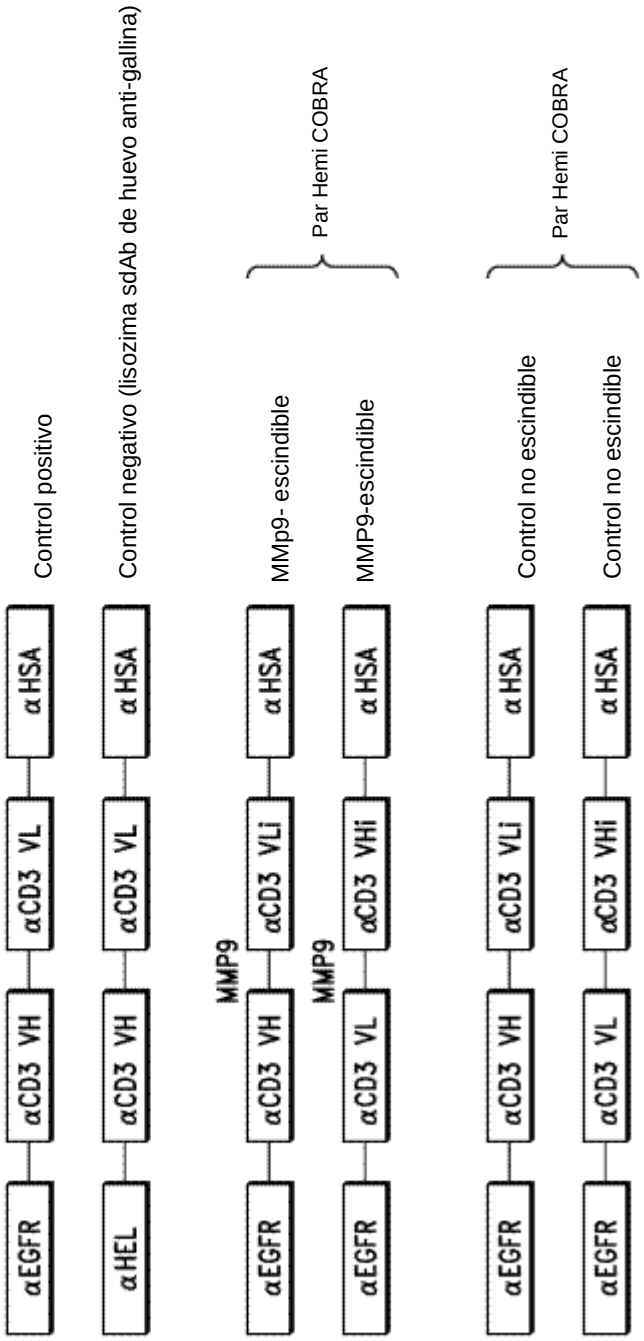

Pro51
αEGFR
αCD3 VH
αCD3 VL
α HSA
Control positivo
Pro98
α HEL
αCD3 VH
αCD3 VL
α HSA
Control negativo (lisozima sdAb de huevo anti-gallina)
Pro53
αEGFR
αCD3 VH
MMP9
αCD3 VLi
α HSA
MMp9- escindible
Pro77
αEGFR
αCD3 VL
MMP9
αCD3 VHi
α HSA
MMP9-escindible
Par Hemi COBRA
Pro72
αEGFR
αCD3 VH
αCD3 VLi
α HSA
Control no escindible
Pro74
αEGFR
αCD3 VL
αCD3 VHi
α HSA
Control no escindible
Par Hemi COBRA

Figura 15

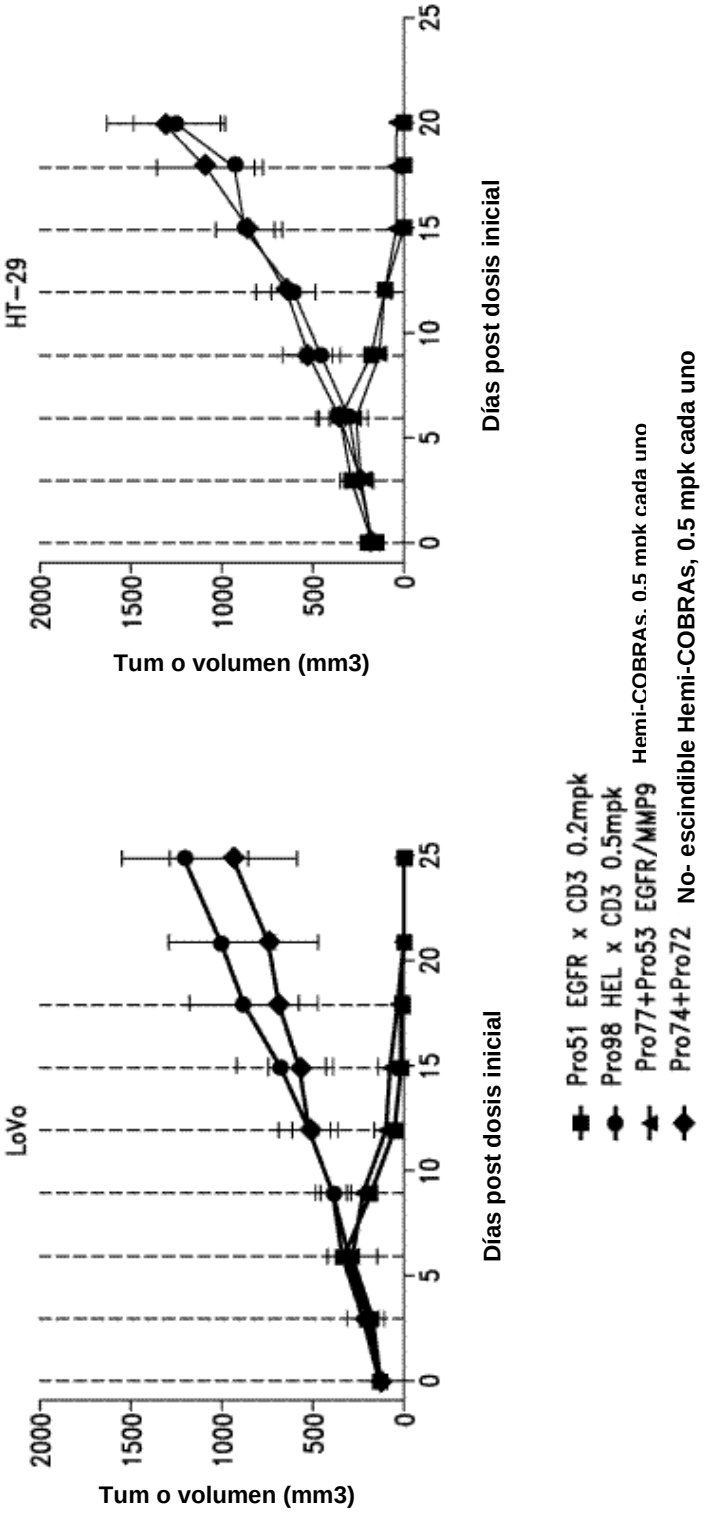

HT-29
LoVo
Tum o volumen (mm3)
Días post dosis inicial
0
500
1000
1500
2000
0
5
10
15
20
25
Pro51 EGFR x CD3 0.2mpk
Pro98 HEL x CD3 0.5mpk
Pro77+Pro53 EGFR/MMP9 Hemi-COBRAs, 0.5 mpk cada uno
Pro74+Pro72 No- escindible Hemi-COBRAs, 0.5 mpk cada uno

Figura 16

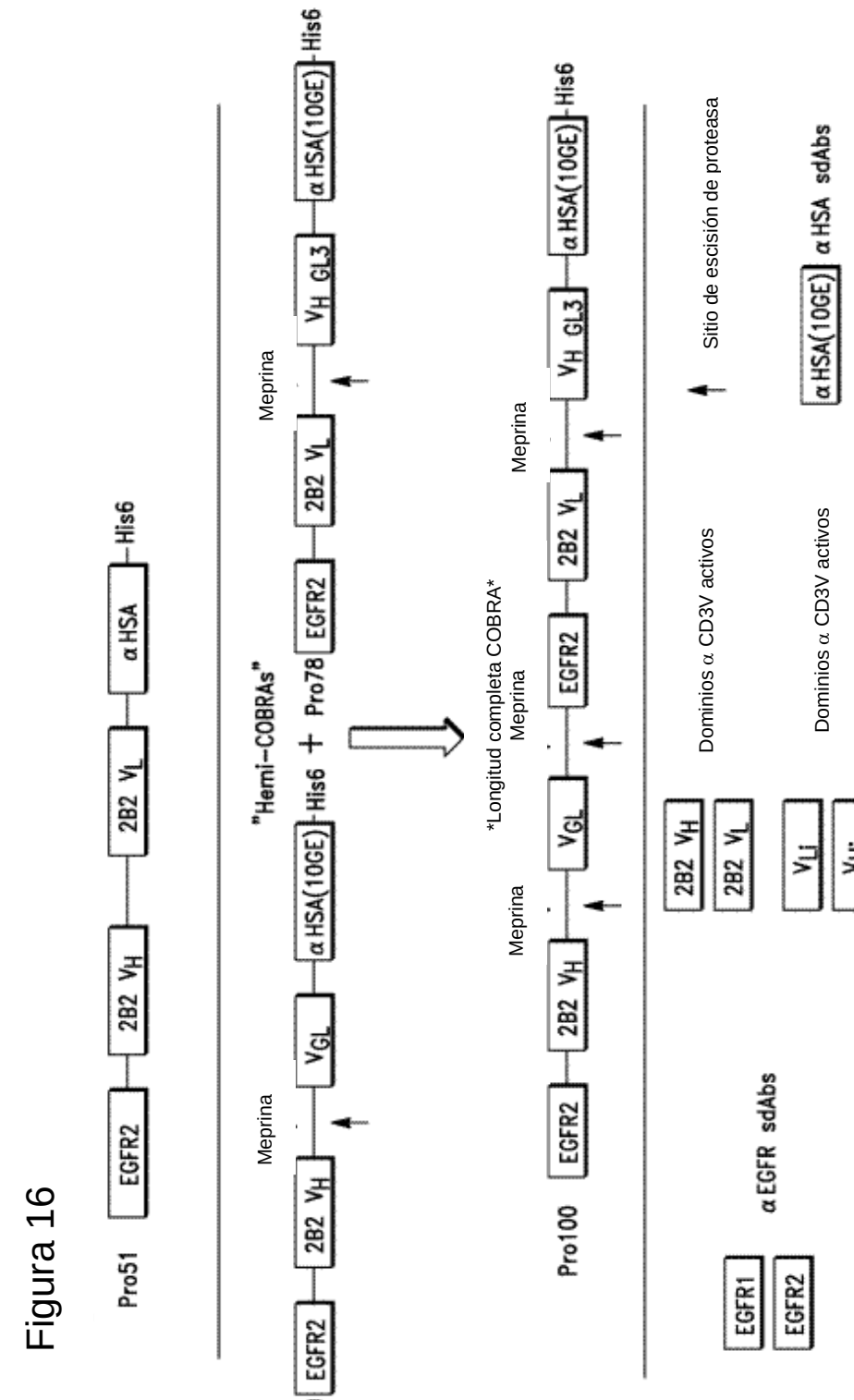

Pro51
EGFR2
2B2 VH
2B2 VL
α HSA
His6
"Hemi-COBRAs"
Meprina
Pro80
EGFR2
2B2 VH
VGL
α HSA(10GE)
His6
+
Pro78
EGFR2
2B2 VL
VH GL3
α HSA(10GE)
His6
*Longitud completa COBRA*
Meprina
Pro100
EGFR2
2B2 VH
VGL
EGFR2
2B2 VL
VH GL3
α HSA(10GE)
His6
Dominios α CD3V activos
Sitio de escisión de proteasa
EGFR1
EGFR2
α EGFR sdAbs
2B2 VH
2B2 VL
VLi
VHi
Dominios α CD3V activos
α HSA(10GE)
α HSA sdAbs

Figura 17

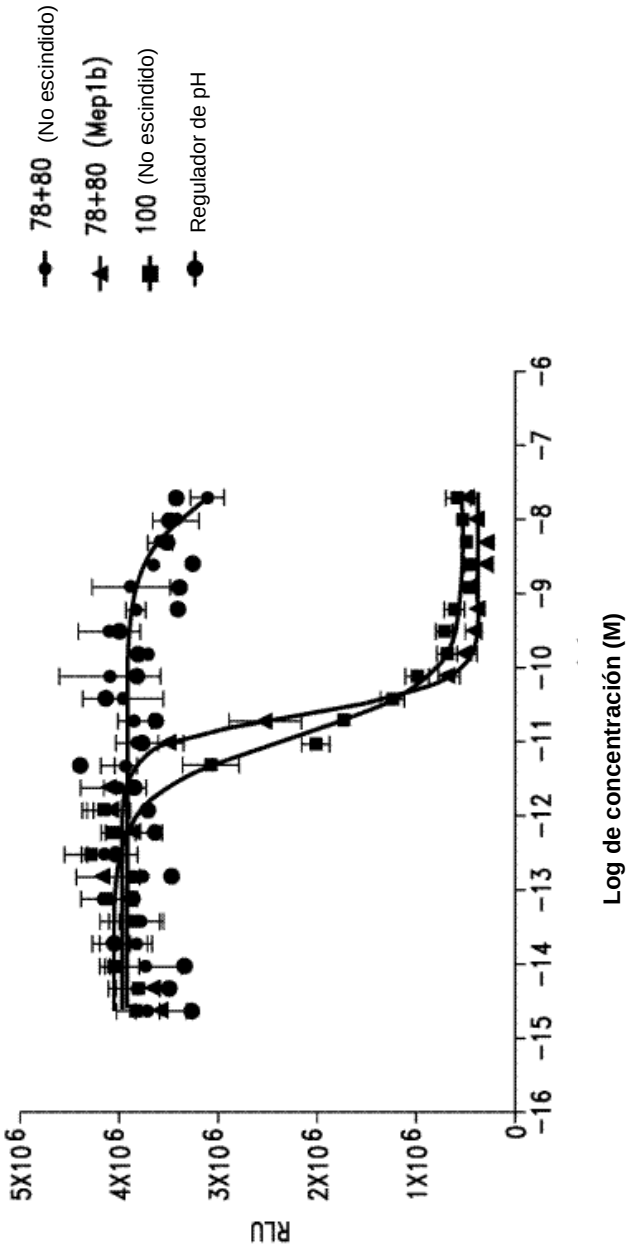

78+80 (No escindido)
78+80 (Mep1b)
100 (No escindido)
Regulador de pH
RLU
5X10 6
4X10 6
3X10 6
2X10 6
1X10 6
0
−16 −15 −14 −13 −12 −11 −10 −9 −8 −7 −6
Log de concentración (M)

Figura 18

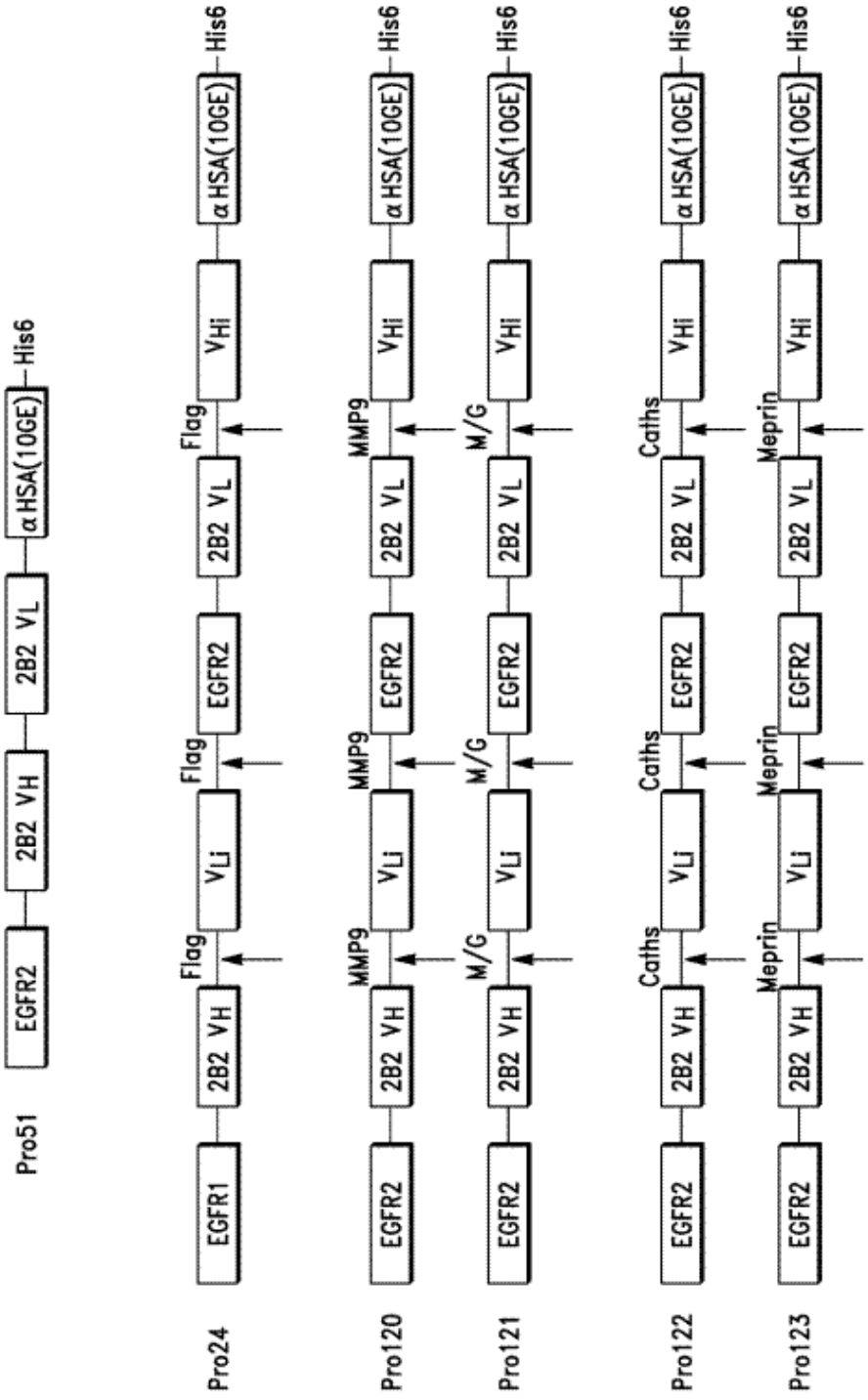

Pro51
EGFR2
2B2 VH
2B2 VL
α HSA(10GE)
His6
Pro24
EGFR1
2B2 VH
Flag
VLi
Flag
EGFR2
2B2 VL
Flag
VHi
α HSA(10GE)
His6
Pro120
EGFR2
2B2 VH
MMP9
VLi
MMP9
EGFR2
2B2 VL
MMP9
VHi
α HSA(10GE)
His6
Pro121
EGFR2
2B2 VH
M/G
VLi
M/G
EGFR2
2B2 VL
M/G
VHi
α HSA(10GE)
His6
Pro122
EGFR2
2B2 VH
Caths
VLi
Caths
EGFR2
2B2 VL
Caths
VHi
α HSA(10GE)
His6
Pro123
EGFR2
2B2 VH
Meprin
VLi
Meprin
EGFR2
2B2 VL
Meprin
VHi
α HSA(10GE)
His6

Figura 19

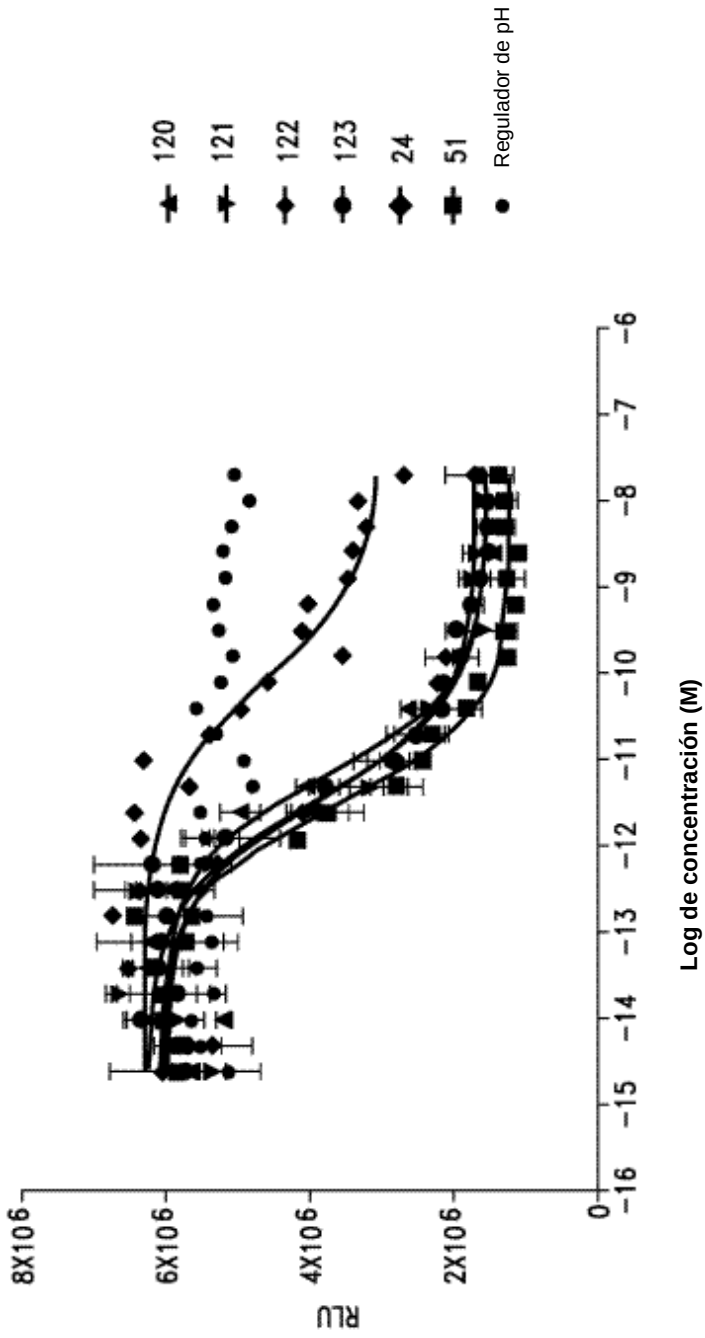
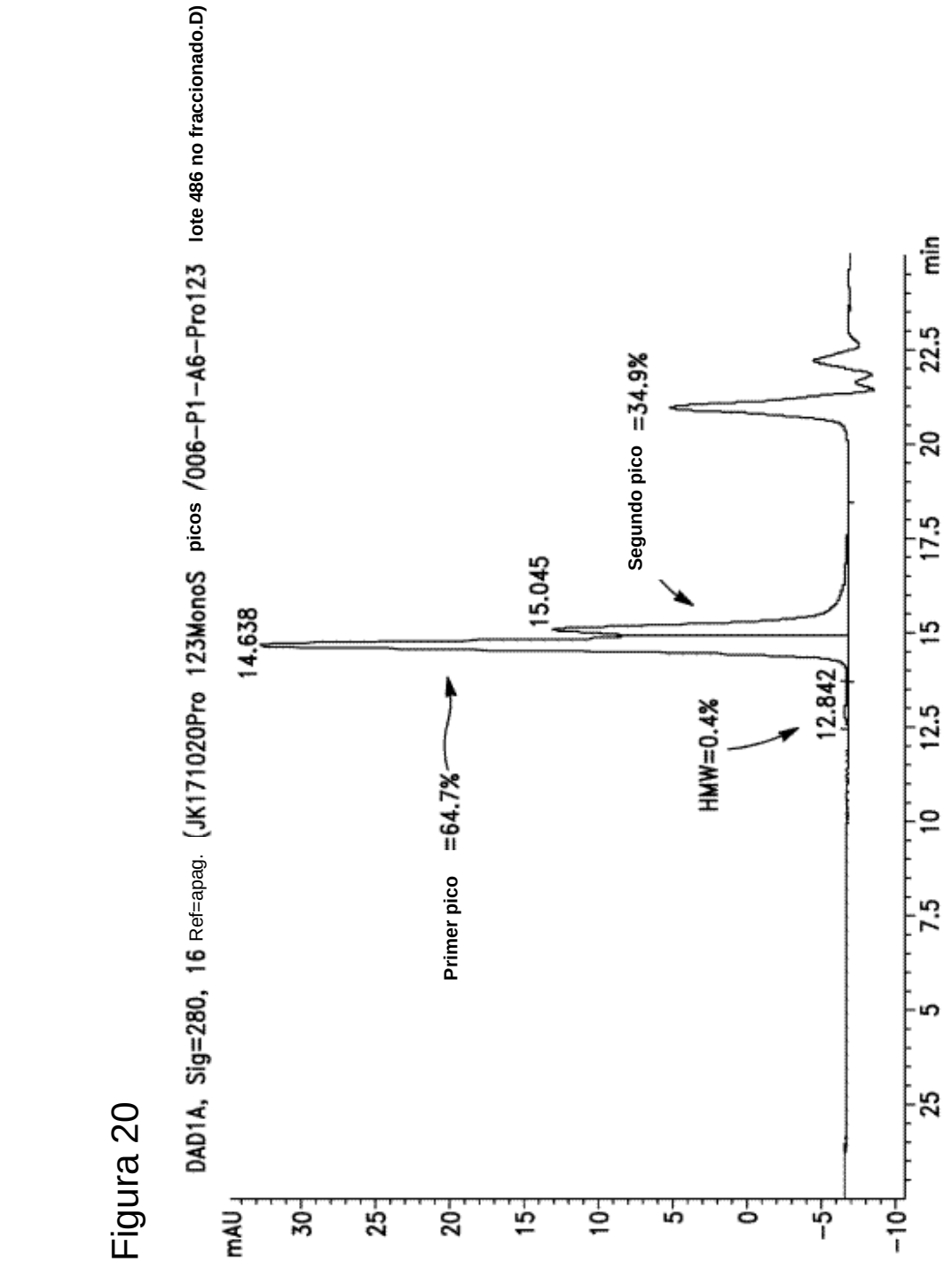

120
121
122
123
24
51
Regulador de pH
8X10^6
6X10^6
4X10^6
2X10^6
0
RLU
-16
-15
-14
-13
-12
-11
-10
-9
-8
-7
-6
Log de concentración (M)

Figura 20




Pro123

Figura 21

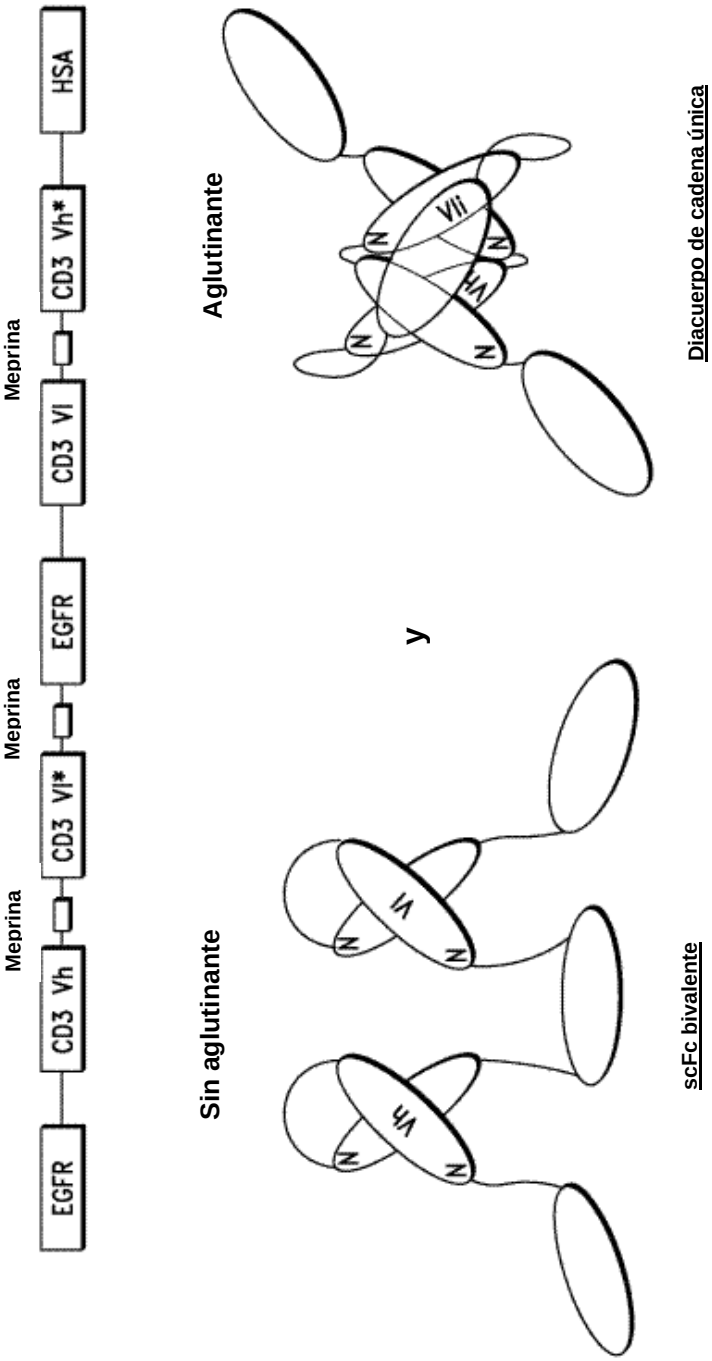

EGFR
CD3 Vh
Meprina
CD3 Vl*
Meprina
EGFR
Meprina
CD3 Vl
CD3 Vh*
HSA
Sin aglutinante
y
Aglutinante
scFc bivalente
Diacuerpo de cadena única

Figura 22

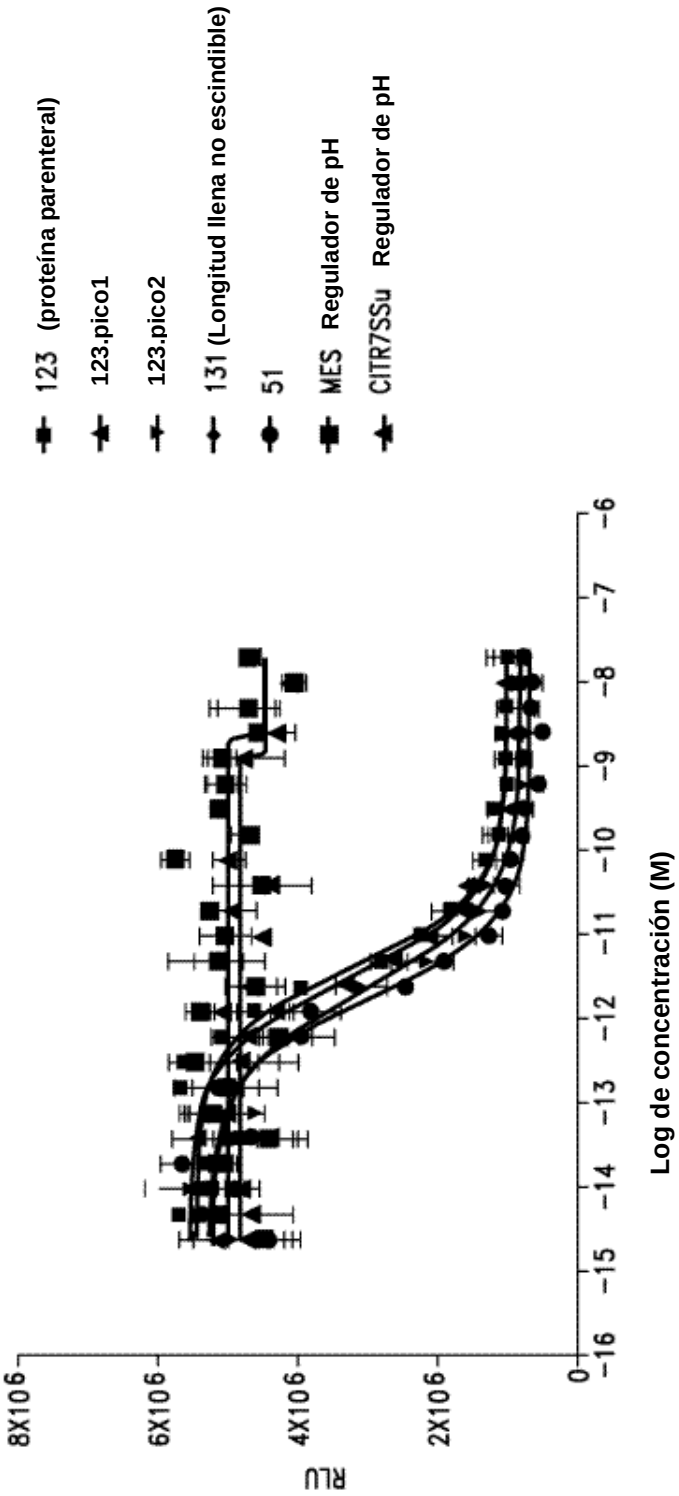

123 (proteína parenteral)
123.pico1
123.pico2
131 (Longitud llena no escindible)
51
MES Regulador de pH
CITR7SSu Regulador de pH
RLU
8X106
6X106
4X106
2X106
0
-16
-15
-14
-13
-12
-11
-10
-9
-8
-7
-6
Log de concentración (M)

Figura 23A

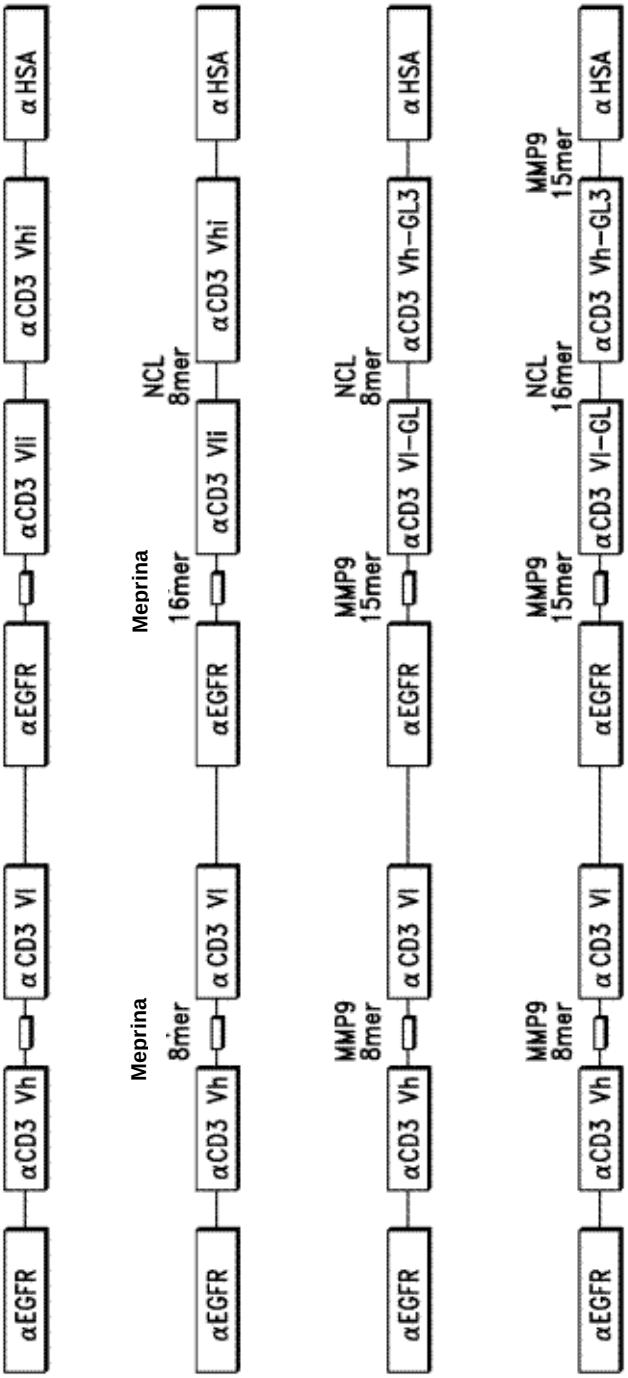

Pro140
αEGFR
αCD3 Vh
MMP9 8mer
αCD3 Vl
αEGFR
MMP9 15mer
αCD3 Vli
NCL 8mer
αCD3 Vhi
α HSA
Pro140b
αEGFR
αCD3 Vh
Meprina 8mer
αCD3 Vl
αEGFR
Meprina 16mer
αCD3 Vli
NCL 8mer
αCD3 Vhi
α HSA
Pro141
αEGFR
αCD3 Vh
MMP9 8mer
αCD3 Vl
αEGFR
MMP9 15mer
αCD3 Vl-GL
NCL 8mer
αCD3 Vh-GL3
α HSA
Pro160
αEGFR
αCD3 Vh
MMP9 8mer
αCD3 Vl
αEGFR
MMP9 15mer
αCD3 Vl-GL
NCL 16mer
αCD3 Vh-GL3
MMP9 15mer
α HSA

Figura 23B

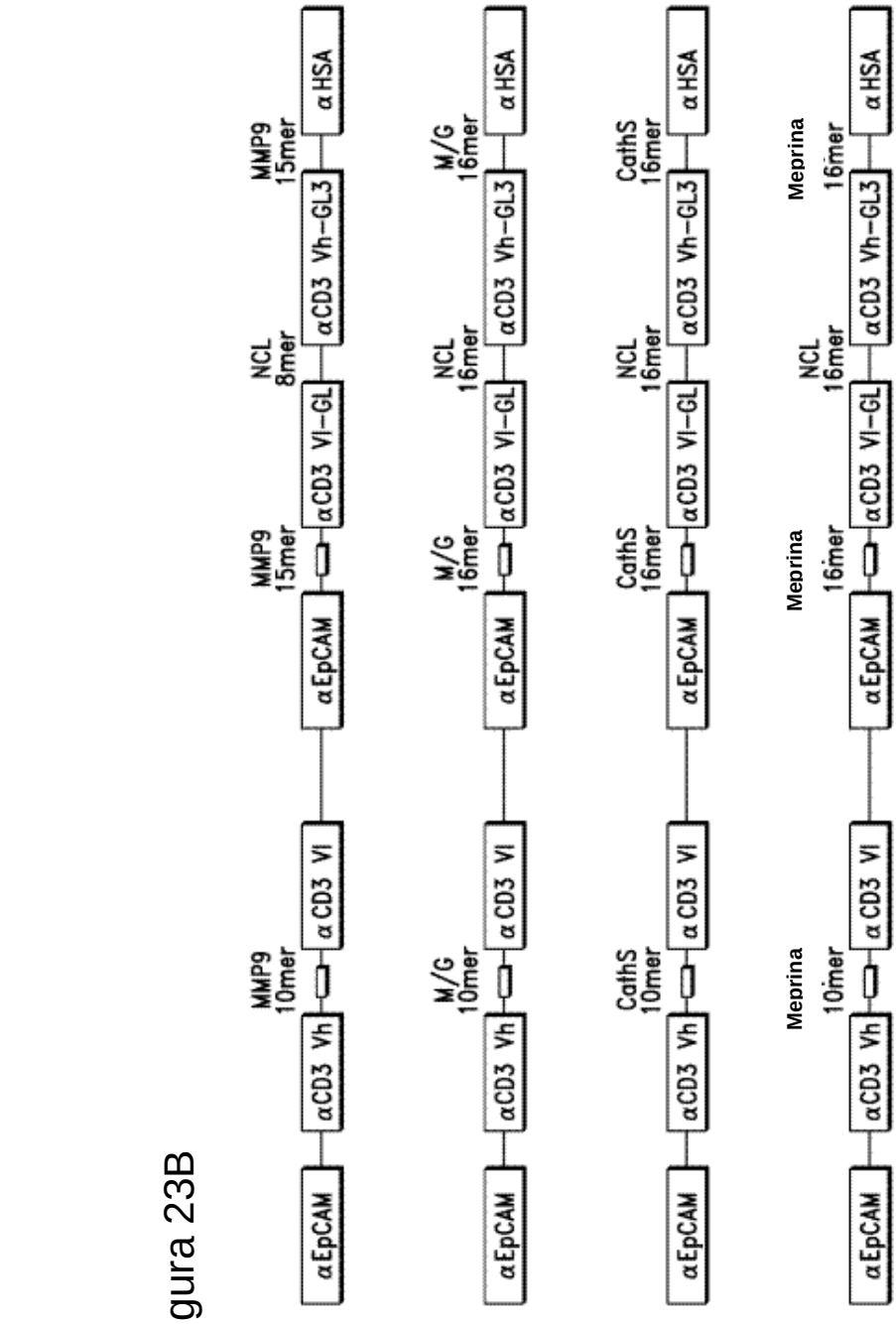

Pro161
αEpCAM
αCD3 Vh
MMP9 10mer
αCD3 Vl
αEpCAM
MMP9 15mer
αCD3 Vl-GL
NCL 8mer
αCD3 Vh-GL3
MMP9 15mer
αHSA
Pro162
αEpCAM
αCD3 Vh
M/G 10mer
αCD3 Vl
αEpCAM
M/G 16mer
αCD3 Vl-GL
NCL 16mer
αCD3 Vh-GL3
M/G 16mer
αHSA
Pro163
αEpCAM
αCD3 Vh
CathS 10mer
αCD3 Vl
αEpCAM
CathS 16mer
αCD3 Vl-GL
NCL 16mer
αCD3 Vh-GL3
CathS 16mer
αHSA
Pro164
αEpCAM
αCD3 Vh
Meprina 10mer
αCD3 Vl
αEpCAM
Meprina 16mer
αCD3 Vl-GL
NCL 16mer
αCD3 Vh-GL3
Meprina 16mer
αHSA

Figura 23C

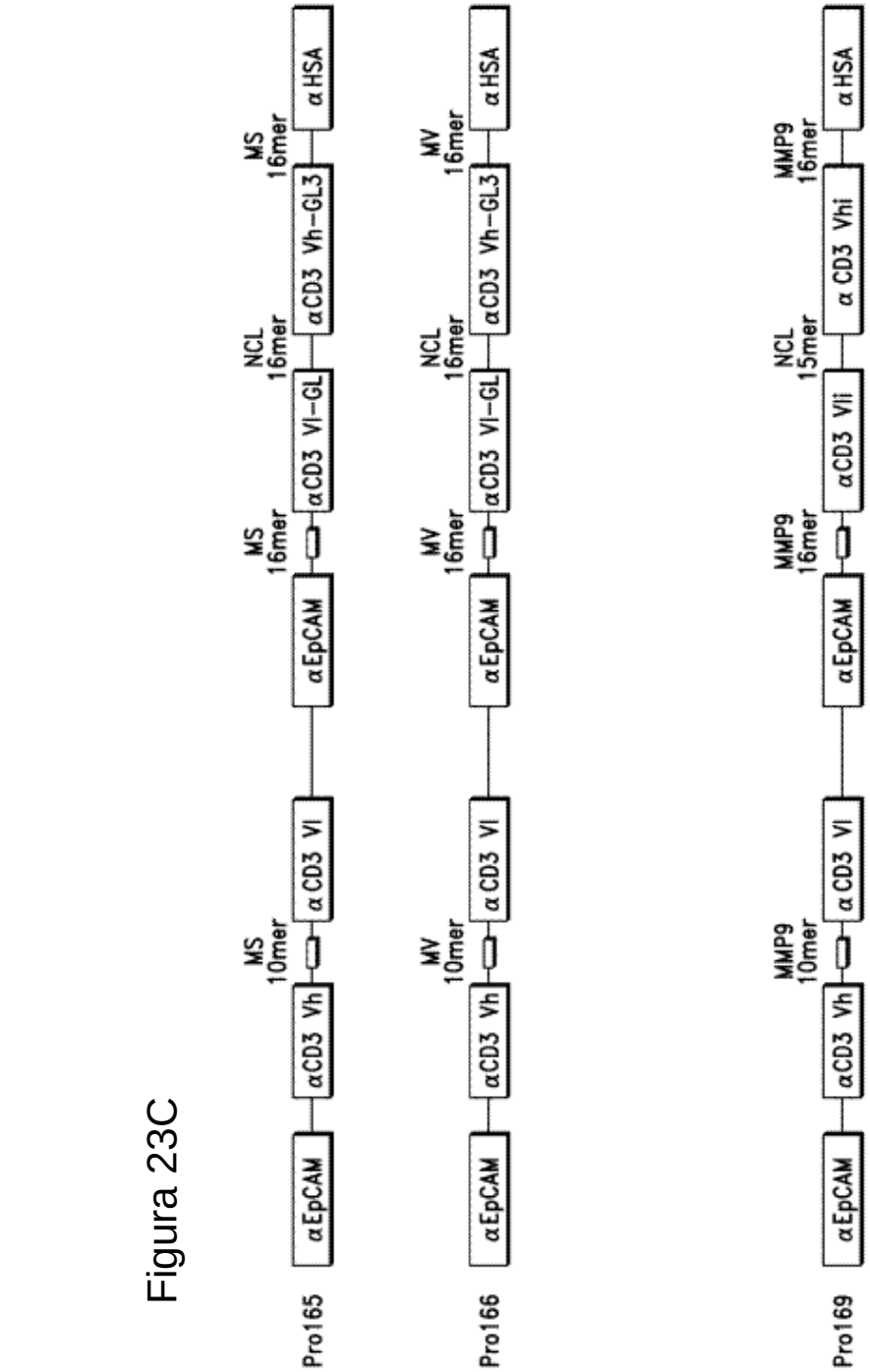

Pro165
αEpCAM
αCD3 Vh
MS 10mer
αCD3 Vl
αEpCAM
MS 16mer
αCD3 Vl-GL
NCL 16mer
αCD3 Vh-GL3
MS 16mer
αHSA
Pro166
αEpCAM
αCD3 Vh
MV 10mer
αCD3 Vl
αEpCAM
MV 16mer
αCD3 Vl-GL
NCL 16mer
αCD3 Vh-GL3
MV 16mer
αHSA
Pro169
αEpCAM
αCD3 Vh
MMP9 10mer
αCD3 Vl
αEpCAM
MMP9 16mer
αCD3 Vli
NCL 15mer
α CD3 Vhi
MMP9 16mer
αHSA

Figura 23D

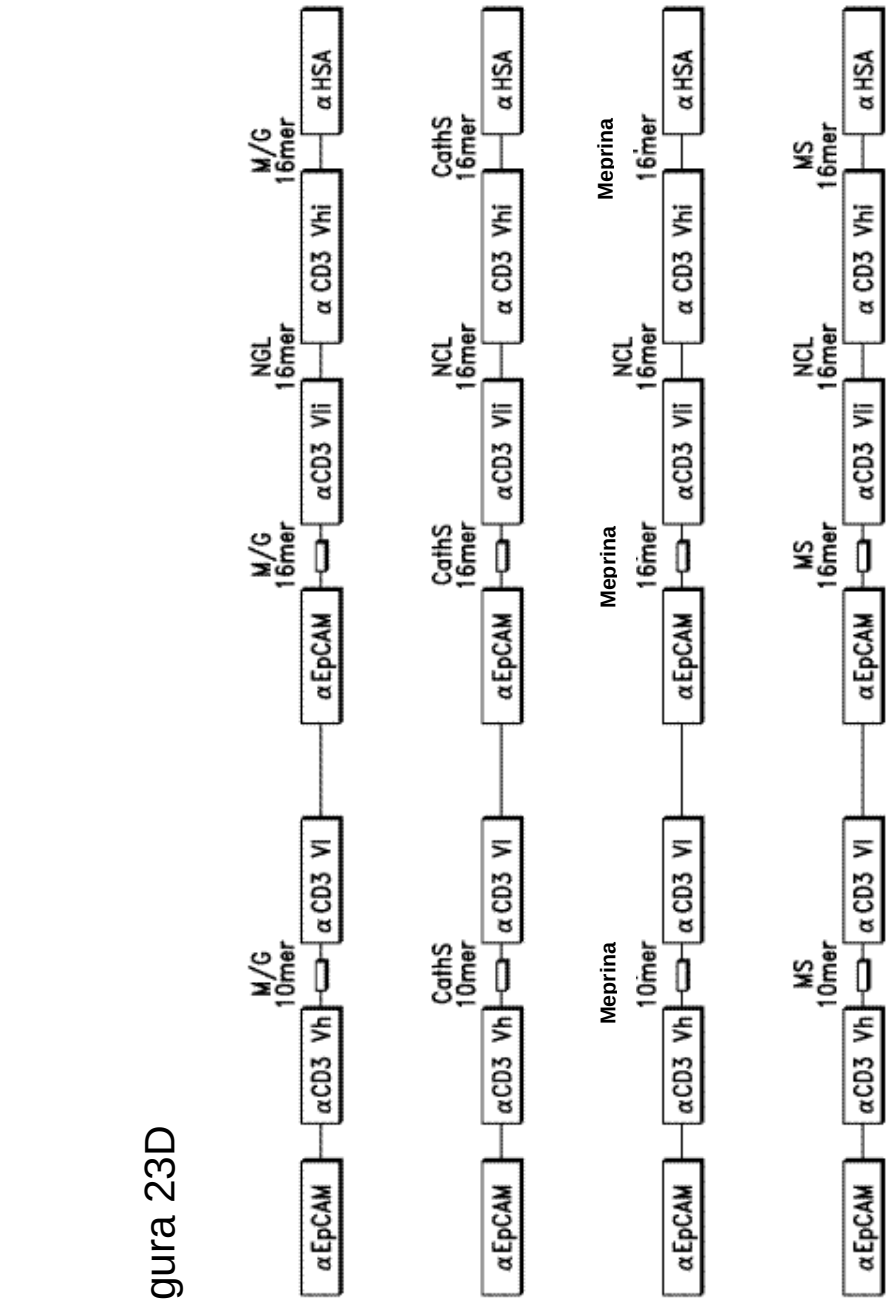

Pro170
αEpCAM
αCD3 Vh
M/G 10mer
αCD3 Vl
αEpCAM
M/G 16mer
αCD3 Vli
NGL 16mer
α CD3 Vhi
M/G 16mer
α HSA
Pro171
αEpCAM
αCD3 Vh
CathS 10mer
αCD3 Vl
αEpCAM
CathS 16mer
αCD3 Vli
NCL 16mer
α CD3 Vhi
CathS 16mer
α HSA
Pro172
αEpCAM
αCD3 Vh
Meprina 10mer
αCD3 Vl
αEpCAM
Meprina 16mer
αCD3 Vli
NCL 16mer
α CD3 Vhi
Meprina 16mer
α HSA
Pro173
αEpCAM
αCD3 Vh
MS 10mer
αCD3 Vl
αEpCAM
MS 16mer
αCD3 Vli
NCL 16mer
α CD3 Vhi
MS 16mer
α HSA

Figura 23E

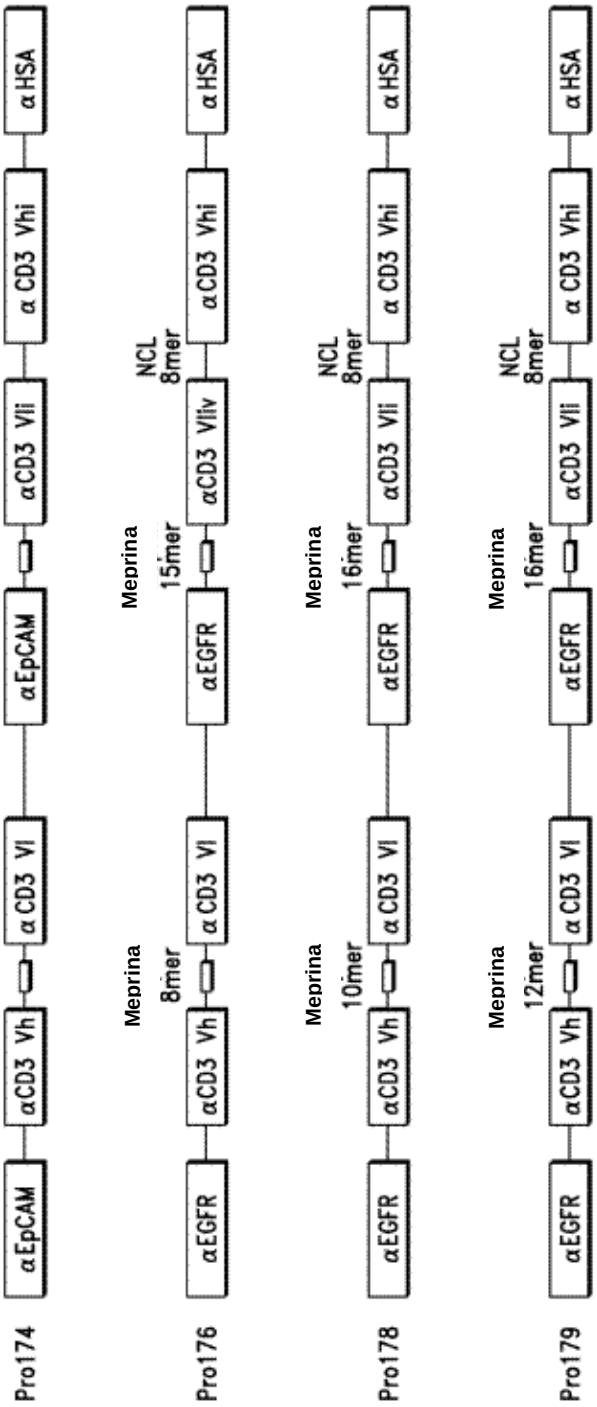

Pro174
αEpCAM
αCD3 Vh
MV
10mer
α CD3 Vl
αEpCAM
MV
16mer
αCD3 Vli
NCL
16mer
α CD3 Vhi
MV
16mer
α HSA
Pro176
αEGFR
αCD3 Vh
Meprina
8mer
α CD3 Vl
αEGFR
Meprina
15mer
αCD3 Vliv
NCL
8mer
α CD3 Vhi
α HSA
Pro178
αEGFR
αCD3 Vh
Meprina
10mer
α CD3 Vl
αEGFR
Meprina
16mer
αCD3 Vli
NCL
8mer
α CD3 Vhi
α HSA
Pro179
αEGFR
αCD3 Vh
Meprina
12mer
α CD3 Vl
αEGFR
Meprina
16mer
αCD3 Vli
NCL
8mer
α CD3 Vhi
α HSA

Figura 23F

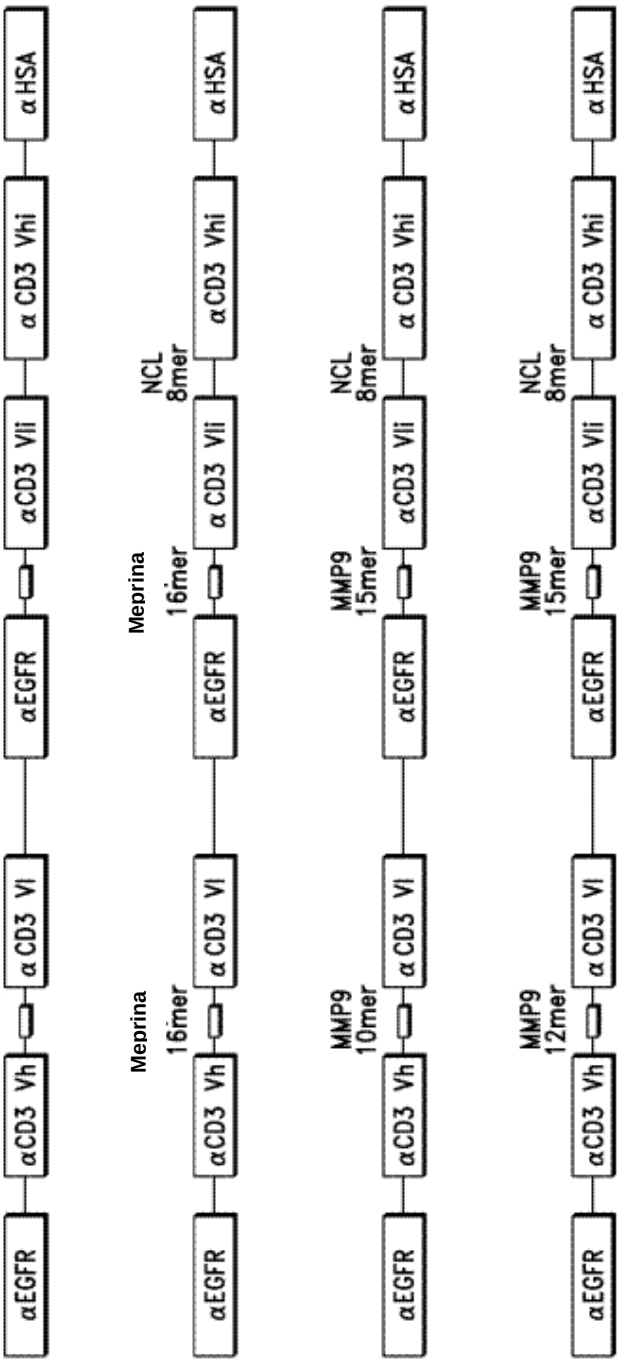

Pro180
αEGFR
αCD3 Vh
Meprina
14mer
α CD3 Vl
αEGFR
Meprina
16mer
αCD3 Vli
NCL
8mer
α CD3 Vhi
α HSA
Pro181
αEGFR
αCD3 Vh
Meprina
16mer
α CD3 Vl
αEGFR
Meprina
16mer
α CD3 Vli
NCL
8mer
α CD3 Vhi
α HSA
Pro182
αEGFR
αCD3 Vh
MMP9
10mer
α CD3 Vl
αEGFR
MMP9
15mer
αCD3 Vli
NCL
8mer
α CD3 Vhi
α HSA
Pro183
αEGFR
αCD3 Vh
MMP9
12mer
α CD3 Vl
αEGFR
MMP9
15mer
αCD3 Vli
NCL
8mer
α CD3 Vhi
α HSA

Figura 23G

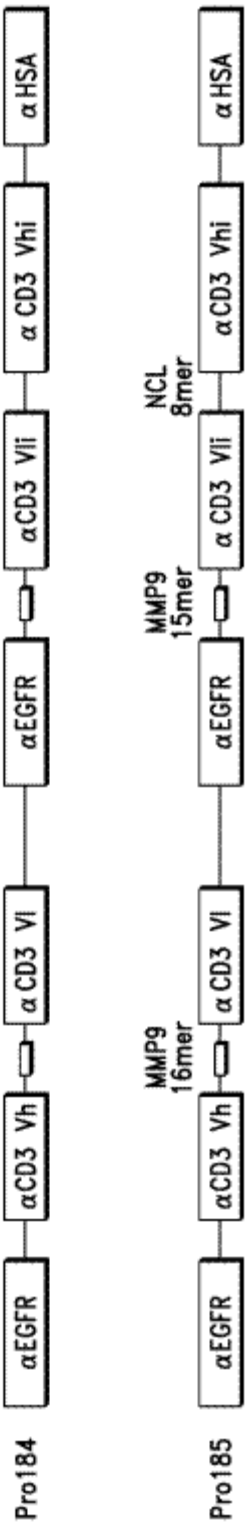

Pro184
αEGFR
αCD3 Vh
MMP9
14mer
α CD3 Vl
αEGFR
MMP9
15mer
αCD3 Vli
NCL
8mer
α CD3 Vhi
α HSA
Pro185
αEGFR
αCD3 Vh
MMP9
16mer
α CD3 Vl
αEGFR
MMP9
15mer
α CD3 Vli
NCL
8mer
αCD3 Vhi
α HSA

Figura 24

DAD1A, Sig=280,16 Ref= apag(C:\CHEM32\...ATA\JK171027 SEC LOTES 503 a 508\V003-P1-A4PRO Lote PL-0506.DO 4°C
DAD1A, Sig=280,16 Ref= apag(JK17 1030 Pro140 y 41 y 42 a 37\003-P1-A4-Pro 140 a 37 C.D) 37°C 72 hrs

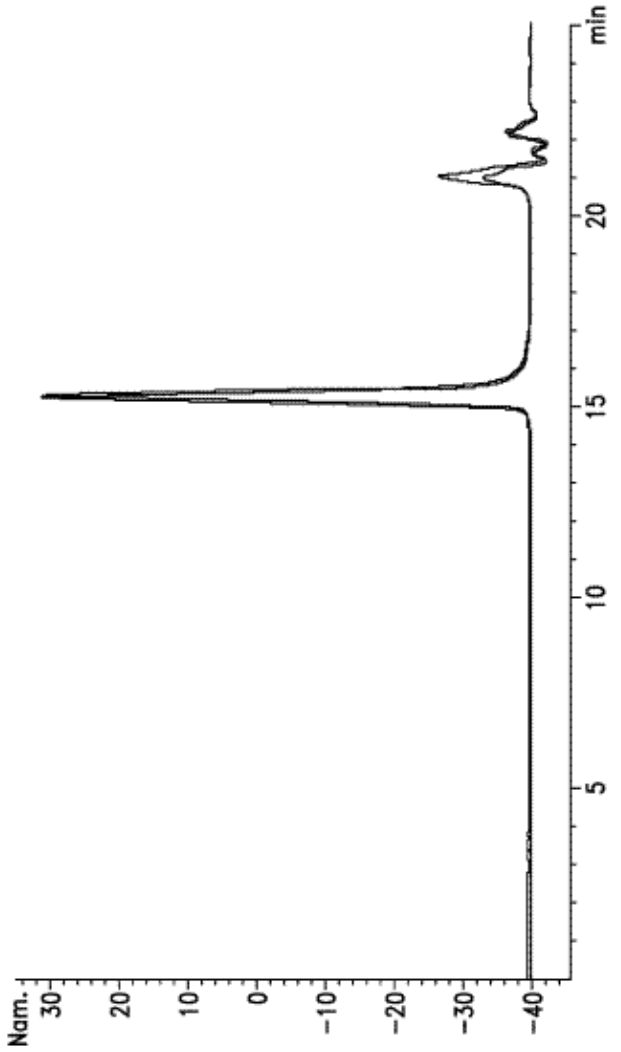


Figura 25

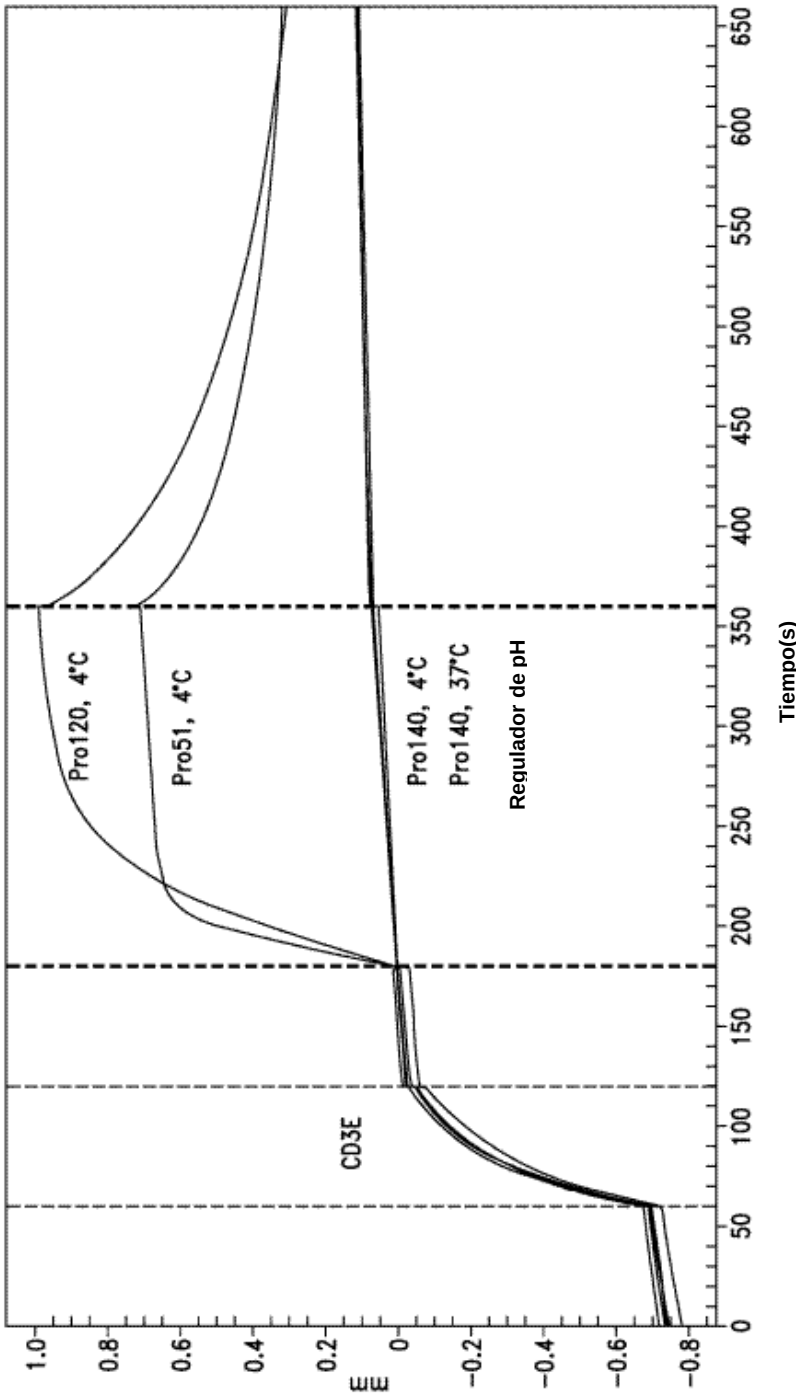

Pro120, 4°C
Pro51, 4°C
Pro140, 4°C
Pro140, 37°C
Regulador de pH
CD3E
mDeg
Tiempo(s)
1.0
0.8
0.6
0.4
0.2
0
−0.2
−0.4
−0.6
−0.8
0
50
100
150
200
250
300
350
400
450
500
550
600
650

Figura 26

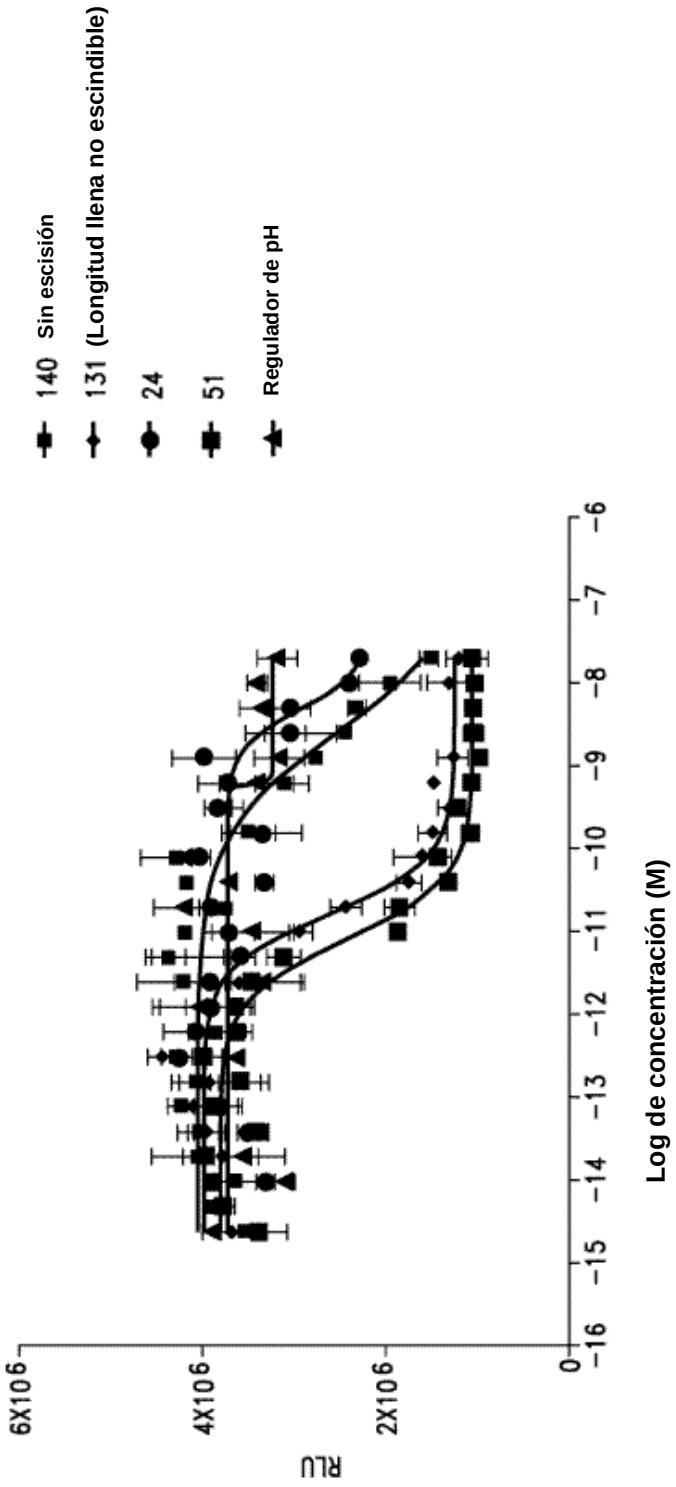
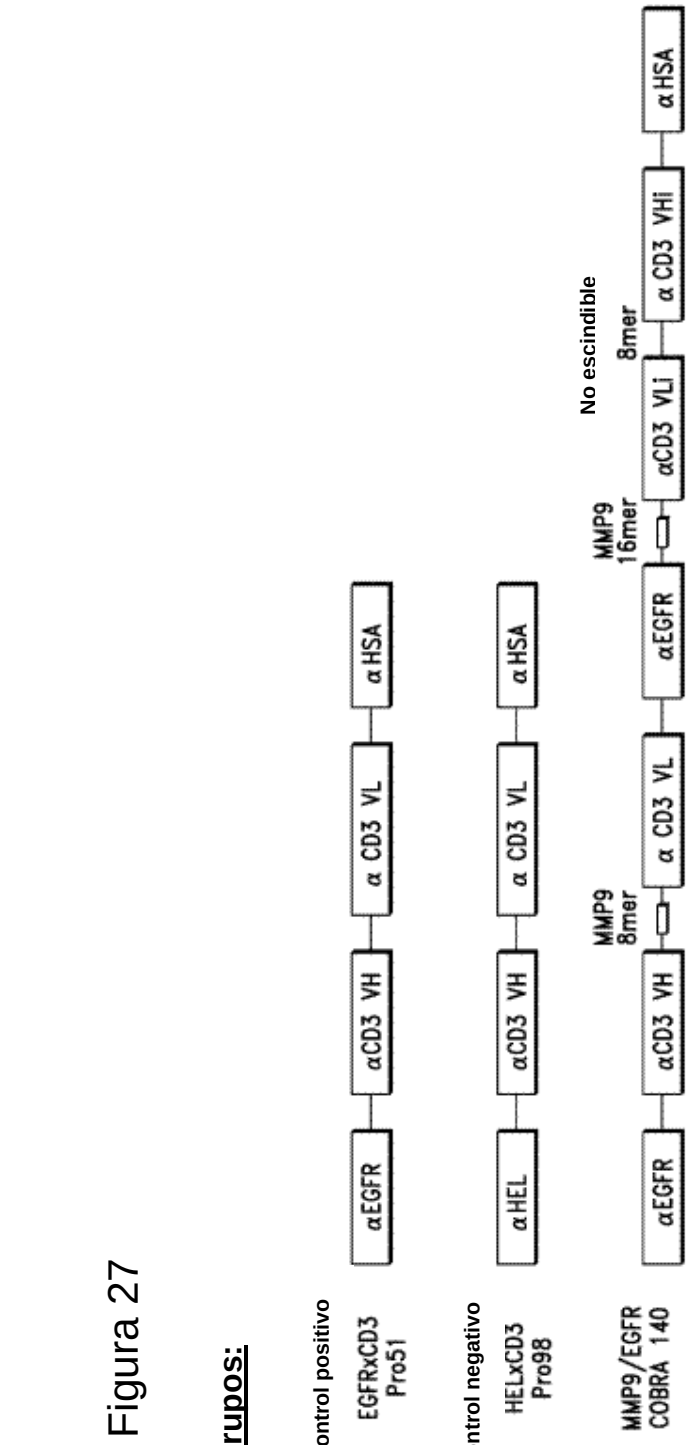

140 Sin escisión
131 (Longitud llena no escindible)
24
51
Regulador de pH
RLU
6X10 6
4X10 6
2X10 6
0
−16 −15 −14 −13 −12 −11 −10 −9 −8 −7 −6
Log de concentración (M)

Figura 27

**Grupos:**



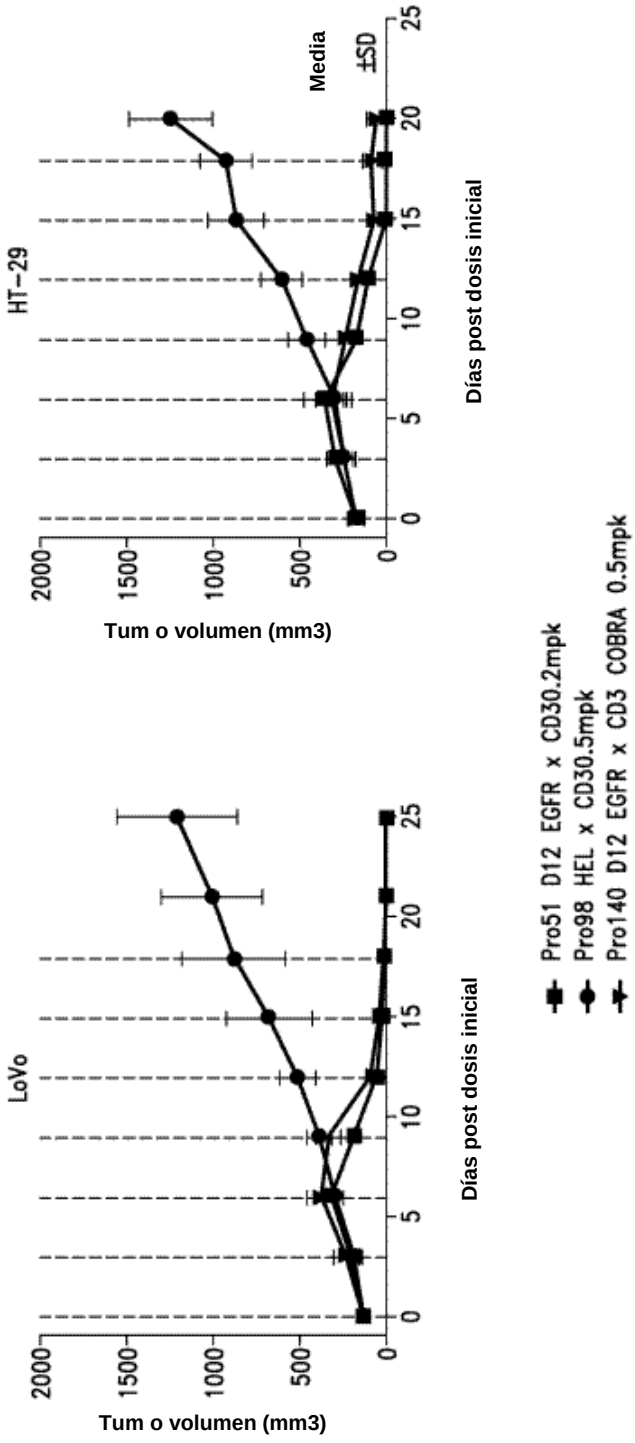
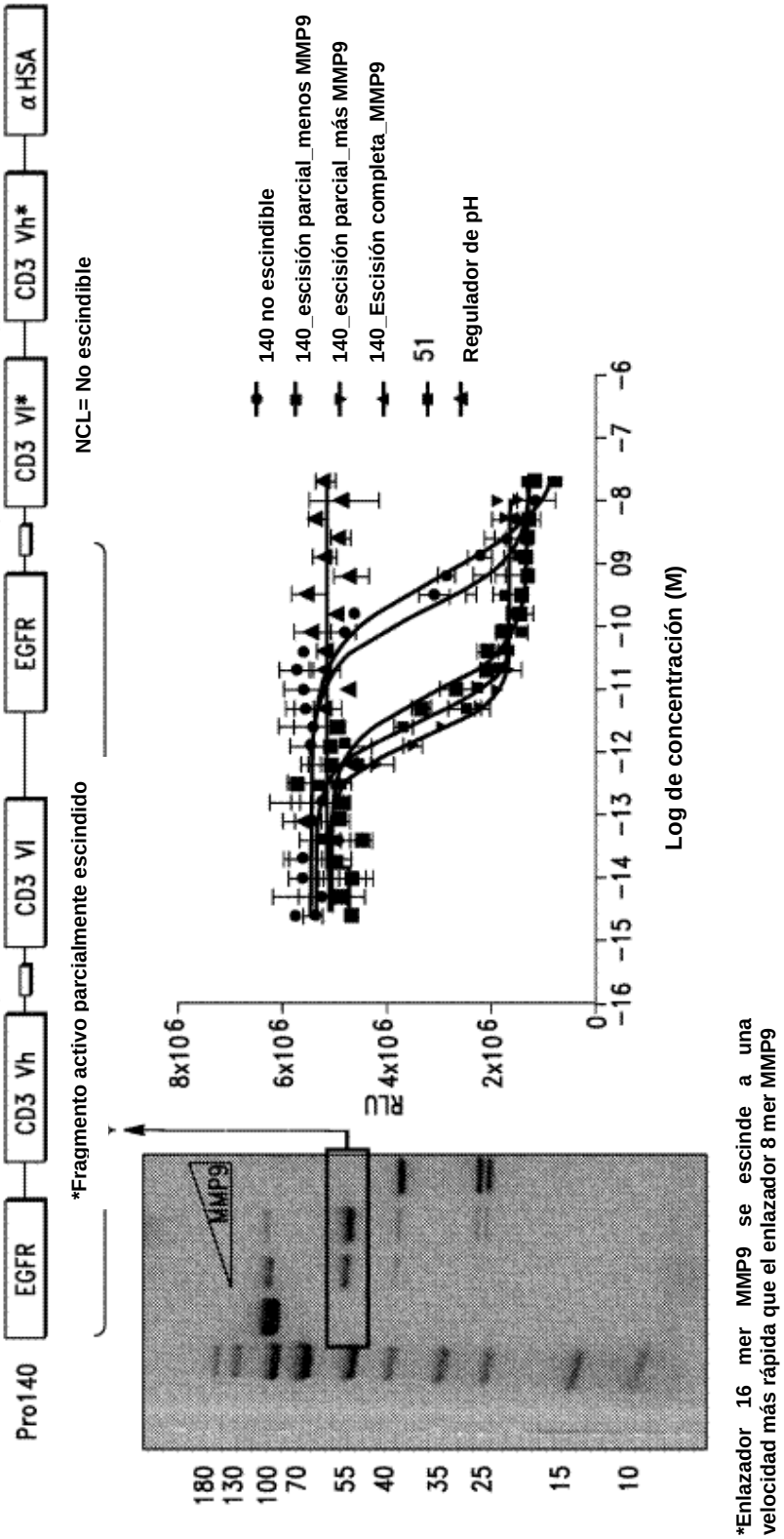



Figura 28A

Figura 28B

Figura 29




*Enlazador 16 mer MMP9 se escinde a una velocidad más rápida que el enlazador 8 mer MMP9

Figura 30

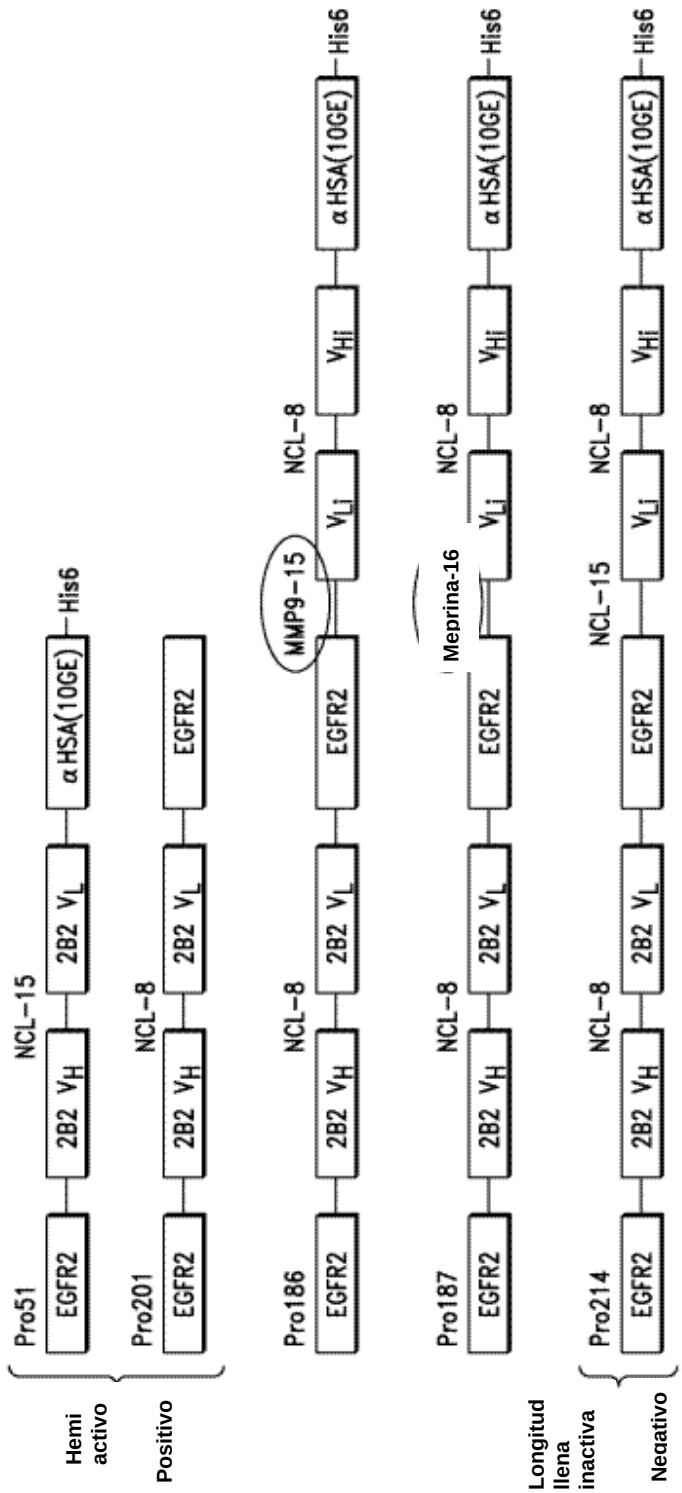

Pro51
EGFR2
NCL-15
2B2 VH
2B2 VL
α HSA(10GE)
His6
Hemi activo
Pro201
EGFR2
NCL-8
2B2 VH
2B2 VL
EGFR2
Positivo
Pro186
EGFR2
NCL-8
2B2 VH
2B2 VL
EGFR2
MMP9-15
NCL-8
VLi
VHi
α HSA(10GE)
His6
Pro187
EGFR2
NCL-8
2B2 VH
2B2 VL
EGFR2
Meprina-16
NCL-8
VLi
VHi
α HSA(10GE)
His6
Longitud llena inactiva
Pro214
EGFR2
NCL-8
2B2 VH
2B2 VL
EGFR2
NCL-15
NCL-8
VLi
VHi
α HSA(10GE)
His6
Negativo

Figura 31

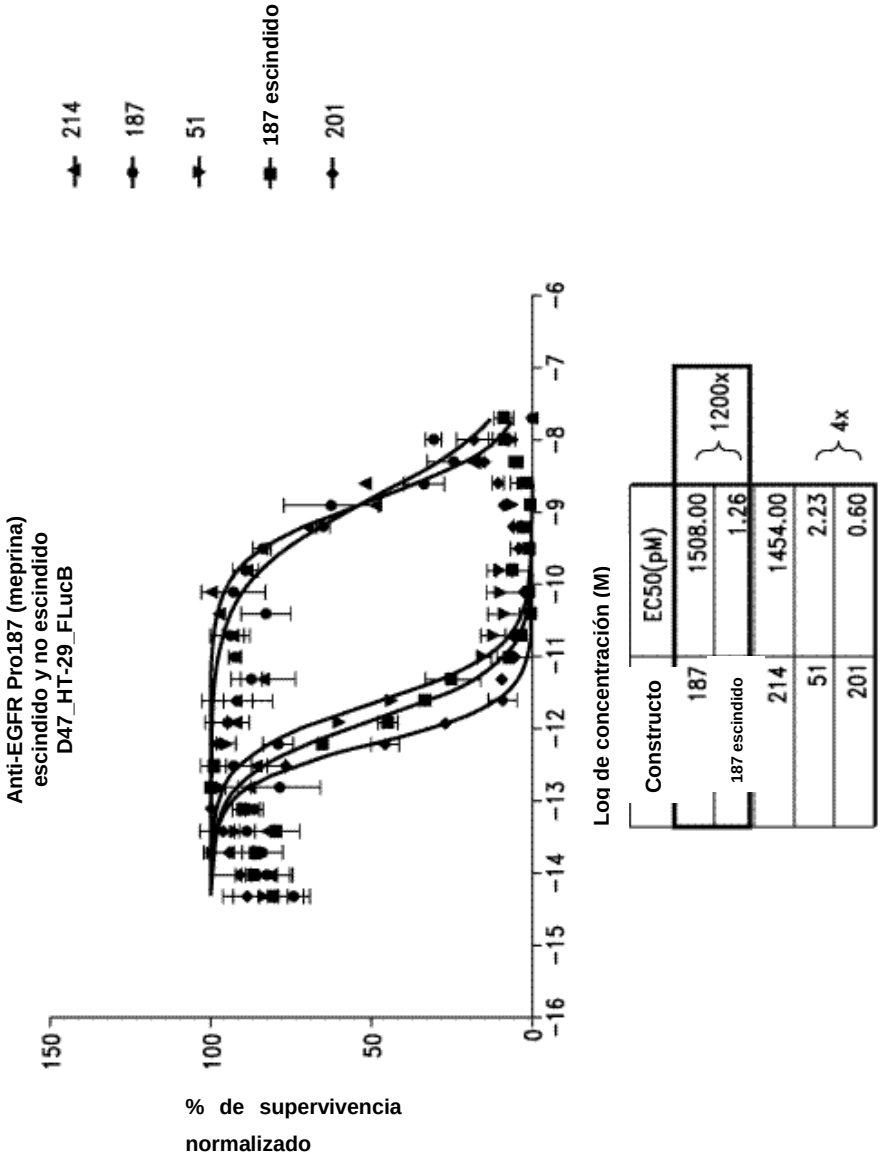

Anti-EGFR Pro187 (meprina) escindido y no escindido D47_HT-29_FLucB
214
187
51
187 escindido
201
% de supervivencia normalizado
150
100
50
0
−16
−15
−14
−13
−12
−11
−10
−9
−8
−7
−6
Log de concentración (M)
Constructo
EC50(pM)
187
1508.00
187 escindido
1.26
1200x
214
1454.00
51
2.23
4x
201
0.60

Figura 32

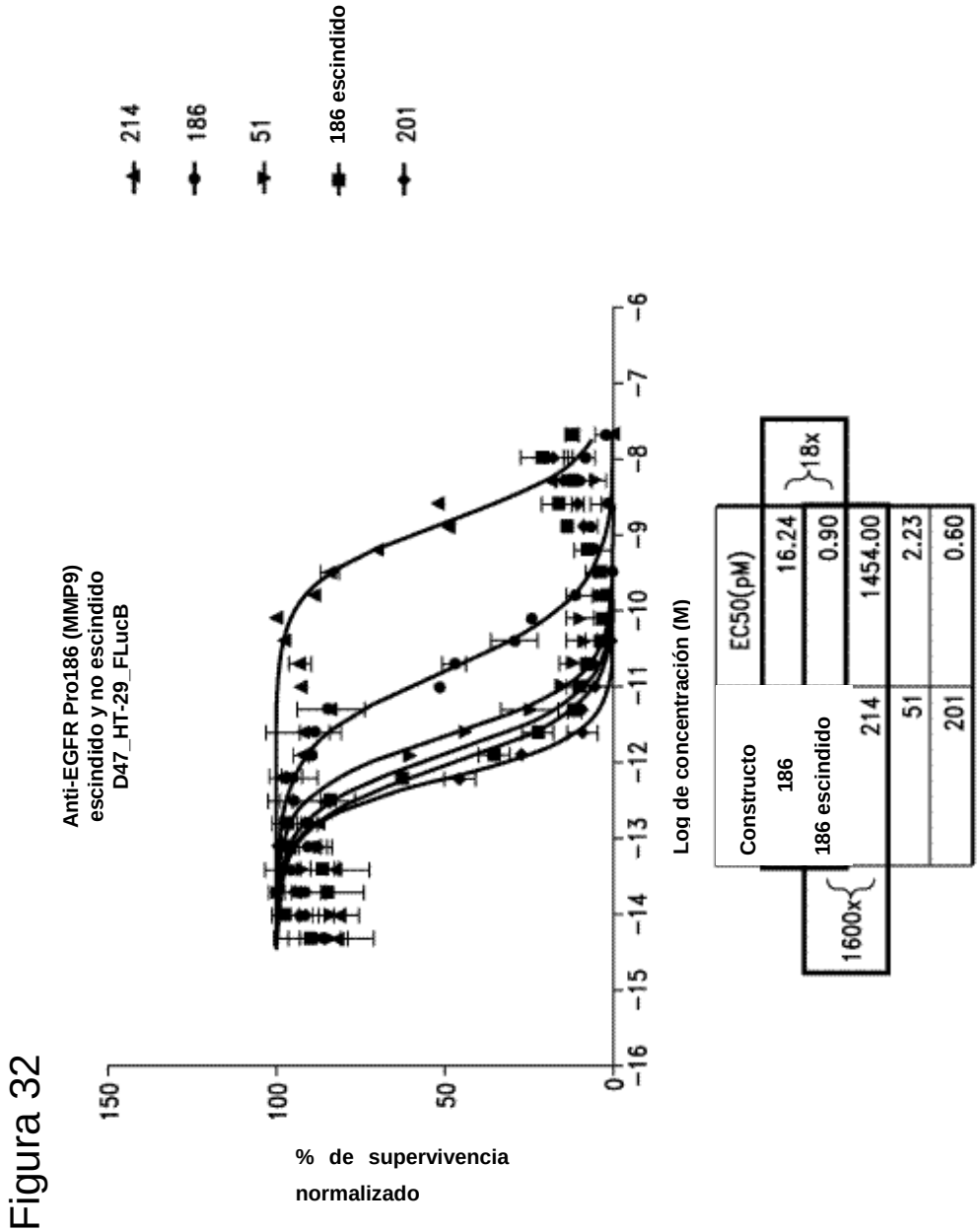

Anti-EGFR Pro186 (MMP9)
escindido y no escindido
D47_HT-29_FLucB
214
186
51
186 escindido
201
% de supervivencia normalizado
Log de concentración (M)
150
100
50
0
−16
−15
−14
−13
−12
−11
−10
−9
−8
−7
−6
Constructo
EC50(pM)
186
16.24
186 escindido
0.90
18x
214
1454.00
1600x
51
2.23
201
0.60

Figura 33

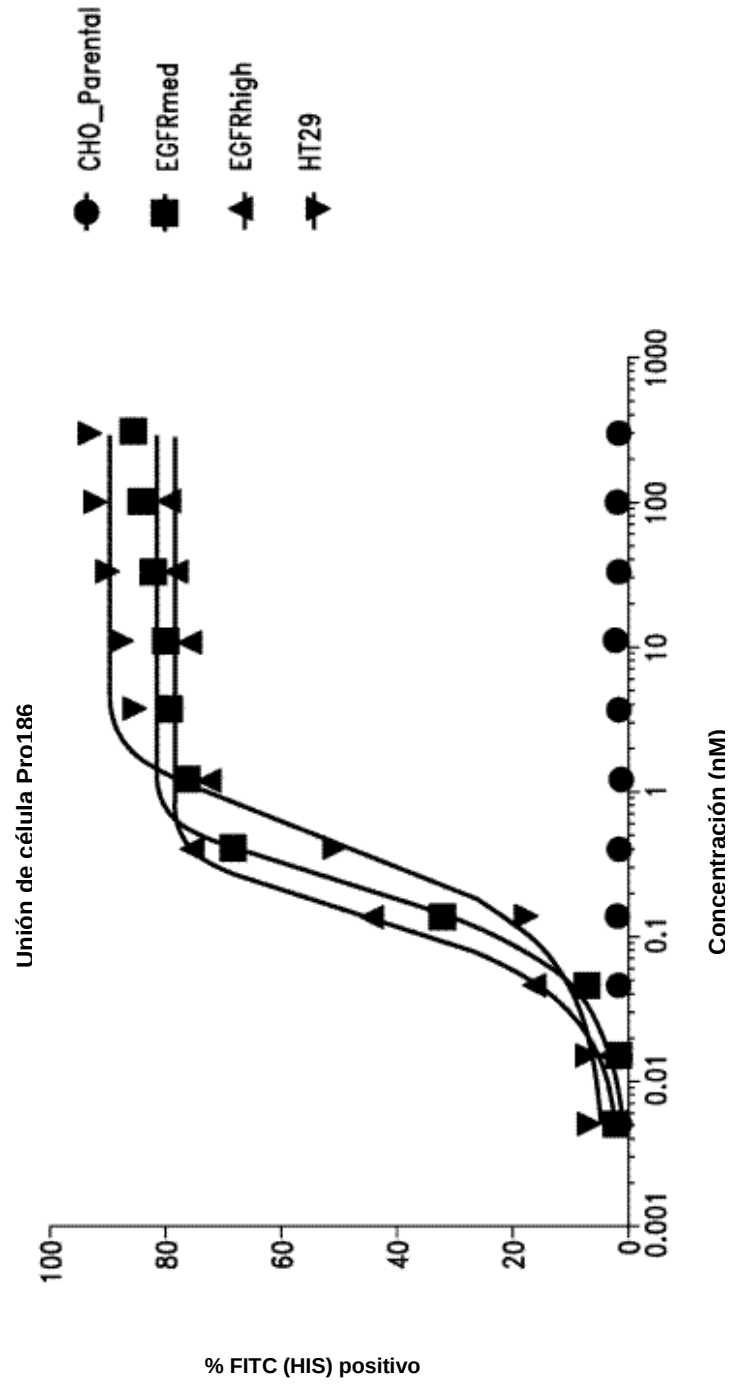

CHO_Parental
EGFRmed
EGFRhigh
HT29
Unión de célula Pro186
% FITC (HIS) positivo
Concentración (nM)
100
80
60
40
20
0
0.001
0.01
0.1
1
10
100
1000

Figura 34

**Grupos:**

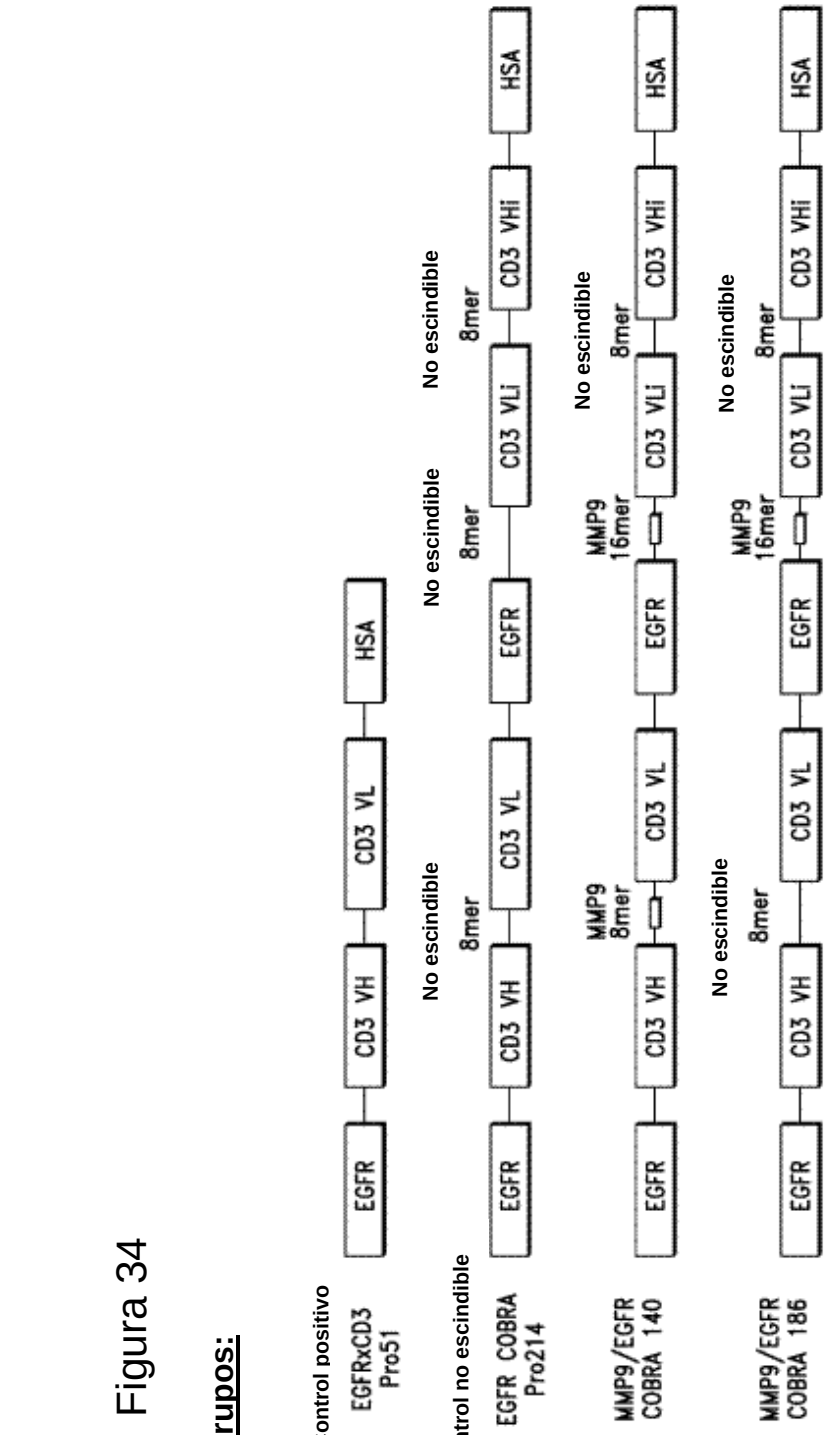


Figura 35

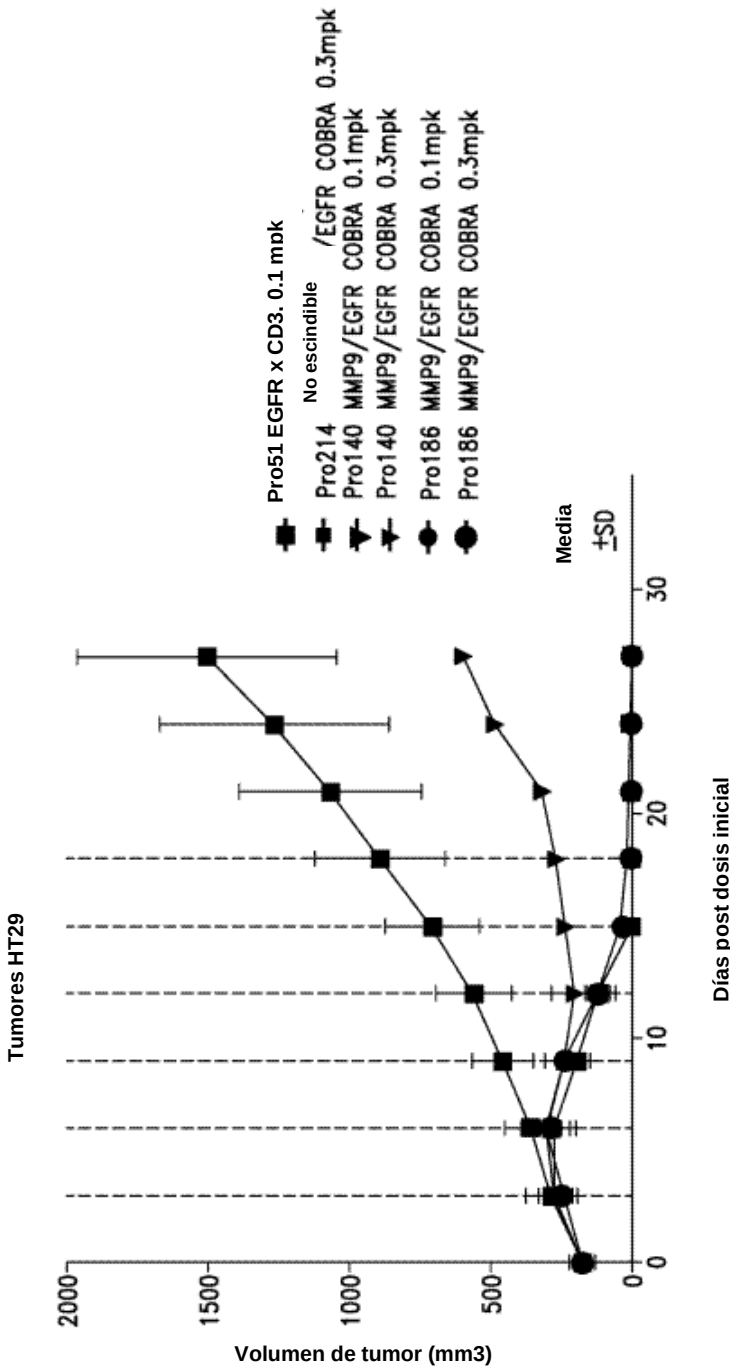
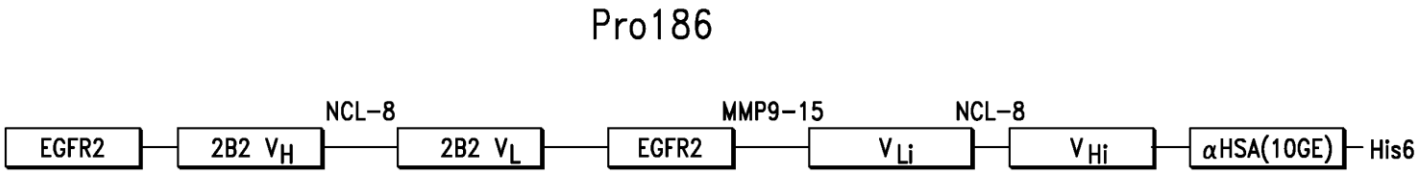

Pro51 EGFR x CD3. 0.1 mpk
No escindible
Pro214
Pro140 MMP9/EGFR COBRA 0.1mpk
Pro140 MMP9/EGFR COBRA 0.3mpk
Pro186 MMP9/EGFR COBRA 0.1mpk
Pro186 MMP9/EGFR COBRA 0.3mpk
/EGFR COBRA 0.3mpk
Media
±SD
Tumores HT29
Volumen de tumor (mm3)
2000
1500
1000
500
0
0
10
20
30
Días post dosis inicial

Figura 36




| Pro | BS1 | | DL1 | CD3Vl- | BS2 | AL | | DL2 | CD3Vh- | |
|---|---|---|---|---|---|---|---|---|---|---|
| 393 | EGFR2 | Vh | NCL-8 | Vl | EGFR2 | S9 | Vli | NCL-8 | Vhi | αHSA |
| 394 | EGFR2 | Vh | NCL-8 | Vl | EGFR2 | ST14(MV) | Vli | NCL-8 | Vhi | αHSA |
| 395 | EGFR2 | Vh | NCL-8 | Vl | EGFR2 | Cats | Vli | NCL-8 | Vhi | αHSA |
| 396 | EGFR2 | Vh | NCL-8 | Vl | EGFR2 | MMP9v | Vli | NCL-8 | Vhi | αHSA |
| 429 | EGFR2 | Vh | NCL-8 | Vl | EGFR2 | Mep/GrandB | Vli | NCL-8 | Vhi | αHSA |
| 430 | EGFR2 | Vh | NCL-8 | Vl | EGFR2 | MMP9-2 | Vli | NCL-8 | Vhi | αHSA |
| 431 | EGFR2 | Vh | NCL-8 | Vl | EGFR2 | ST14(MS) | Vli | NCL-8 | Vhi | αHSA |

Figura 37

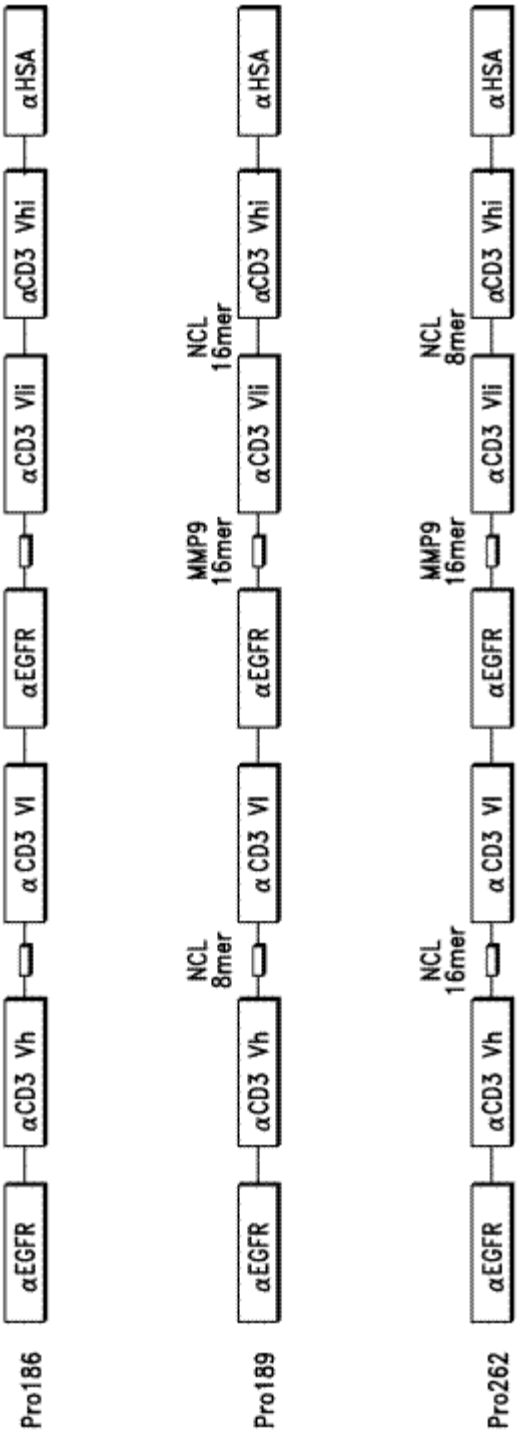
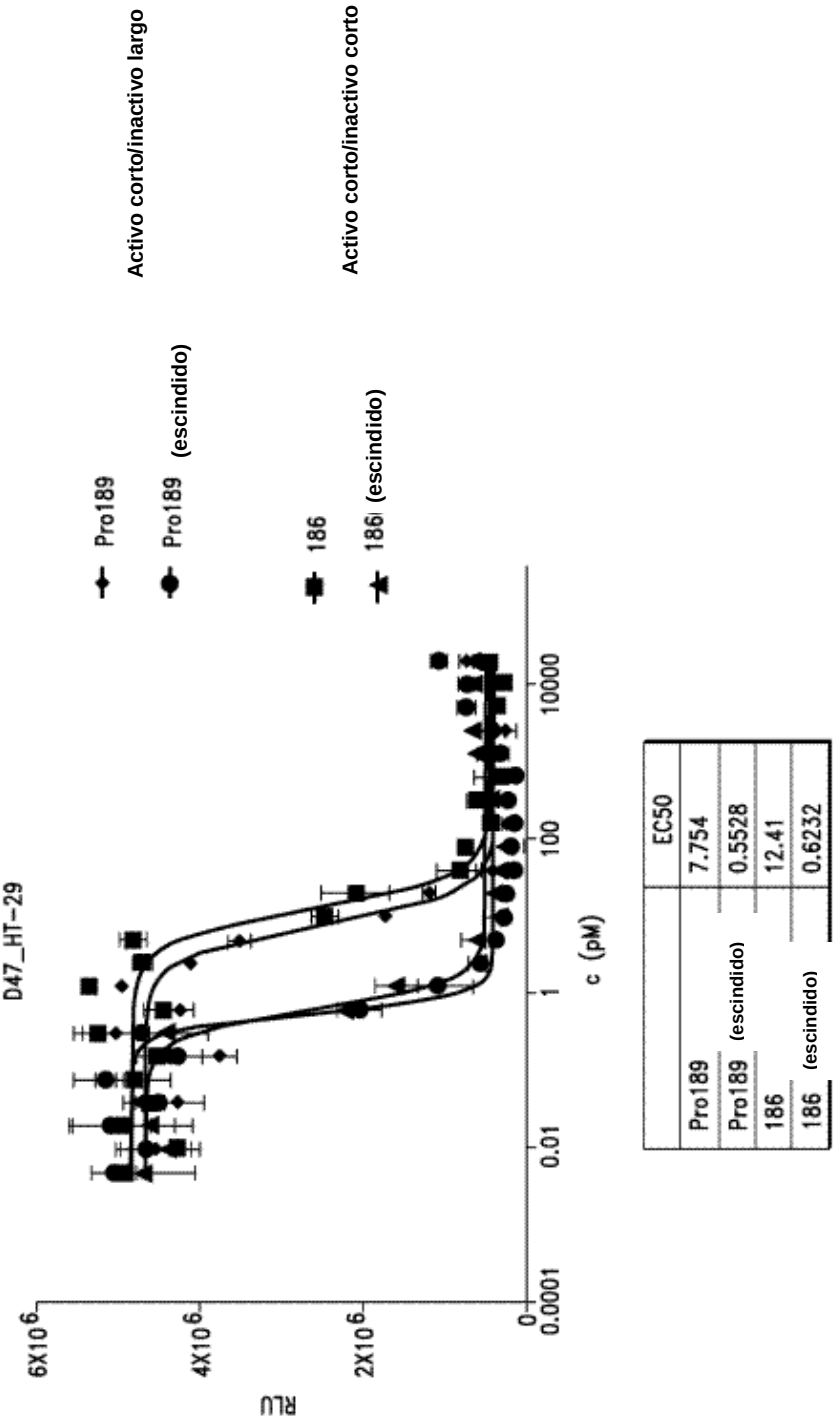

Pro186
αEGFR
αCD3 Vh
NCL 8mer
α CD3 VI
αEGFR
MMP9 16mer
αCD3 Vii
αCD3 Vhi
αHSA
Pro189
αEGFR
αCD3 Vh
NCL 8mer
α CD3 VI
αEGFR
MMP9 16mer
αCD3 Vii
NCL 16mer
αCD3 Vhi
αHSA
Pro262
αEGFR
αCD3 Vh
NCL 16mer
α CD3 VI
αEGFR
MMP9 16mer
αCD3 Vii
NCL 8mer
αCD3 Vhi
αHSA

Figura 38




| | EC50 |
|---|---|
| Pro189 | 7.754 |
| Pro189 (escindido) | 0.5528 |
| 186 | 12.41 |
| 186 (escindido) | 0.6232 |

Figura 39

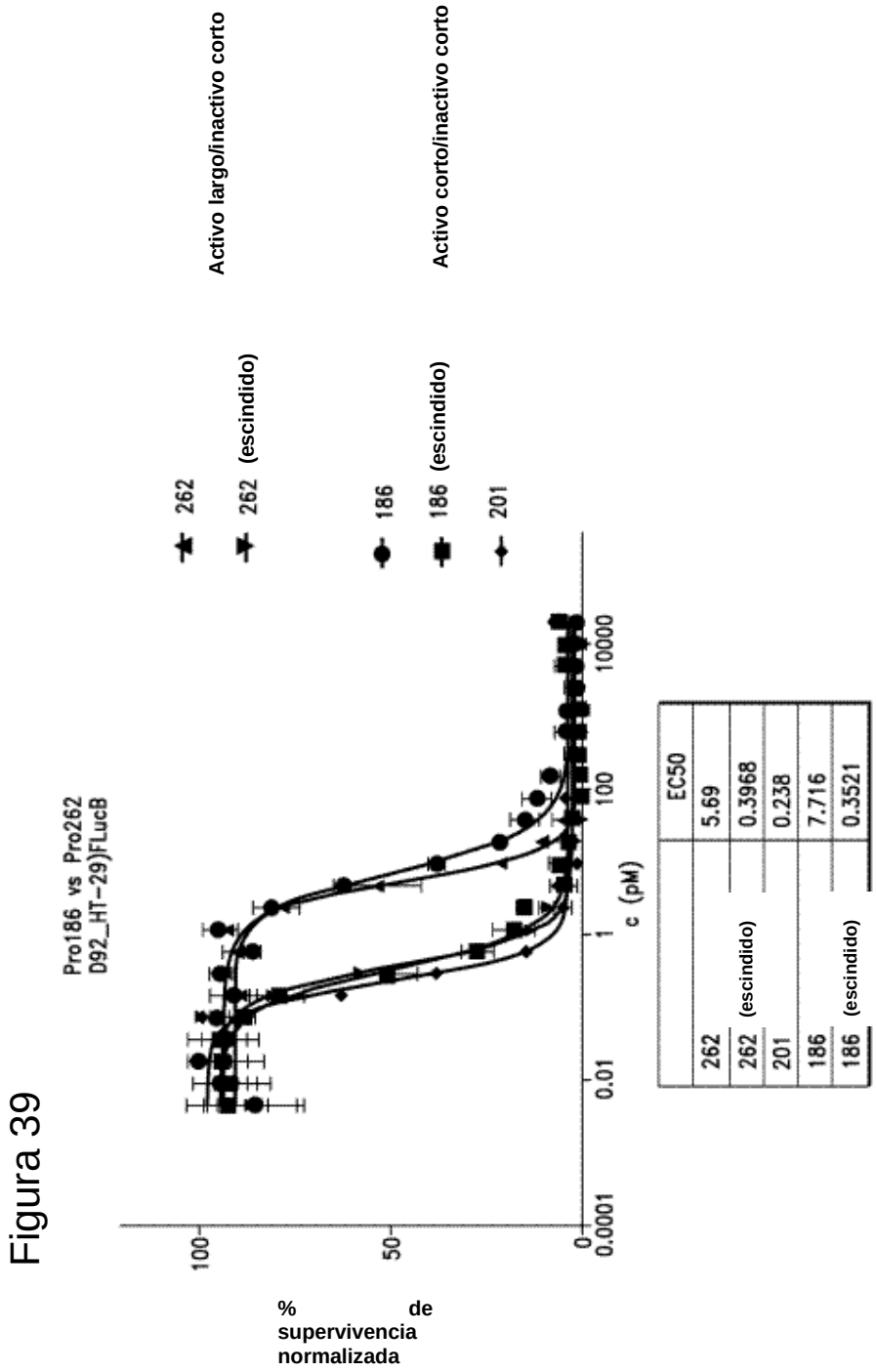

Pro186 vs Pro262
D92_HT-29)FLucB
Activo largo/inactivo corto
Activo corto/inactivo corto
262
262 (escindido)
186
186 (escindido)
201
% de supervivencia normalizada
100
50
0
0.0001
0.01
1
100
10000
c (pM)
EC50
262 5.69
262 (escindido) 0.3968
201 0.238
186 7.716
186 (escindido) 0.3521

Figura 40A

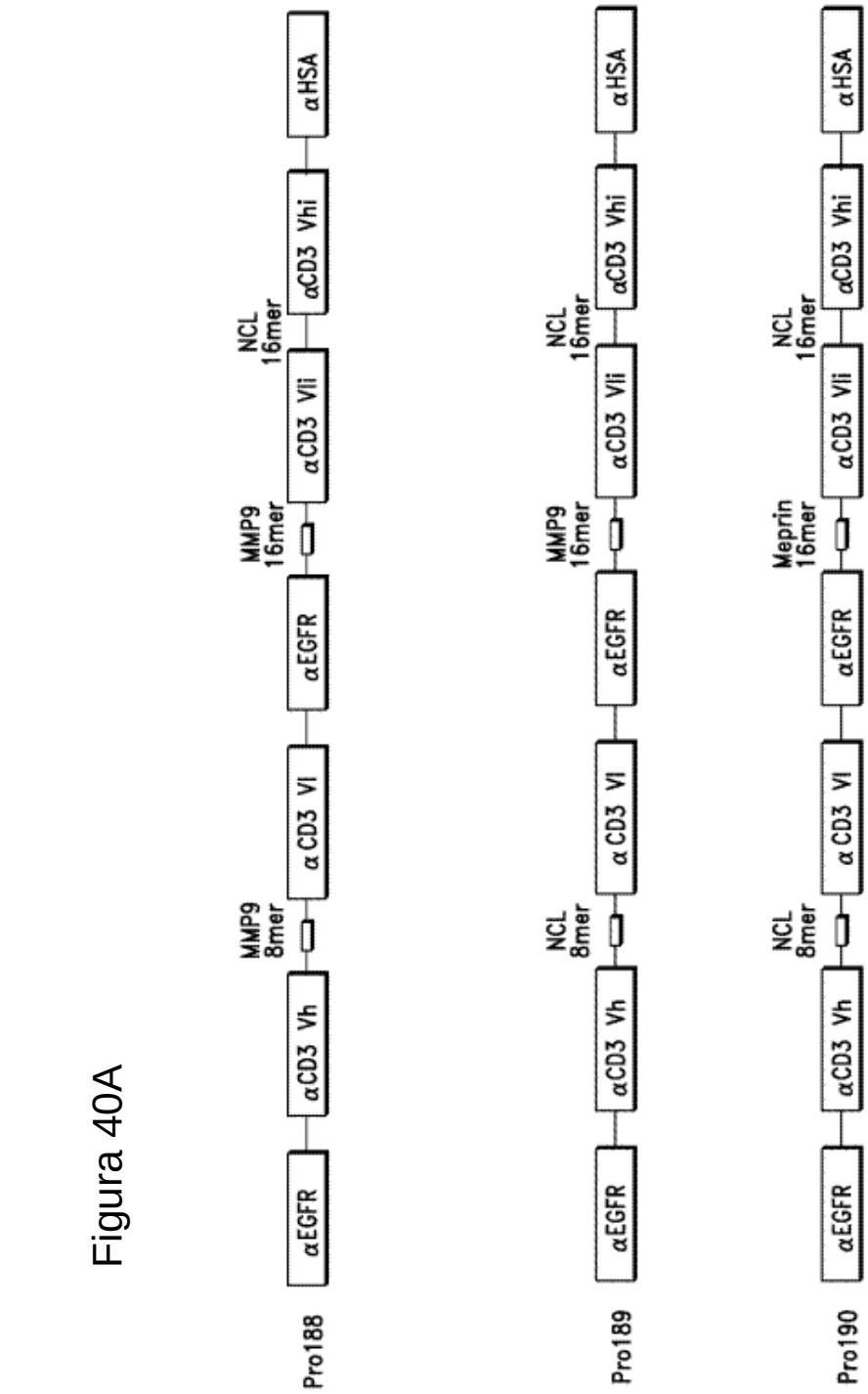

Pro188
αEGFR
αCD3 Vh
MMP9 8mer
αCD3 Vl
αEGFR
MMP9 16mer
αCD3 Vli
NCL 16mer
αCD3 Vhi
αHSA
Pro189
αEGFR
αCD3 Vh
NCL 8mer
αCD3 Vl
αEGFR
MMP9 16mer
αCD3 Vli
NCL 16mer
αCD3 Vhi
αHSA
Pro190
αEGFR
αCD3 Vh
NCL 8mer
αCD3 Vl
αEGFR
Meprin 16mer
αCD3 Vli
NCL 16mer
αCD3 Vhi
αHSA

Figura 40B

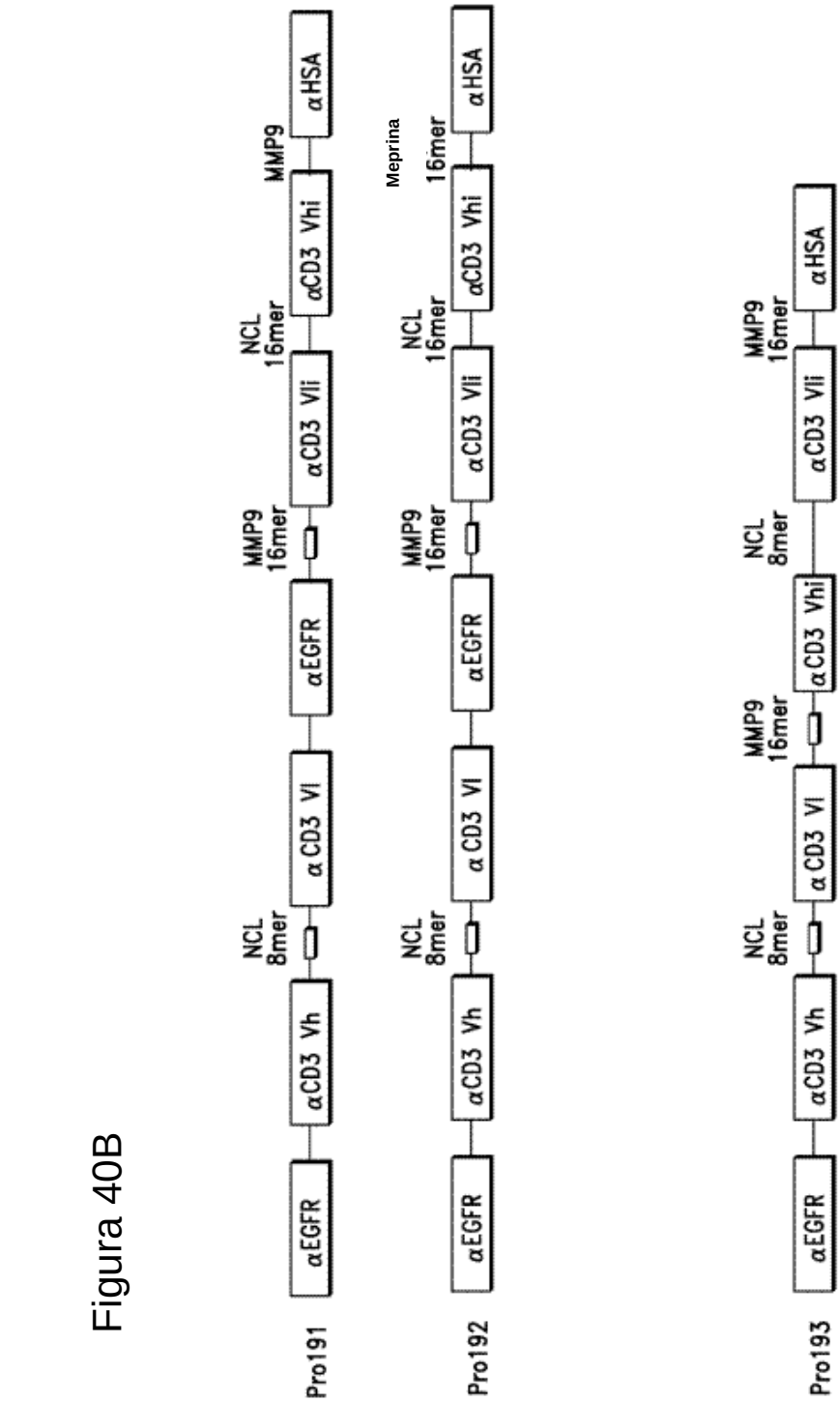

Pro191
αEGFR
αCD3 Vh
NCL 8mer
α CD3 Vl
MMP9 16mer
αEGFR
NCL 16mer
αCD3 Vli
MMP9
αHSA
Meprina
Pro192
αEGFR
αCD3 Vh
NCL 8mer
α CD3 Vl
MMP9 16mer
αEGFR
NCL 16mer
αCD3 Vli
16mer
αHSA
Pro193
αEGFR
αCD3 Vh
NCL 8mer
α CD3 Vl
MMP9 16mer
αCD3 Vhi
NCL 8mer
αCD3 Vli
MMP9 16mer
αHSA

Figura 40C

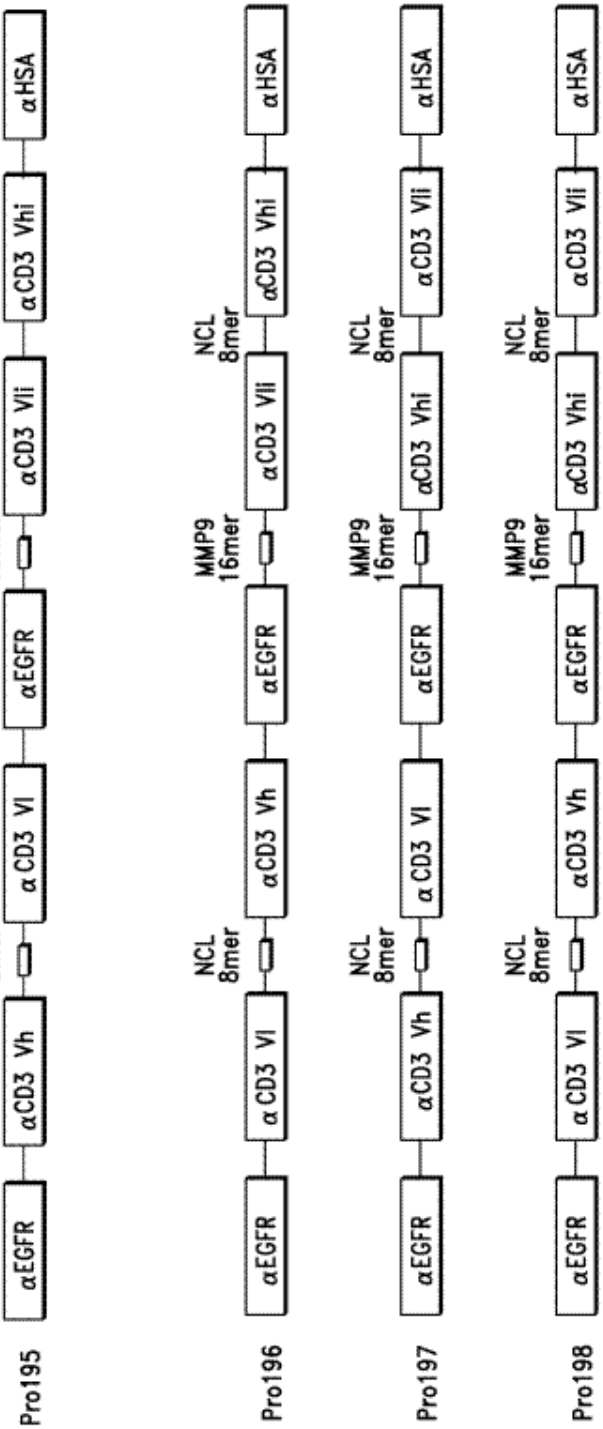

Pro195
αEGFR
αCD3 Vh
NCL 8mer
α CD3 Vl
αEGFR
MMP9 16mer
αCD3 Vli
NCL 16mer
αCD3 Vhi
αHSA
Pro196
αEGFR
α CD3 Vl
NCL 8mer
αCD3 Vh
αEGFR
MMP9 16mer
αCD3 Vli
NCL 8mer
αCD3 Vhi
αHSA
Pro197
αEGFR
αCD3 Vh
NCL 8mer
α CD3 Vl
αEGFR
MMP9 16mer
αCD3 Vhi
NCL 8mer
αCD3 Vli
αHSA
Pro198
αEGFR
α CD3 Vl
NCL 8mer
αCD3 Vh
αEGFR
MMP9 16mer
αCD3 Vhi
NCL 8mer
αCD3 Vli
αHSA

Figura 41

| sdAb | | Unión de proteína: $K_D$ (nM) | | | Unión de célula: | | TDCC $EC_{50}$ (pM) | |
|---|---|---|---|---|---|---|---|---|
| MVK ID | Familia | Humano | Rhesus | Ratón | Humano | Rhesus | IGROV1 | OVAR8 |
| 77-2 | 2 | 2 | 3 | 7 | +++ | +++ | 2 | 0.2 |
| 59-3 | 3 | 15 | 53 | NB | +++ | +++ | 30 | 6 |
| 22-4 | 4 | 2 | 11 | NB | +++ | +++ | 8 | 1 |
| Pro51 | | | | | | | 41 | 2 |

Figura 42

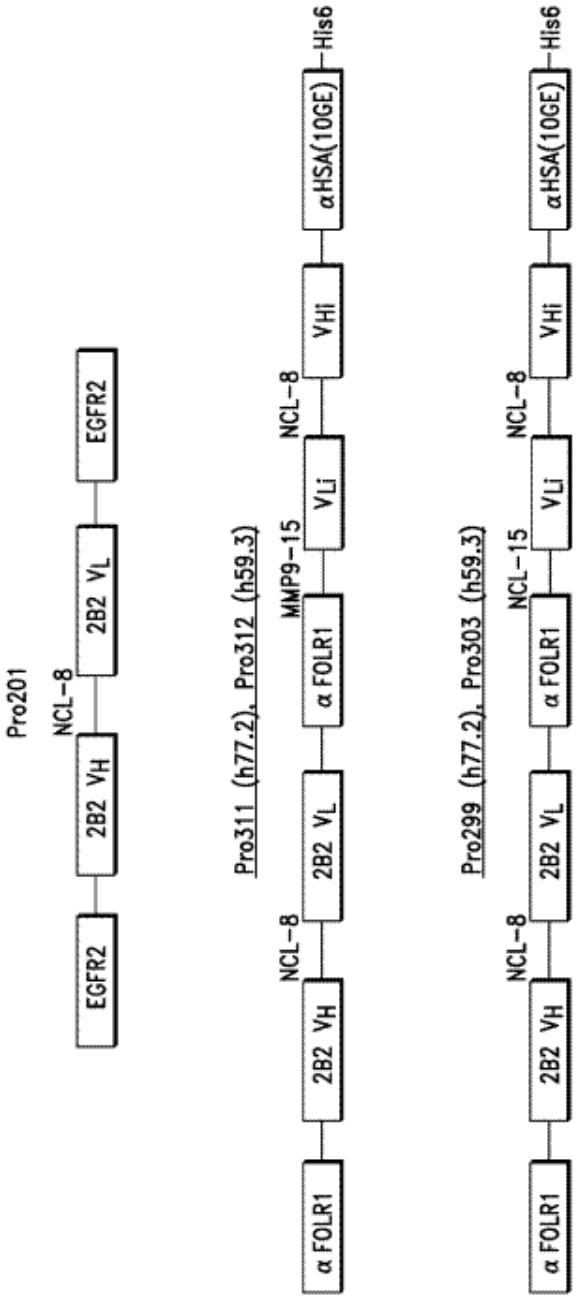

Pro201
EGFR2
2B2 VH
NCL-8
2B2 VL
EGFR2
Pro311 (h77.2), Pro312 (h59.3)
α FOLR1
2B2 VL
NCL-8
2B2 VH
α FOLR1
MMP9-15
VLi
NCL-8
VHi
αHSA(10GE)
His6
Pro299 (h77.2), Pro303 (h59.3)
α FOLR1
2B2 VL
NCL-8
2B2 VH
α FOLR1
NCL-15
VLi
NCL-8
VHi
αHSA(10GE)
His6

Figura 43

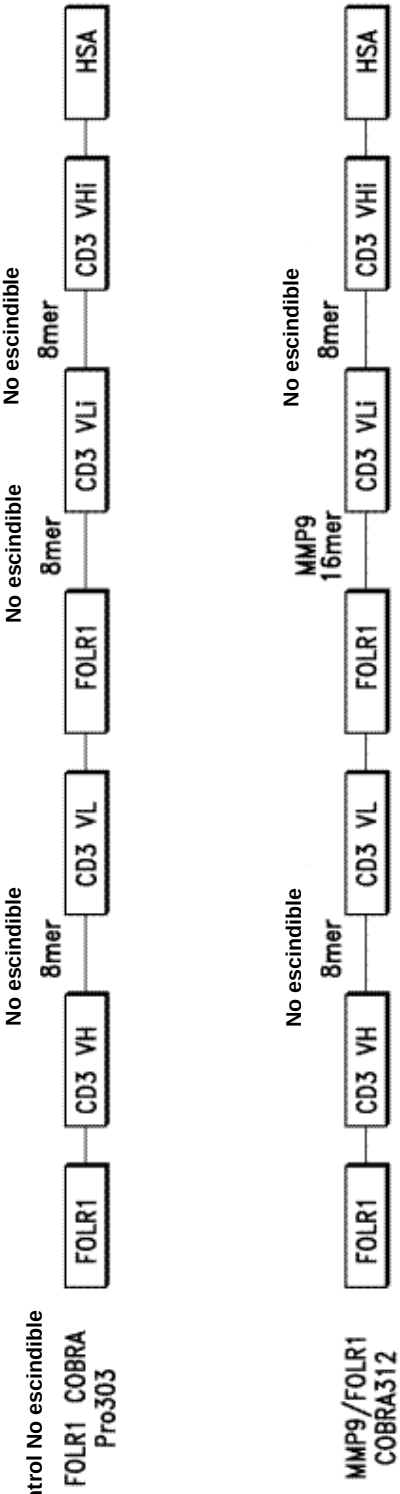

Control No escindible
FOLR1 COBRA Pro303
FOLR1
CD3 VH
No escindible
8mer
CD3 VL
FOLR1
No escindible
8mer
CD3 VLi
No escindible
8mer
CD3 VHi
HSA
MMP9/FOLR1 COBRA312
FOLR1
CD3 VH
No escindible
8mer
CD3 VL
FOLR1
MMP9 16mer
CD3 VLi
No escindible
8mer
CD3 VHi
HSA

Figura 44

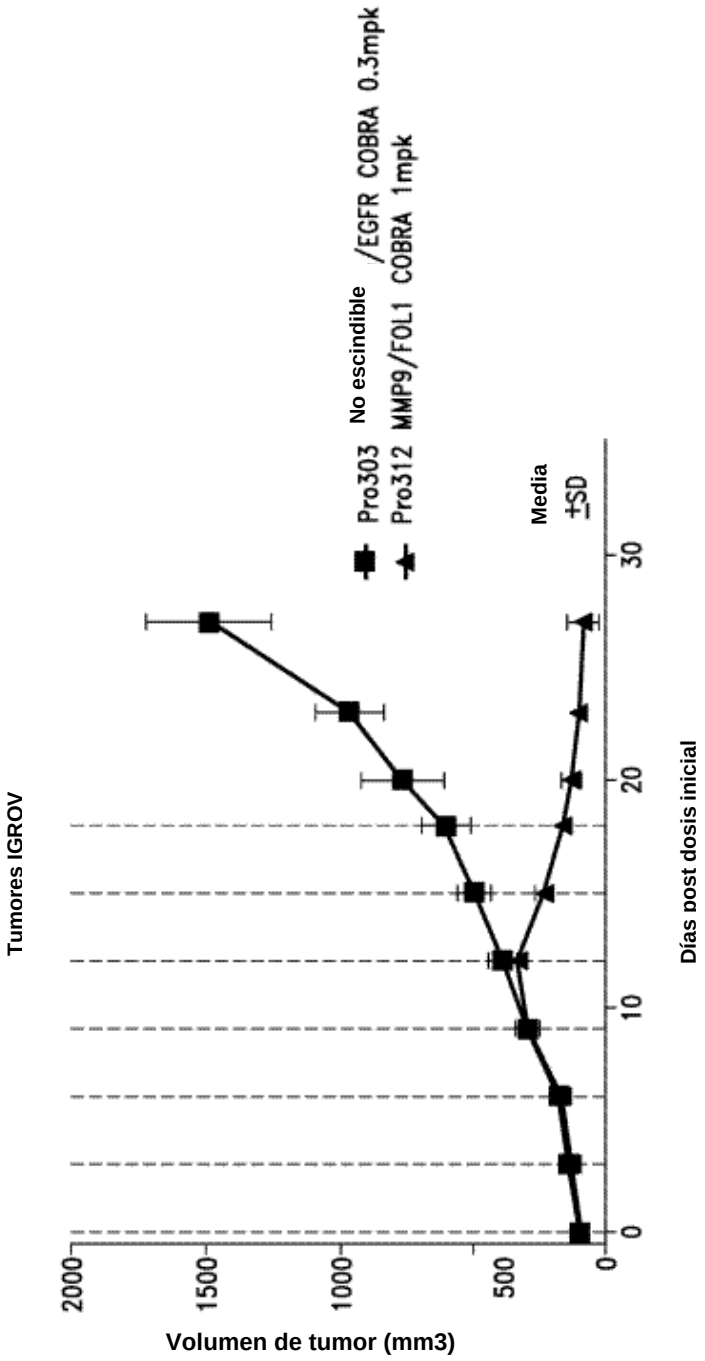

Tumores IGROV
Pro303 No escindible /EGFR COBRA 0.3mpk
Pro312 MMP9/FOL1 COBRA 1mpk
Media
±SD
Volumen de tumor (mm3)
Días post dosis inicial
2000
1500
1000
500
0
0
10
20
30

Figura 45

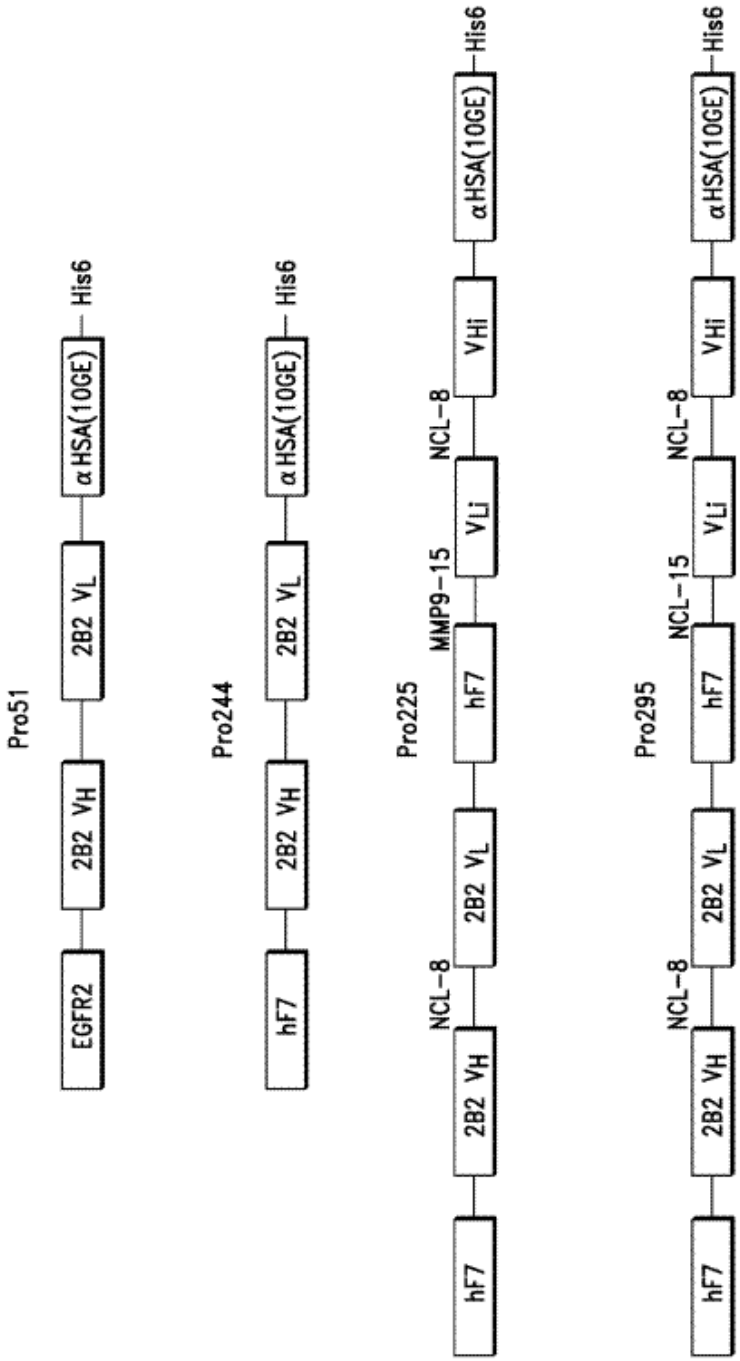
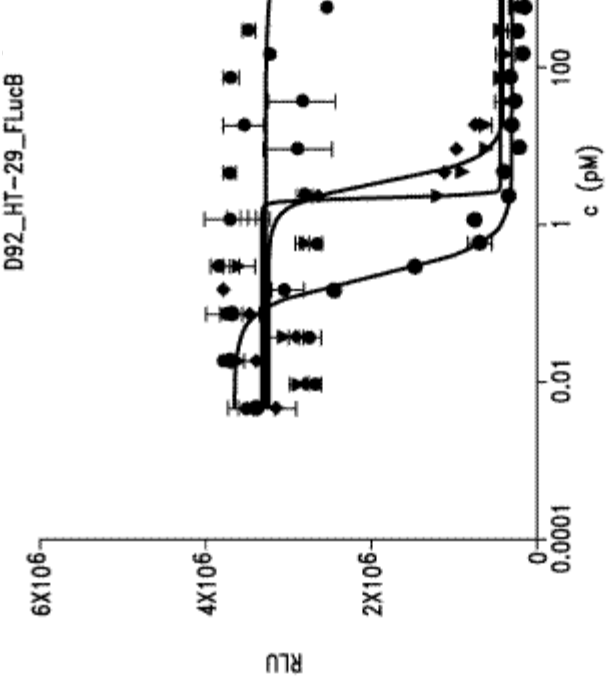

Pro51
EGFR2
2B2 VH
2B2 VL
αHSA(10GE)
His6
Pro244
hF7
2B2 VH
2B2 VL
αHSA(10GE)
His6
Pro225
hF7
NCL-8
2B2 VH
2B2 VL
MMP9-15
hF7
VLi
NCL-8
VHi
αHSA(10GE)
His6
Pro295
hF7
NCL-8
2B2 VH
2B2 VL
NCL-15
hF7
VLi
NCL-8
VHi
αHSA(10GE)
His6

Figura 46




| | | EC50 | |
|---|---|---|---|
| 225 | escindido | ~2.313 | 2000x |
| 225 | | 3.757 | |
| 295 | | 8497 | |
| 201 | | 0.2374 | |

Figura 47

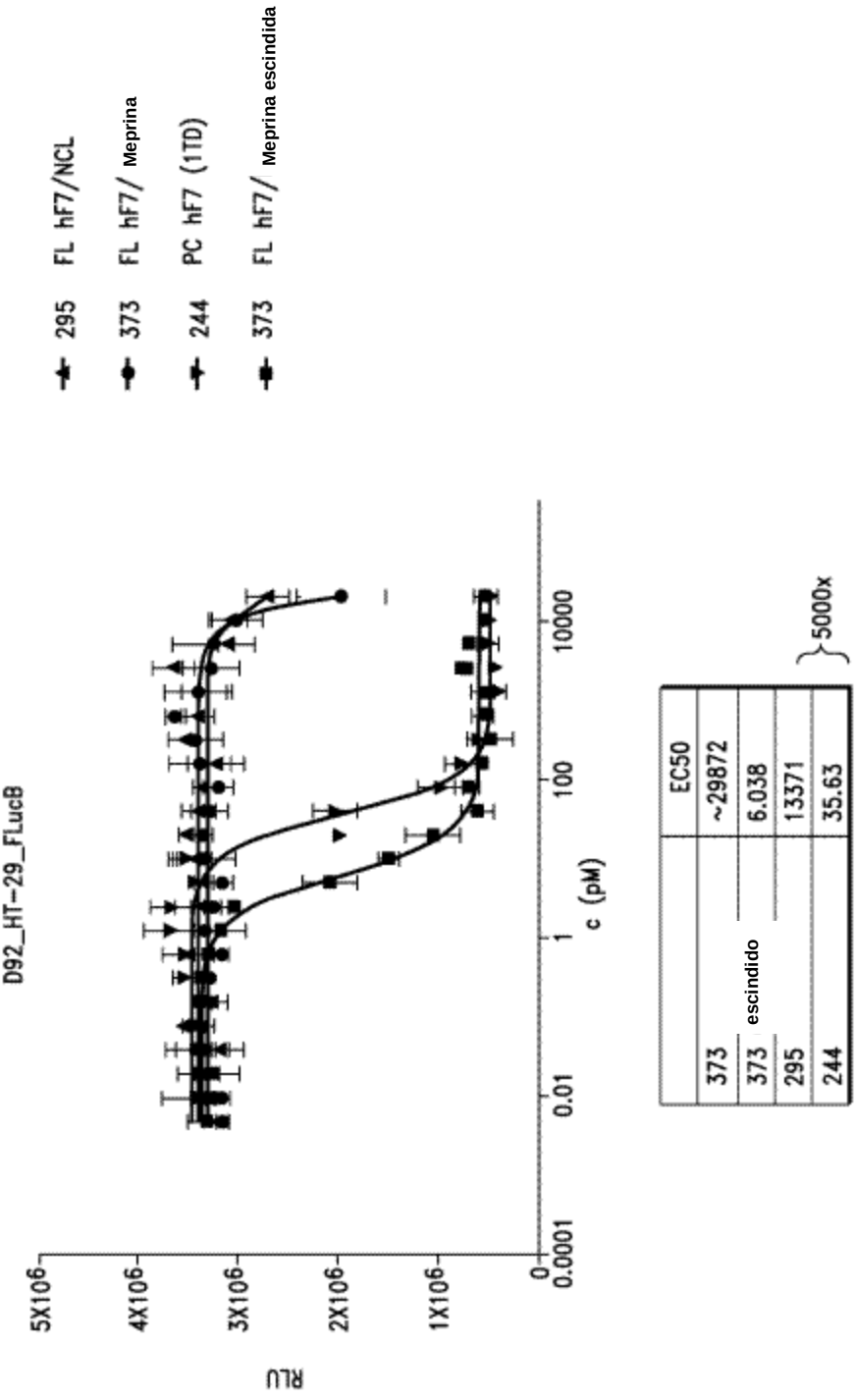

anti-B7H3 hF7 Longitud llena
D92_HT-29_FLucB
295 FL hF7/NCL
373 FL hF7/ Meprina
244 PC hF7 (1TD)
373 FL hF7/ Meprina escindida
RLU
5X10^6
4X10^6
3X10^6
2X10^6
1X10^6
0
0.0001
0.01
1
100
10000
c (pM)
EC50
373 ~29872
373 escindido 6.038
295 13371
244 35.63
5000x

Figura 48

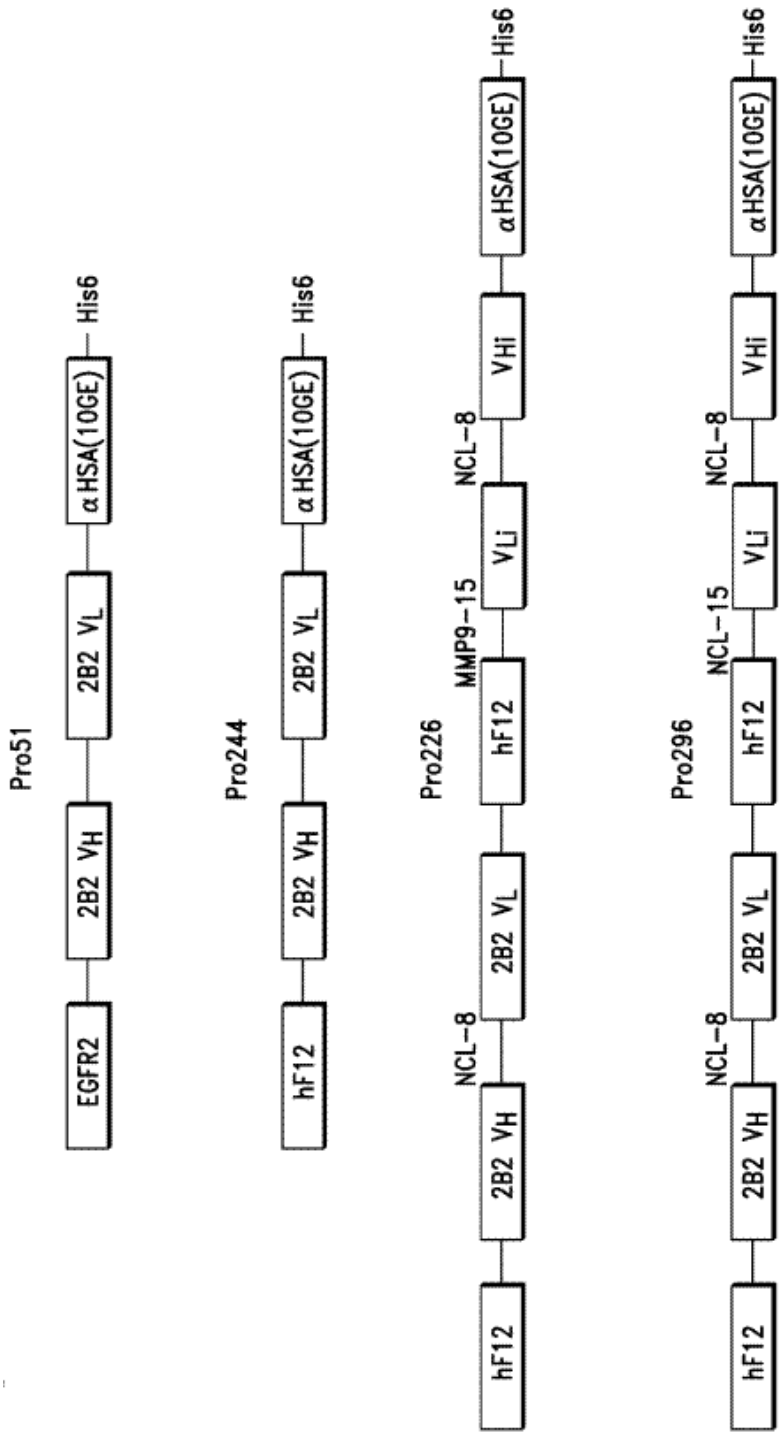
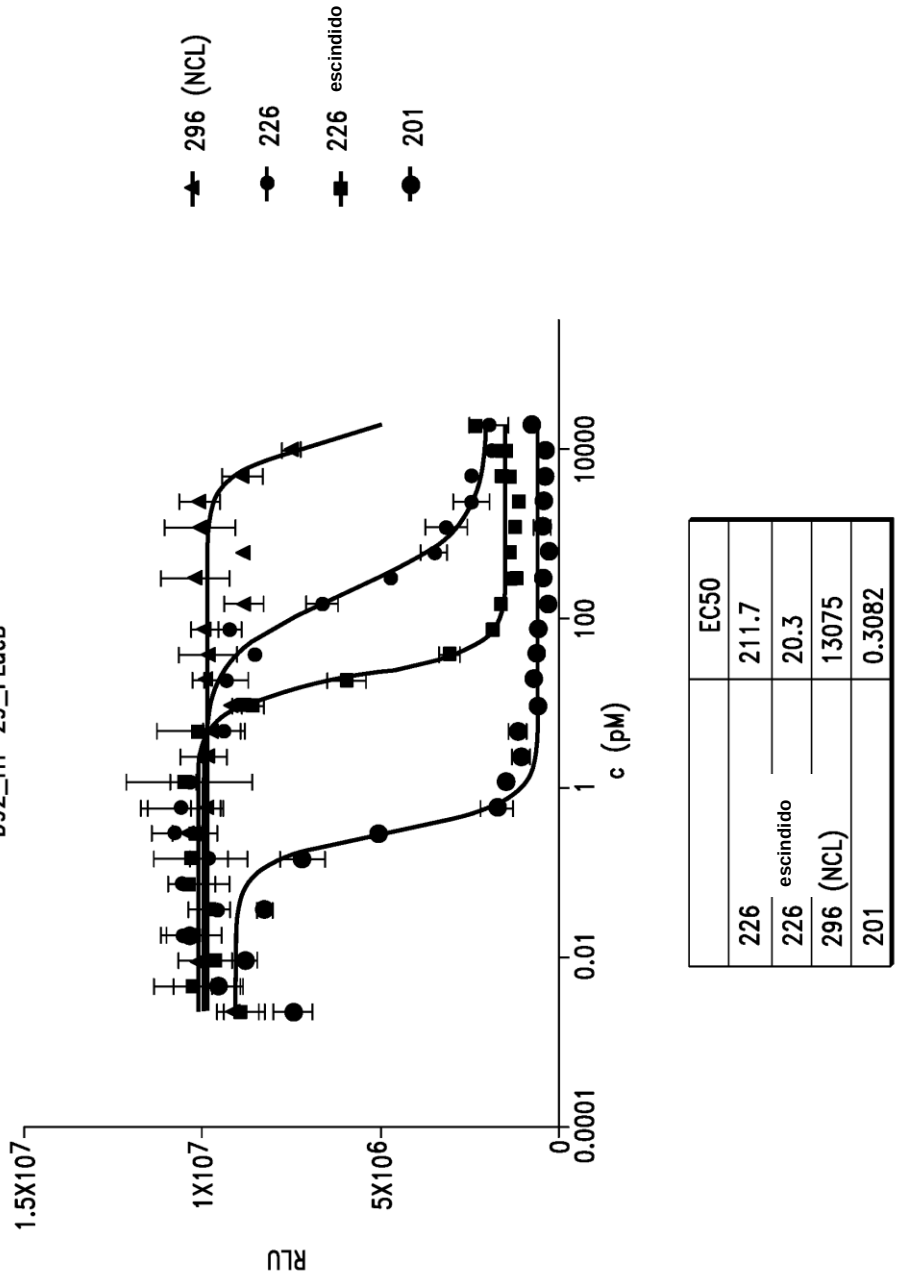

Pro51
EGFR2
2B2 VH
2B2 VL
αHSA(10GE)
His6
Pro244
hF12
2B2 VH
2B2 VL
αHSA(10GE)
His6
Pro226
hF12
NCL-8
2B2 VH
2B2 VL
MMP9-15
hF12
VLi
NCL-8
VHi
αHSA(10GE)
His6
Pro296
hF12
NCL-8
2B2 VH
2B2 VL
NCL-15
hF12
VLi
NCL-8
VHi
αHSA(10GE)
His6

Figura 49




| | EC50 |
|---|---|
| 226 | 211.7 |
| 226 escindido | 20.3 |
| 296 (NCL) | 13075 |
| 201 | 0.3082 |

Figura 50

| Clon | Afinidad de unión (nM) | | Reactividad cruzada |
|---|---|---|---|
| | Humano | Cino | Cino/humano |
| VIB-13 | 2.3 | 11.6 | 5 |
| hVIB-13 | 2.8 | 12.7 | 4.5 |
| | | | |
| VIB-23 | 4.2 | 46.7 | 11.1 |
| hVIB-23 | 4.1 | 51.8 | 12.6 |

Figura 51

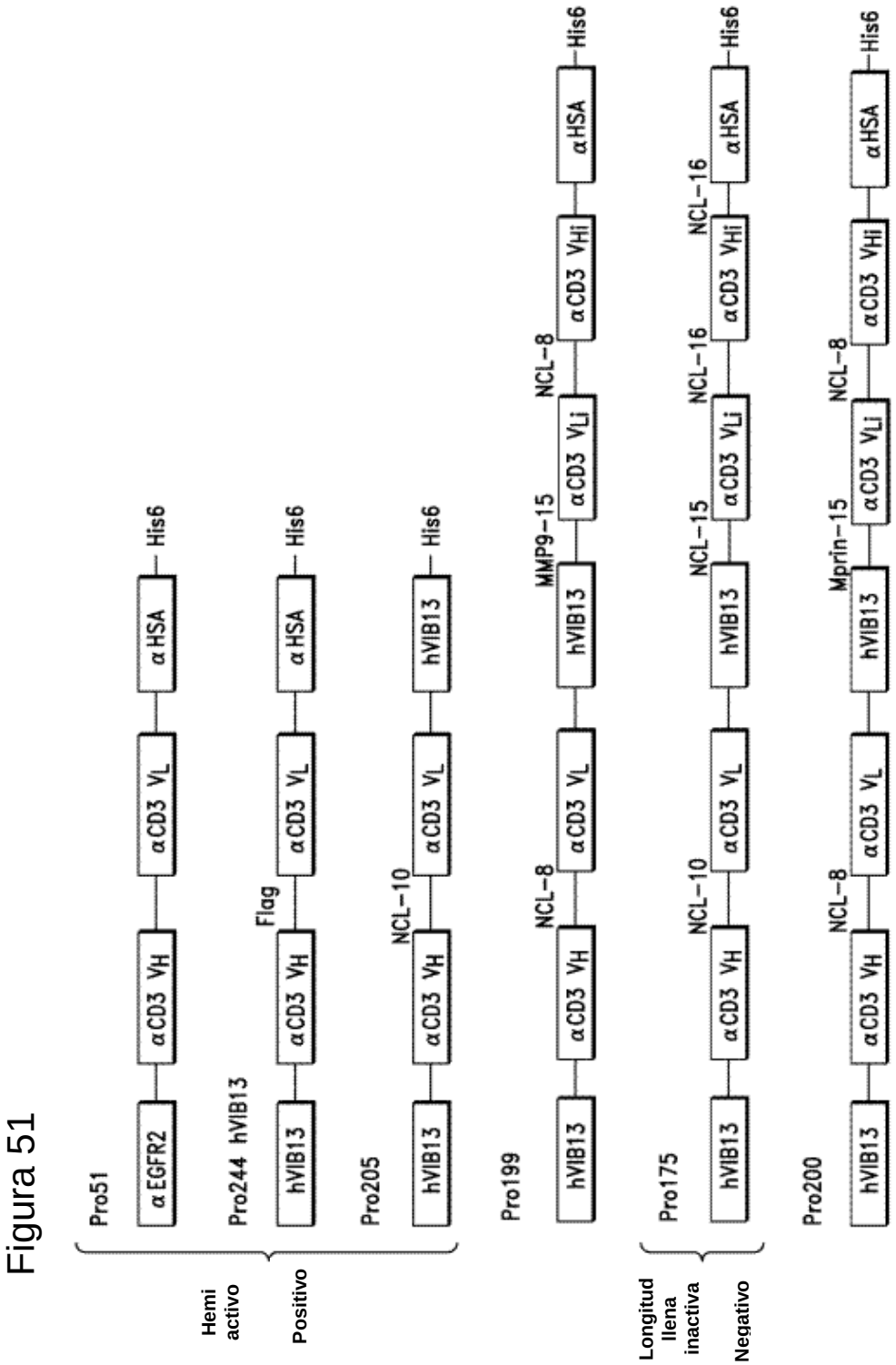
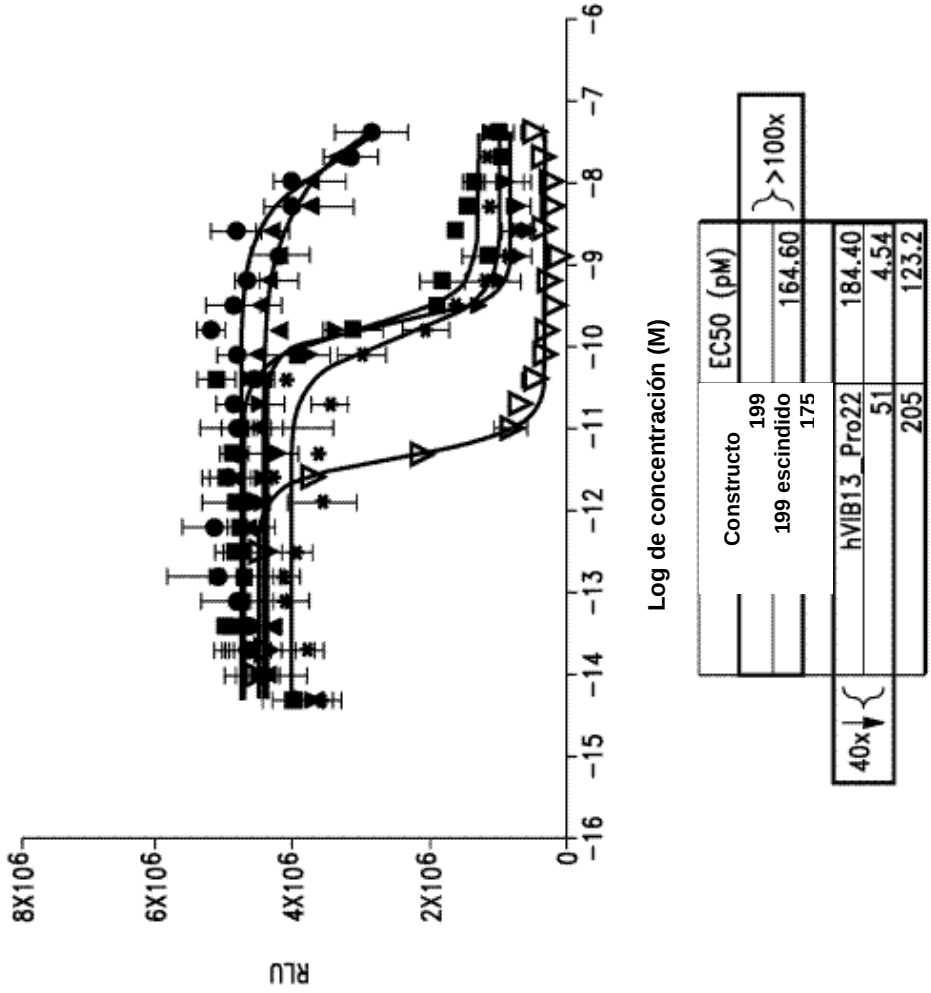
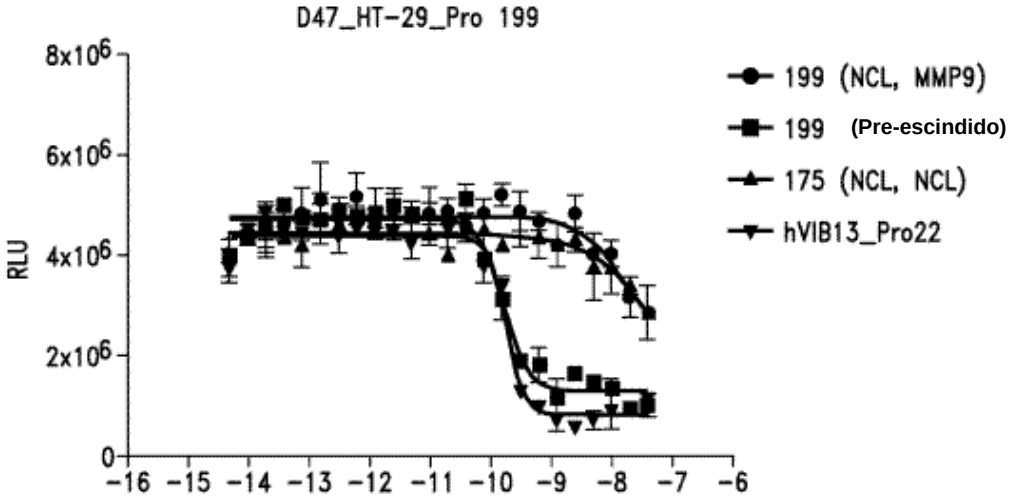

Pro51
αEGFR2
αCD3 VH
αCD3 VL
αHSA
His6
Hemi activo
Positivo
Pro244 hVIB13
hVIB13
αCD3 VH
Flag
αCD3 VL
αHSA
His6
Pro205
hVIB13
αCD3 VH
NCL-10
αCD3 VL
hVIB13
His6
Pro199
hVIB13
αCD3 VH
NCL-8
αCD3 VL
hVIB13
MMP9-15
αCD3 VLi
NCL-8
αCD3 VHi
αHSA
His6
Longitud llena inactiva
Negativo
Pro175
hVIB13
αCD3 VH
NCL-10
αCD3 VL
hVIB13
NCL-15
αCD3 VLi
NCL-16
αCD3 VHi
αHSA
His6
Pro200
hVIB13
αCD3 VH
NCL-8
αCD3 VL
hVIB13
Mprin-15
αCD3 VLi
NCL-8
αCD3 VHi
αHSA
His6

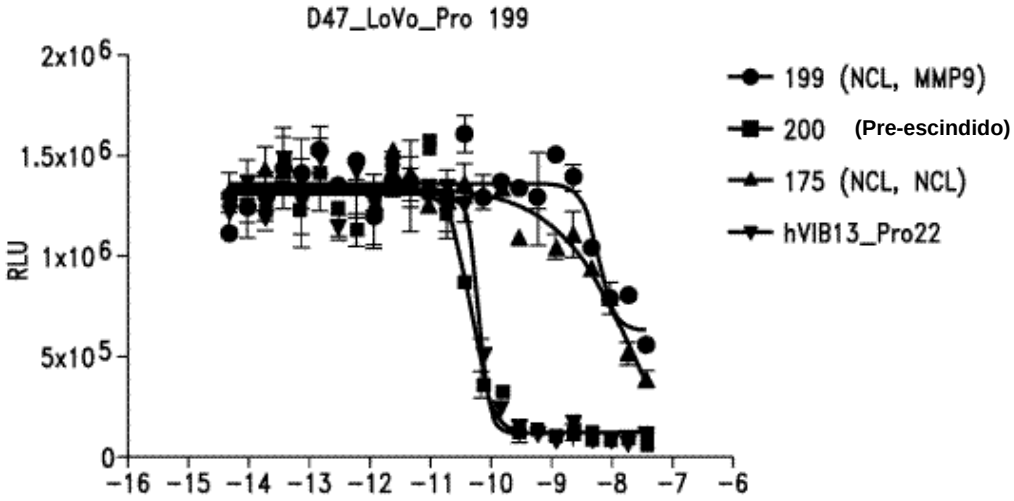
Figura 52


D47_HT-29_Pro199
199
175
199 (Pre-escindido)
hVIB13_Pro22
205
51
RLU
8X106
6X106
4X106
2X106
0
-16
-15
-14
-13
-12
-11
-10
-9
-8
-7
-6
Log de concentración (M)
Constructo
EC50 (pM)
199
199 escindido
175
hVIB13_Pro22
51
205
164.60
184.40
4.54
123.2
>100x
40x



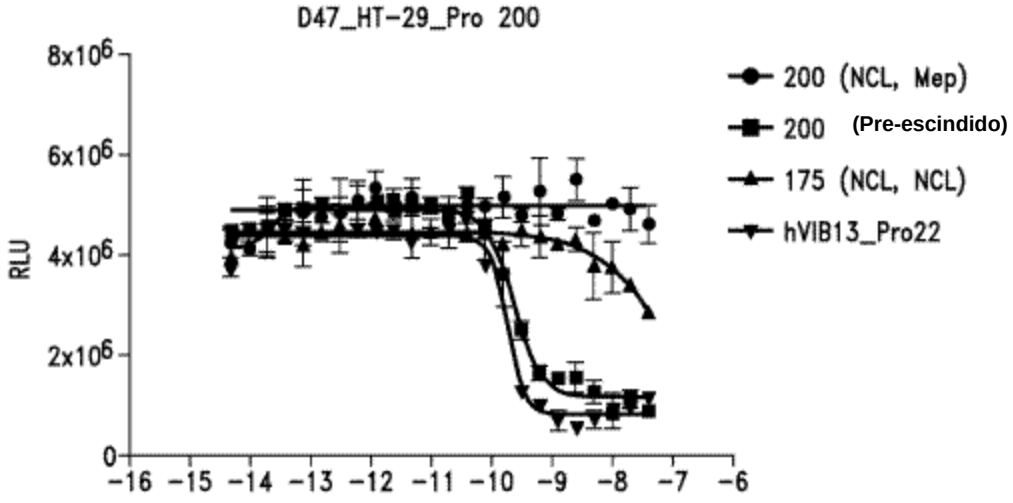

| | EC50 |
|---|---|
| 199 (NCL, MMP9) | 1.657e-008 |
| 199 (Pre-escindido) | 1.646e-010 |
| 175 (NCL, NCL) | 7.461e-008 |
| hVIB13_Pro22 | 1.844e-010 |

Figura 53A



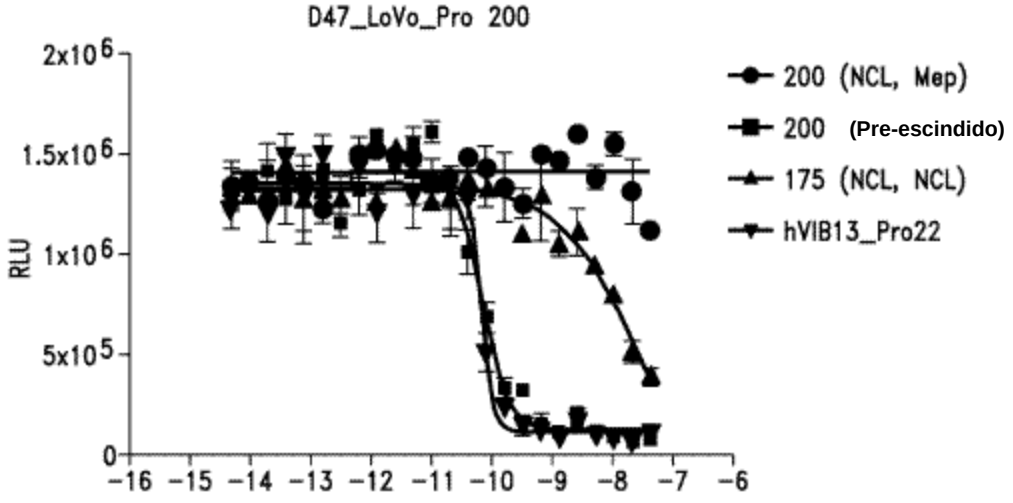

| | EC50 |
|---|---|
| 199 (NCL, MMP9) | 6.344e-009 |
| 199 (Pre-escindido) | 4.912e-011 |
| 175 (NCL, NCL) | 3.882e-008 |
| hVIB13_Pro22 | 6.75e-011 |

Figura 53B




| | EC50 |
|---|---|
| 200 (NCL, Mep) | 2.256e-014 |
| 200 (Pre-escindido) | 2.343e-010 |
| 175 (NCL, NCL) | 7.461e-008 |
| hVIB13_Pro22 | 1.844e-010 |

Figura 54A




| | EC50 |
|---|---|
| 200 (NCL, Mep) | ~4.648e-013 |
| 200 (Pre-escindido) | 6.76e-011 |
| 175 (NCL, NCL) | 3.882e-008 |
| hVIB13_Pro22 | 6.75e-011 |

Figura 54B

Figura 55

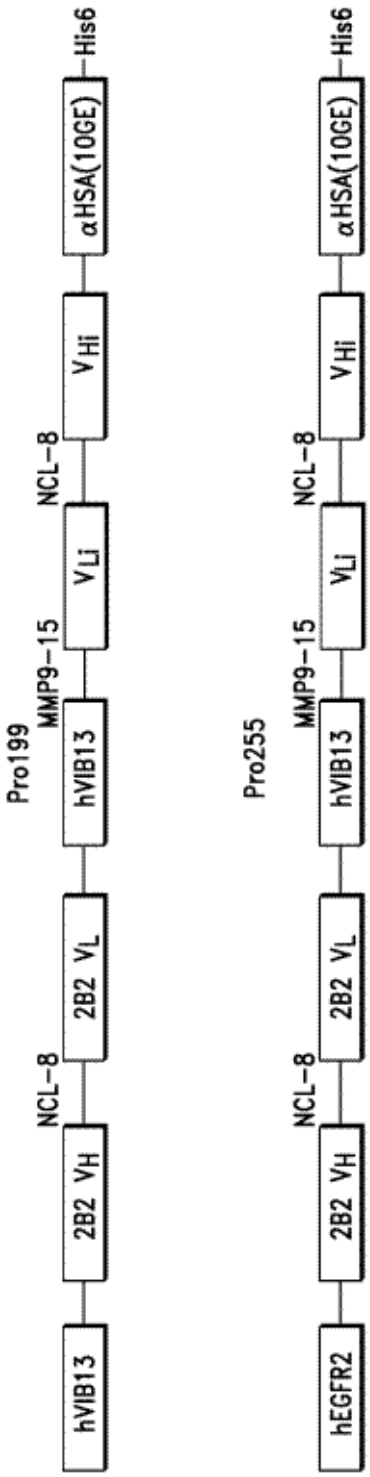
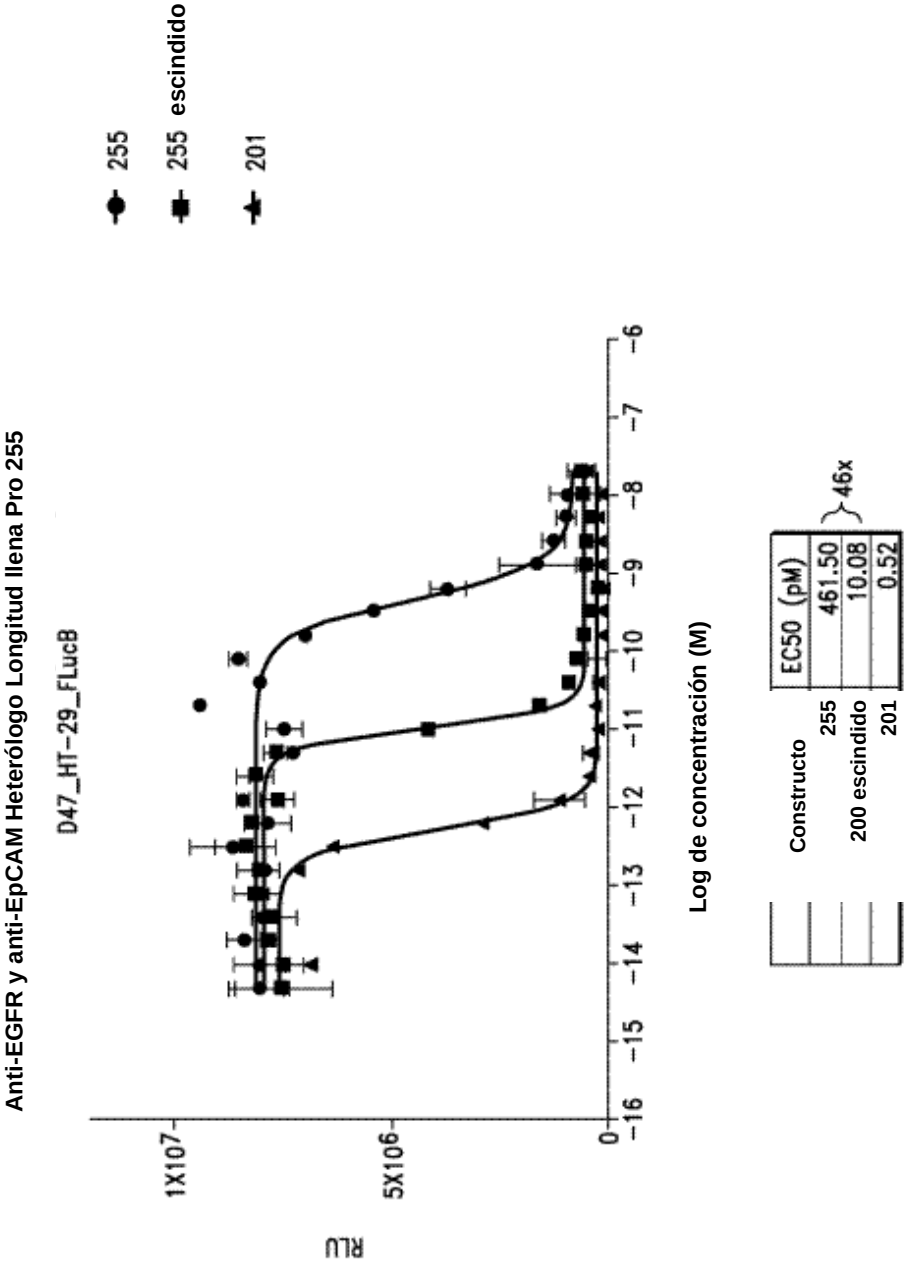

Pro199
hVIB13
NCL-8
2B2 VH
2B2 VL
MMP9-15
hVIB13
VLi
NCL-8
VHi
αHSA(10GE)
His6
Pro255
hEGFR2
NCL-8
2B2 VH
2B2 VL
MMP9-15
hVIB13
VLi
NCL-8
VHi
αHSA(10GE)
His6

Figura 56


Anti-EGFR y anti-EpCAM Heterólogo Longitud llena Pro 255
D47_HT-29_FLucB
255
255 escindido
201
RLU
1X10^7
5X10^6
0
-16
-15
-14
-13
-12
-11
-10
-9
-8
-7
-6
Log de concentración (M)
Constructo
EC50 (pM)
255
461.50
200 escindido
10.08
201
0.52
46x

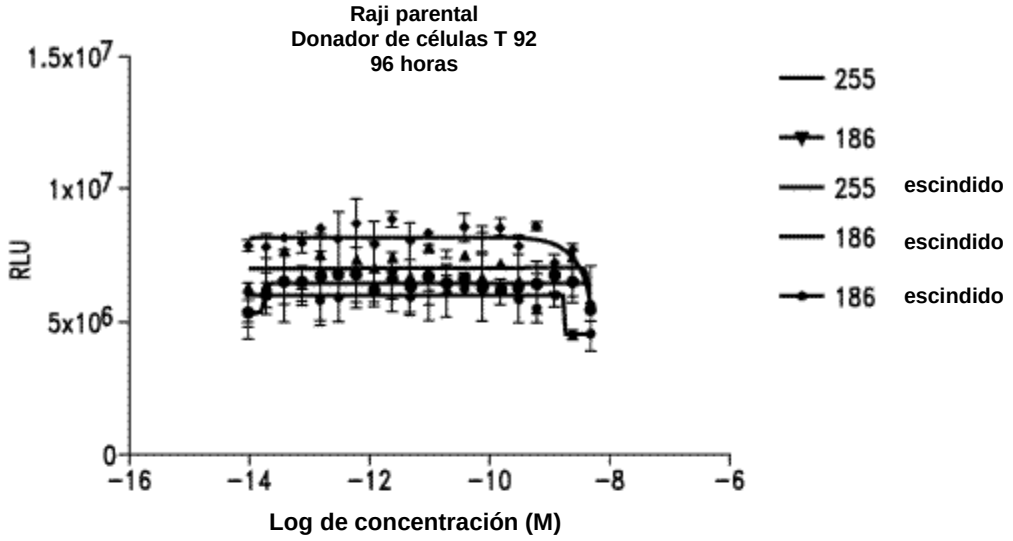



Figura 57A

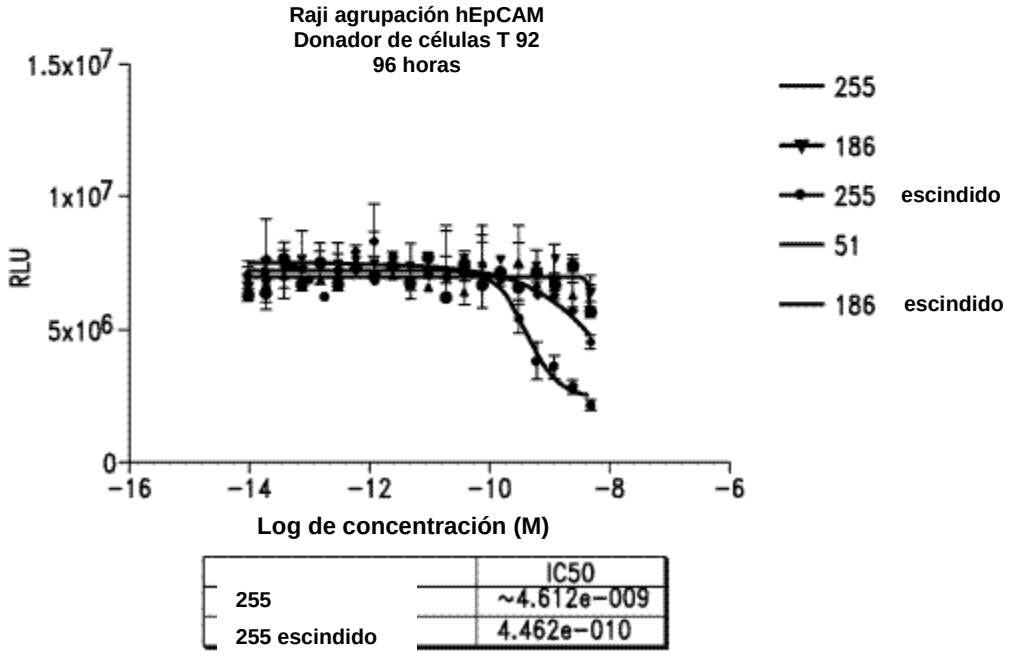
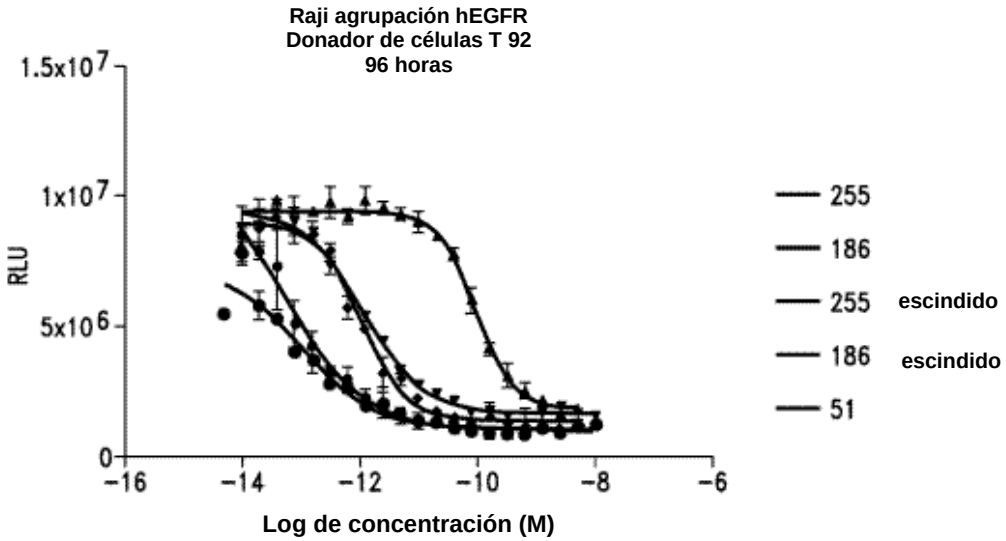
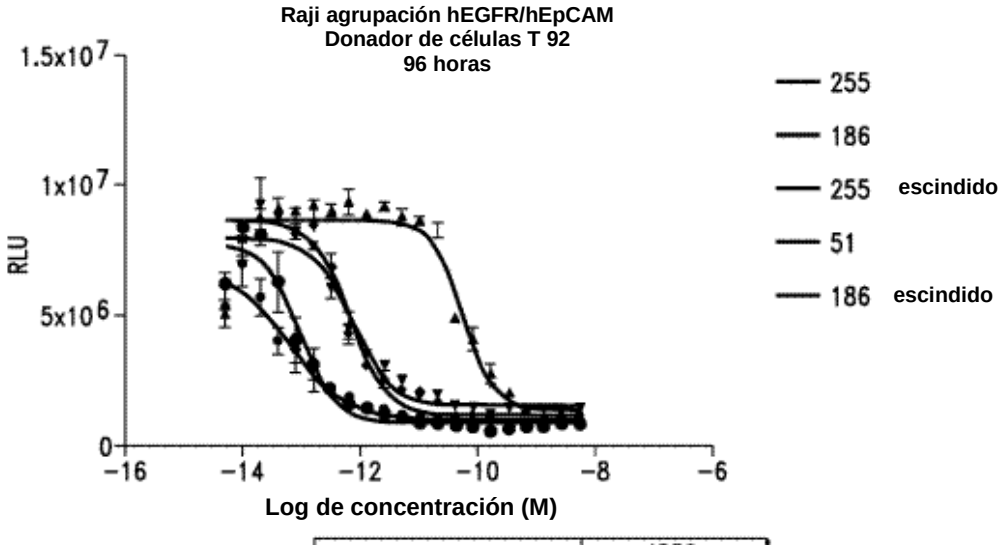



Figura 57B




| | IC50 |
|---|---|
| 255 | 9.205e−011 |
| 186 | 1.132e−012 |
| 255 escindido | 1.082e−012 |
| 186 escindido | 1.013e−013 |
| 51 | 5.329e−014 |

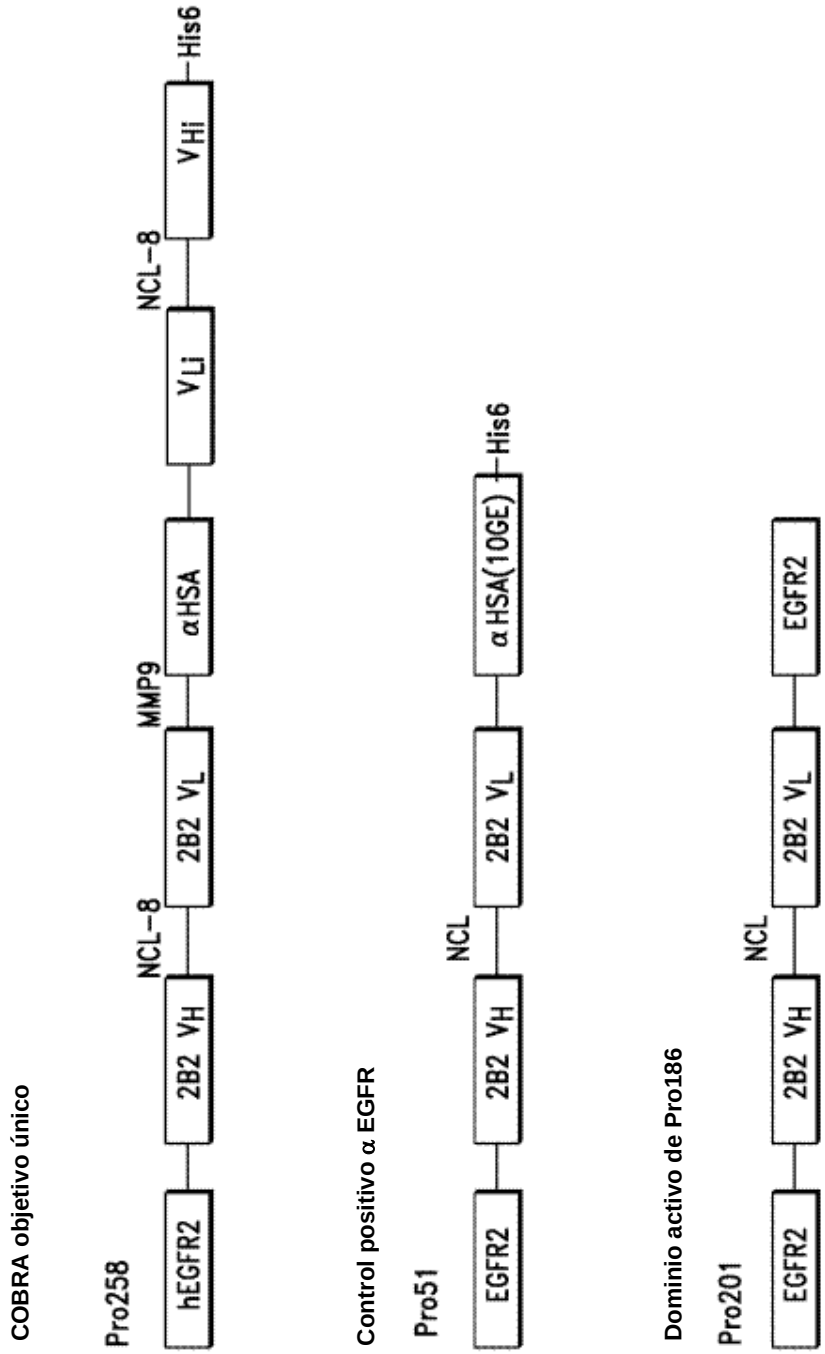
Figura 57C

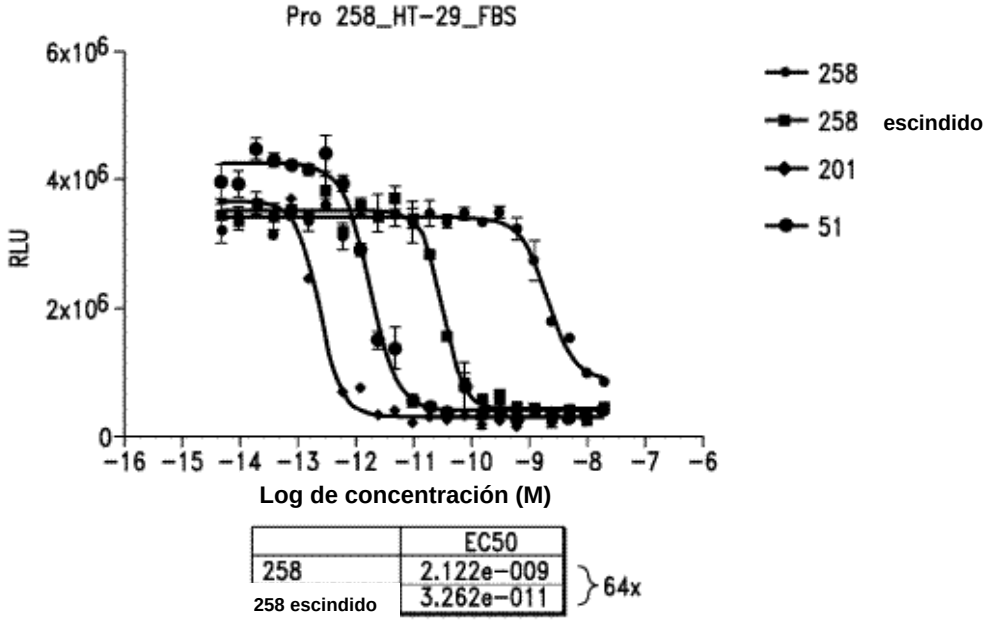



| | IC50 |
|---|---|
| 255 | 5.29e−011 |
| 186 | 7.07e−013 |
| 255 escindido | 6.288e−013 |
| 51 | 9.237e−014 |
| 186 escindido | 5.862e−014 |

Figura 57D

Figura 58

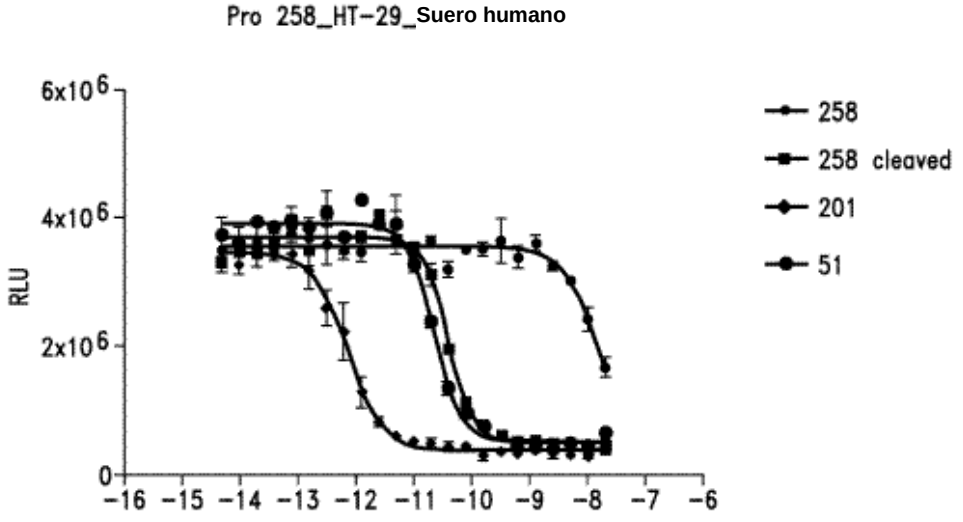

• COBRA objetivo único
Pro258
hEGFR2
2B2 VH
NCL-8
2B2 VL
MMP9
αHSA
VLi
NCL-8
VHi
His6
• Control positivo α EGFR
Pro51
EGFR2
2B2 VH
NCL
2B2 VL
α HSA(10GE)
His6
• Dominio activo de Pro186
Pro201
EGFR2
2B2 VH
NCL
2B2 VL
EGFR2




| | EC50 |
|---|---|
| 258 | 2.122e−009 |
| 258 escindido | 3.262e−011 |

64x

Figura 59A




| | EC50 |
|---|---|
| 258 | 1.51e−008 |
| 258 cleaved | 3.921e−011 |

387x

Figura 59B

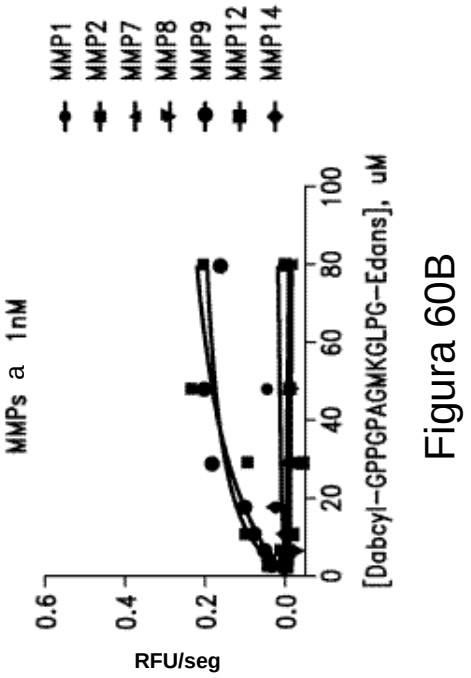



Figura 60B

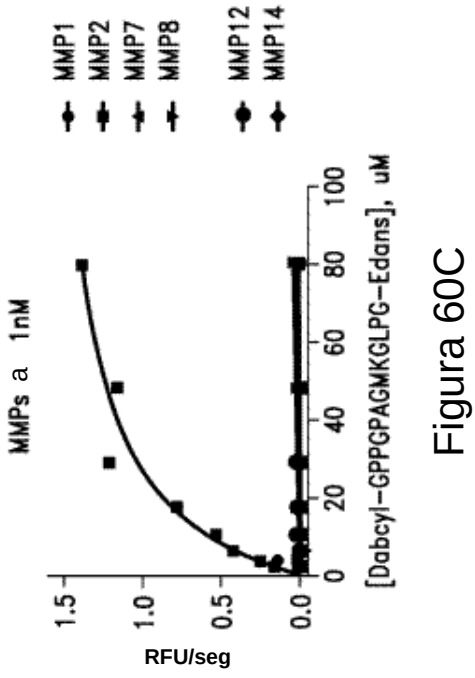



Figura 60C

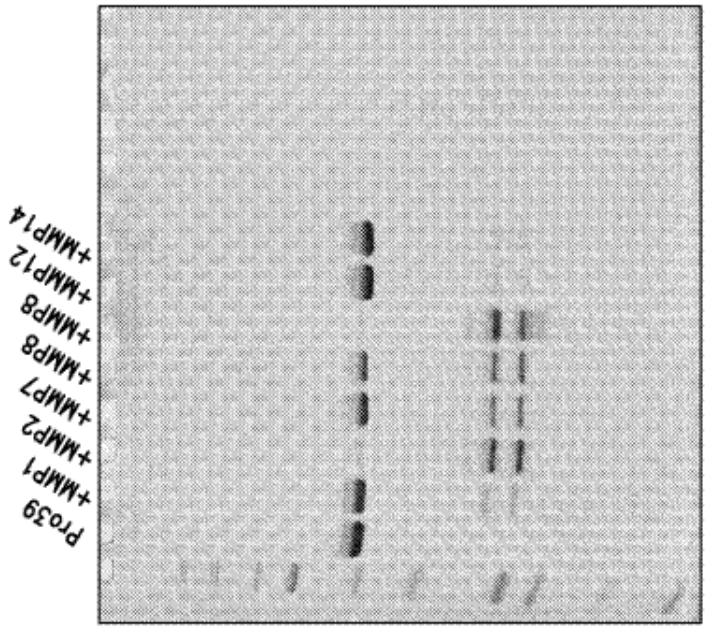



Figura 60A

# Figura 61A

**Formato 2**

Pro186 – EGFR2/MMP9 (aEGFR),

Pro225 – hF7/MMP9 (aB7H3)

Pro226 – hF12/MMP9 (aB7H3)

Pro233 – hEGFR2/MMP9 (aEGFR)

Pro311 – h77.2/MMP9 (aFOLR1)

Pro312 – h59.3/MMP9 (aFOLR1)

Pro313 – h22.4/MMP9 (aFOLR1)

Pro495 – hF7 MMP9 Vli2 + Vhi2 (aB7H3)

**Formato 2 - heterólogo**

Pro246 – hEGFR1/hEGFR2 MMP9 (aEGFR)

Pro254 – hEGFR2/hEGFR1 MMP9 (aEGFR)

Pro255 – hEGFR2/h13 MMP9 (aEGFR/aEpCAM)

Pro256 – h13/hEGFR2 MMP9 (aEpCAM/aEGFR)

Pro420 – h77.2/hEGFR2 MMP9 (aFOLR1/aEGFR)

Pro421 – hEGFR2/h77.2 MMP9 (aEGFR/aFOLR1)

Pro432 - h13/hEGFR1 MMP9 (aEpCAM/aEGFR)

Pro479 – hF7/hF12 MMP9 (aB7H3)

Pro480 – hF12/hF7 MMP9 (aB7H3)

**Hemis de direccionamiento doble (Formato 3)**

Pro448 – h77.2/hEGFR2 MMP9 VH (aFOLR1/aEGFR)

Pro449 – hEGFR2/h77.2 MMP9 VH (aEGFR/aFOLR1)

Pro450 – h77.2/hEGFR2 MMP9 VL (aFOLR1/aEGFR)

Pro451 – hEGFR2/h77.2 MMP9 VL (aEGFR/aFOLR1)

# Figura 61B

**Formato 1**

Pro140 – EGFR2 MMP9 (aEGFR)

Pro140b – EGFR2 Meprin (aEGFR)

**Formato 2 - Variantes del enlazador escindible**

Pro187 – EGFR2/Meprin (aEGFR)

Pro221 – EGFR2/KLK7-6 (aEGFR)

Pro222 – EGFR2/KLK7-13 (aEGFR)

Pro223 – EGFR2/KLK7-11 (aEGFR)

Pro224 – EGFR2/KLK7-10 (aEGFR)

Pro393 – EGFR2/S9 (aEGFR)

Pro394 – EGFR2/ST14MV (aEGFR)

Pro395 – EGFR2/CathS (aEGFR)

Pro396 – EGFR2/MMP9v (aEGFR)

Pro429 – EGFR2/Meprin/GranzymeB (aEGFR)

Pro430 – EGFR2/MMP9-2 (aEGFR)

Pro431 – EGFR2/ST14MS (aEGFR)

**Formato 4**

Pro258 – hEGFR2 MMP9 (aEGFR)

Pro356 – hEGFR1 MMP9 (aEGFR)

Pro359 – hF7 MMP9 (aB7H3)

Pro388 – h77.2 MMP9 (aFOLR1)

Pro364 – h59.3 MMP9 (aFOLR1)

# Figura 62A

**Pro140 (Formato 1)**

QVKLEESGGGSVQTGGSLRLTCAAS**GRTSRSYGMG**WFRQAPGKEREFVS**GISWRGDST**
**GYADSVKG**RFTISRDNAKNTVDLQMNSLKPEDTAIYYCAA**AAGSAWYGTLYEYDY**WGQG
TQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGK
GLEWVA**RIRSKYNNYATYYADQVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HAN**
**FGNSYISYWAY**WGQGTLVTVSS/*GPAGMKGL*/QTVVTQEPSLTVSPGGTVTLTC**ASSTGA**
**VTSGNYPN**WVQQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGKAALTLSGVQPEDEAE
YYC**TLWYSNRWV**FGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAAS**GR**
**TSRSYGMG**WFRQAPGKEREFVS**GISWRGDSTGYADSVKG**RFTISRDNAKNTVDLQMNSL
KPEDTAIYYCAA**AAGSAWYGTLYEYDY**WGQGTQVTVSS/*SGGPGPAGMKGLPGS*/QTVV
TQEPSLTVSPGGTVTLTC**GSSTGAVTSGNYPN**WVQQKPGQAPRGLIG**DYKDDDDK**GTPA
RFSGSLLGGKAALTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL/GGGSGGGS/EVQ
LVESGGGLVQPGGSLKLSCAAS**GFTFNKYAMN**WVRQAPGKGLEWVA**RIRSKYDYKDDD**
**DKADSVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGT
LVTVSS/GGGGSGGGS/EVQLVESGGGLVQPGNSLRLSCAAS**GFTFSKFGMS**WVRQAPG
KGLEWVS**SISGSGRDTLYAESVKG**RFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI**GGSLS**
**V**SSQGTLVTVSS (SEQ ID NO:143)

**Pro140b Formato 1**

QVKLEESGGGSVQTGGSLRLTCAAS**GRTSRSYGMG**WFRQAPGKEREFVS**GISWRGDST**
**GYADSVKG**RFTISRDNAKNTVDLQMNSLKPEDTAIYYCAA**AAGSAWYGTLYEYDY**WGQG
TQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGK
GLEWVA**RIRSKYNNYATYYADQVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HAN**
**FGNSYISYWAY**WGQGTLVTVSS/*KKLADEPE*/QTVVTQEPSLTVSPGGTVTLTC**ASSTGAV**
**TSGNYPN**WVQQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGKAALTLSGVQPEDEAEY
YC**TLWYSNRWV**FGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAAS**GRT**
**SRSYGMG**WFRQAPGKEREFVS**GISWRGDSTGYADSVKG**RFTISRDNAKNTVDLQMNSLK
PEDTAIYYCAA**AAGSAWYGTLYEYDY**WGQGTQVTVSS/*GGGSKKLADEPEGGGS*/QTVVT
QEPSLTVSPGGTVTLTC**GSSTGAVTSGNYPN**WVQQKPGQAPRGLIG**DYKDDDDK**GTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL/GGGSGGGS/EVQL
VESGGGLVQPGGSLKLSCAAS**GFTFNKYAMN**WVRQAPGKGLEWVA**RIRSKYDYKDDDD**
**KADSVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGTL
VTVSS/GGGGSGGGS/EVQLVESGGGLVQPGNSLRLSCAAS**GFTFSKFGMS**WVRQAPGK
GLEWVS**SISGSGRDTLYAESVKG**RFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI**GGSLSV**
SSQGTLVTVSS (SEQ ID NO:144)

Figura 62B

**Pro186 Formato 2**

QVKLEESGGGSVQTGGSLRLTCAAS**GRTSRSYGMG**WFRQAPGKEREFVS**GISWRGDST**
**GYADSVKG**RFTISRDNAKNTVDLQMNSLKPEDTAIYYCAA**AAGSAWYGTLYEYDY**WGQG
TQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGK
GLEWVA**RIRSKYNNYATYYADQVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HAN**
**FGNSYISYWAY**WGQGTLVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTC**ASSTGA**
**VTSGNYPN**WVQQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGKAALTLSGVQPEDEAE
YYC**TLWYSNRWV**FGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAAS**GR**
**TSRSYGMG**WFRQAPGKEREFVS**GISWRGDSTGYADSVKG**RFTISRDNAKNTVDLQMNSL
KPEDTAIYYCAA**AAGSAWYGTLYEYDY**WGQGTQVTVSS/*SGGPGPAGMKGLPGS*/QTVV
TQEPSLTVSPGGTVTLTC**GSSTGAVTSGNYPN**WVQQKPGQAPRGLIG**DYKDDDDK**GTPA
RFSGSLLGGKAALTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL/GGGSGGGS/EVQ
LVESGGGLVQPGGSLKLSCAAS**GFTFNKYAMN**WVRQAPGKGLEWVA**RIRSKYDYKDDD**
**DKADSVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGT
LVTVSS/GGGGSGGGS/EVQLVESGGGLVQPGNSLRLSCAAS**GFTFSKFGMS**WVRQAPG
KGLEWVS**SISGSGRDTLYAESVKG**RFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI**GGSLS**
**V**SSQGTLVTVSS (SEQ ID NO:145)

**Pro187 Formato 2**

QVKLEESGGGSVQTGGSLRLTCAAS**GRTSRSYGMG**WFRQAPGKEREFVS**GISWRGDST**
**GYADSVKG**RFTISRDNAKNTVDLQMNSLKPEDTAIYYCAA**AAGSAWYGTLYEYDY**WGQG
TQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGK
GLEWVA**RIRSKYNNYATYYADQVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HAN**
**FGNSYISYWAY**WGQGTLVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTC**ASSTGA**
**VTSGNYPN**WVQQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGKAALTLSGVQPEDEAE
YYC**TLWYSNRWV**FGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAAS**GR**
**TSRSYGMG**WFRQAPGKEREFVS**GISWRGDSTGYADSVKG**RFTISRDNAKNTVDLQMNSL
KPEDTAIYYCAA**AAGSAWYGTLYEYDY**WGQGTQVTVSS/*GGGSKKLADEPEGGGS*/QTVV
TQEPSLTVSPGGTVTLTC**GSSTGAVTSGNYPN**WVQQKPGQAPRGLIG**DYKDDDDK**GTPA
RFSGSLLGGKAALTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL/GGGSGGGS/EVQ
LVESGGGLVQPGGSLKLSCAAS**GFTFNKYAMN**WVRQAPGKGLEWVA**RIRSKYDYKDDD**
**DKADSVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGT
LVTVSS/GGGGSGGGS/EVQLVESGGGLVQPGNSLRLSCAAS**GFTFSKFGMS**WVRQAPG
KGLEWVS**SISGSGRDTLYAESVKG**RFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI**GGSLS**
**V**SSQGTLVTVSS (SEQ ID NO:146)

# Figura 62C

**Pro225 (enlazador FL aB7H3 hF7 MMP9) Formato 2**

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGST
VYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCAPSRRT
FHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDNSKNTLYLQMNSLR
AEDTAVYYCAAGGATTQRATEASYDYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVT
VSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:147)

**Pro226 (enlazador FL aB7H3 hF12 MMP9) Formato 2**

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTS
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGTLVT
VSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW
VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS
YISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSG
NYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTL
WYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCEASPRTFSTY
SMAWFRQAPGKERSFVAAINWSGGNTSYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA
VYYCAAGGVLAHHNYEYDYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEPSLTV
SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLG
GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGL
VQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDR
FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/**GGG
GSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSIS
GSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTV
SS/HHHHHH (SEQ ID NO:148)

Figura 62D

**Pro233 (Pro186 humanizado) Formato 2**

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRPGGSLTLSCAASGRT
SRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNSLYLQMNSLR
AEDTALYYCAAAAGSAWYGTLYEYDYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVT
VSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:149)

**Pro311 (enlazador FL aFOLR1 h77.2 MMP9) Formato 2**

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYAD
SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGTLVTVSS/**GGGSGG
GS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNN
YATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ
GTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKP
GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGG
GTKLTVL/**GGGSGGGS**/QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPG
NEREFVAIINSIGITNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIYW
GQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGN
YPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV
LWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKY
AMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKT
EDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/**GGGGSGGGS**/EVQLVESGGGLVQ
PGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRD
NAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/HHHHHH (SEQ ID NO:150)

Figura 62E

**Pro312 (enlazador FL aFOLR1 h59.3 MMP9)**

QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQAPGKQREWVAVTHSDYSTN
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCKHYGIDYWGQGTLVTVSS/**GGGS**
**GGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKY
NNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYW
GQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQ
KPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVF
GGGTKLTVL/**GGGSGGGS**/QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQA
PGKQREWVAVTHSDYSTNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCKHYGI
DYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVT
SGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTF
NKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNN
LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/**GGGGSGGGS**/EVQLVESGGGL
VQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTIS
RDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/HHHHHH (SEQ ID
NO:151)

**Pro313 (enlazador FL aFOLR1 h22.4 MMP9) formato 2**

QVQLVESGGGLVQPGGSLRLSCEASGTTFSRDVMGWYRQAPGKQRELVAIISRGGSTNY
ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNANTATWGRVFWGQGTLVTVSS/**G**
**GGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIR
SKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW
AYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNW
VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNR
WVFGGGTKLTVL/**GGGSGGGS**/QVQLVESGGGLVQPGGSLRLSCEASGTTFSRDVMGWY
RQAPGKQRELVAIISRGGSTNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAN
TATWGRVFWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEPSLTVSPGGTVTLTCG
SSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQ
PEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLS
CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKN
TAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/**GGGGSGGGS**/EV
QLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA
ESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/HHHHHH
(SEQ ID NO:152)

# Figura 62F

**Pro246 (FL haEGFR1/haEGFR2 heterólogo COBRA con enlazador MMP9)**

EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVVAINWSSGSTY
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGYQINSGNYNFKDYEYDYWGQ
GTLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPG
KGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA
NFGNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTG
AVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE
YYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRPGGSLTLSCAASGR
TSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNSLYLQMNSL
RAEDTALYYCAAAAGSAWYGTLYEYDYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVV
TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPA
RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDD
KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLV
TVSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKG
LEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:153)

**Pro256 (FL haEpCAM VIB13/haEGFR1 heterólogo COBRA enlazador MMP9)**

QVQLVESGGGLVQPGGSLTLSCAASGTGSIFSINLMGWYRQAPGKQRELVARITSGDSTV
YADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCNLLLRSSPGATTPYWGQGTLVTV
SS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWV
ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI
SYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNY
PNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWY
SNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGM
GWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALY
YCAAAAGSAWYGTLYEYDYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEPSLTV
SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLG
GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGL
VQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDR
FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/**GGG
GSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSIS
GSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTV
SS/HHHHHH (SEQ ID NO:154)

Figura 62G

**Pro420 (FL aFOLR1 h77.2/haEGFR1 heterólogo COBRA enlazador MMP9)**

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYAD
SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGTLVTVSS/**GGGSGG**
**GS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNN
YATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ
GTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKP
GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGG
GTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPG
KEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAAAAGS
AWYGTLYEYDYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEPSLTVSPGGTVTLT
CGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSG
VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLK
LSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDS
KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/**GGGGSGGGS**/
EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTL
YAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/HHHHH
H (SEQ ID NO:155)

**Pro421 (FL haEGFR1/aFOLR1 h77.2 heterólogo COBRA enlazador MMP9)**

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVQLVESGGGLVQPGGSLRLSCAASGFT
VSNSVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDT
AVYVCNRNFDRIYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEPSLTVSPGGTVT
LTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTL
SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGS
LKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDD
SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/**GGGGSGGGS**
/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTL
YAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/HHHHH
H (SEQ ID NO:156)

Figura 62H

**Pro393 (enlazador Pro186 S9)**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/***GARLQSAAPAGLKGAG***/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVT
VSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:157)

**Pro394 (enlazador Pro186 ST14(MV)**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/***GGGSFTRQARVVGGGS***/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVT
VSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:158)

# Figura 62I

**Pro395 (enlazador Pro186 CatS)**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/***GGGSARLQSAAPGGGS***/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVT
VSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:159)

**Pro396 (enlazador Pro186 MMP9v)**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/***GSGGPGPAGMHGLPGGS***/QTVV
TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPA
RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDD
KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLV
TVSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKG
LEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:160)

# Figura 62J

**Pro429 (enlazador Pro186 Meprina/granzimaB)**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/***SGGGVYADSLEDGGGS***/QTVVTQ
EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARF
SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLV
ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKA
DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTV
SS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE
WVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQ
GTLVTVSS/HHHHHH (SEQ ID NO:161)

**Pro430 (enlazador Pro186 MMP9-2)**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/***SGGPGPAGLKGAPGS***/QTVVTQE
PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFS
GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVE
SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKA
DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTV
SS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE
WVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQ
GTLVTVSS/HHHHHH (SEQ ID NO:162)

Figura 62K

**Pro431 (enlazador Pro186 ST14(MS)**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/***GGGSLSGRSDNHGGGS***/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVT
VSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:163)

**Pro258 (Pro186 con un dominio aEGFR sencillo y un dominio aHSA central)**

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWVFGGGTKLTVL/***SGGPGPAGMKGLPGS***/EVQLVESGGGLVQPGNSLRLS
CAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYL
QMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/**GGGGSGGGS**/QTVVTQEPSLTVSPG
GTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKA
ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQP
GGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTIS
RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/HHHHHH
(SEQ ID NO:164)

Figura 62L

**Pro221**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/***SGGGQNPYSAGRGGGS***/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVT
VSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:165)

**Pro222**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/***SGGGQNPYSAGGGSGG***/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVT
VSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:166)

Figura 62M

**Pro223**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/***SGGGRNVYSAGGGSGG***/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVT
VSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:167)

**Pro224**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/***SGGGQNTWSAGKGGGS***/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVT
VSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:168)

Figura 62N

**Pro254**

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLRLSCAASGRT
FSSYAMGWFRQAPGKEREFVVAINWSSGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRA
EDTAVYYCAAGYQINSGNYNFKDYEYDYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVV
TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPA
RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDD
KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLV
TVSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKG
LEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:169)

**Pro255**

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVQLVESGGGLVQPGGSLTLSCAASGTG
SIFSINLMGWYRQAPGKQRELVARITSGDSTVYADSVKGRFTISRDNSKNTLYLQMNSLRP
EDTAVYYCNLLLRSSPGATTPYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEPSL
TVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSL
LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGG
GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/**G**
**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVS
SISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV
TVSS/HHHHHH (SEQ ID NO:170)

Figura 62O

**Pro262**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG
LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTLVTVSS/**GGGGSGGGGSGGGGS**/QTVVTQEPSLTVSPGGTVTLT
CASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQ
PEDEAEYYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLT
CAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVD
LQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/***SGGPGPAGMKGLPG***
***S***/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDD
KGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGG**
**GS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYD
YKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYW
GQGTLVTVSS/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVR
QAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGTLVTVSS/HHHHHH (SEQ ID NO:171)

**Pro356**

EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVVAINWSSGSTY
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGYQINSGNYNFKDYEYDYWGQ
GTLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPG
KGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA
NFGNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTG
AVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE
YYCTLWYSNRWVFGGGTKLTVL/***SGGPGPAGMKGLPGS***/EVQLVESGGGLVQPGNSLRL
SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLY
LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/**GGGGSGGGS**/QTVVTQEPSLTVSPG
GTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKA
ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQP
GGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTIS
RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/HHHHHH
(SEQ ID NO:172)

# Figura 62P

**Pro359**

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGST
VYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWVFGGGTKLTVL/***SGGPGPAGMKGLPGS***/EVQLVESGGGLVQPGNSLRLS
CAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYL
QMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/**GGGGSGGGS**/QTVVTQEPSLTVSPG
GTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKA
ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQP
GGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTIS
RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/HHHHHH
(SEQ ID NO:173)

**Pro364**

QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQAPGKQREWVAVTHSDYSTN
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCKHYGIDYWGQGTLVTVSS/**GGGS
GGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKY
NNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYW
GQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQ
KPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVF
GGGTKLTVL/***SGGPGPAGMKGLPGS***/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGM
SWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVY
YCTIGGSLSVSSQGTLVTVSS/**GGGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCGSSTGAV
TSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAE
YYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGF
TFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQM
NNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/HHHHHH (SEQ ID NO:174)

Figura 62Q

**Pro388**

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYAD
SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGTLVTVSS/**GGGSGG**
**GS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNN
YATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ
GTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKP
GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGG
GTKLTVL/***SGGPGPAGMKGLPGS***/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSW
VRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT
IGGSLSVSSQGTLVTVSS/**GGGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSG
NYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC
VLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNK
YAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLK
TEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/HHHHHH (SEQ ID NO:175)

Figura 62R

**Pro432**

QVQLVESGGGLVQPGGSLTLSCAASGTGSIFSINLMGWYRQAPGKQRELVARITSGDSTV
YADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCNLLLRSSPGATTPYWGQGTLVTV
SS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWV
ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI
SYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNY
PNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWY
SNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAM
GWFRQAPGKEREFVVAINWSSGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY
YCAAGYQINSGNYNFKDYEYDYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEPSL
TVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSL
LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGG
GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/**G**
**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVS
SISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV
TVSS/HHHHHH (SEQ ID NO:176)

**Pro448**

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYAD
SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGTLVTVSS/**GGGGSG**
**GGS**/QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRG
DSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYW
GQGTLVTVSS/**GGGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQ
APGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV
RHANFGNSYISYWAYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEPSLTVSPGGT
VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAAL
TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGGSGGGS**/EVQLVESGGGLVQP
GNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN
AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/HHHHHH (SEQ ID NO:177)

# Figura 62S

**Pro449**

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQG
TLVTVSS/**GGGGSGGGS**/QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTP
GNEREFVAIINSIGITNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIY
WGQGTLVTVSS/**GGGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR
QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
VRHANFGNSYISYWAYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEPSLTVSPG
GTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKA
ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGGSGGGS**/EVQLVESGGGLV
QPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISR
DNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/HHHHHH (SEQ ID
NO:178)

**Pro450**

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYAD
SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGTLVTVSS/**GGGGSG
GGS**/QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRG
DSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYW
GQGTLVTVSS/**GGGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQ
QKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWV
FGGGTKLTVL/***SGGPGPAGMKGLPGS***/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA
MNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTE
DTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/**GGGGSGGGS**/EVQLVESGGGLVQP
GNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN
AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/HHHHHH (SEQ ID NO:179)

Figura 62T

**Pro451**

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQG
TLVTVSS/**GGGGSGGGS**/QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTP
GNEREFVAIINSIGITNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNRNFDRIY
WGQGTLVTVSS/**GGGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNW
VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNR
WVFGGGTKLTVL/***SGGPGPAGMKGLPGS***/EVQLVESGGGLVQPGGSLKLSCAASGFTFNK
YAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLK
TEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/**GGGGSGGGS**/EVQLVESGGGLV
QPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISR
DNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/HHHHHH (SEQ ID
NO:180)

**Pro479**

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGST
VYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCEASPRT
FSTYSMAWFRQAPGKERSFVAAINWSGGNTSYADSVKGRFTISRDNSKNTLYLQMNSLRA
EDTAVYYCAAGGVLAHHNYEYDYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEP
SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSG
SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVES
GGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKAD
SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVS
S/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEW
VSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT
LVTVSS/HHHHHH (SEQ ID NO:181)

Figura 62U

**Pro480**

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTS
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGTLVT
VSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW
VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS
YISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSG
NYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTL
WYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTY
HMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDT
AVYYCAAGGATTQRATEASYDYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVTQEPS
LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGS
LLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESG
GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSV
KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS/
**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWV
SSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTL
VTVSS/HHHHHH (SEQ ID NO:182)

**Pro495**

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGST
VYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCAPSRRT
FHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDNSKNTLYLQMNSLR
AEDTAVYYCAAGGATTQRATEASYDYWGQGTLVTVSS/***SGGPGPAGMKGLPGS***/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKDDAPGTPARF
SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLV
ESGGGLVQPGGSLKLSCAASGFTFNKHAMNWVRQAPGKGLEWVARIRSKYNNYATAYAD
SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVS
S/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEW
VSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT
LVTVSS/HHHHHH (SEQ ID NO:183)

LISTADO DE SECUENCIAS

<110> MAVERICK THERAPEUTICS, INC.

<120> PROTEÍNAS DE UNIÓN CONDICIONALMENTE ACTIVADAS RESTRINGIDAS

<130> 118459-5005

<150> 62/555,943
<151> 2017-09-08

<150> 62/586,627
<151> 2017-11-15

<150> 62/587,318
<151> 2017-11-16

<160> 272

<170> PatentIn versión 3.5

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

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

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

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

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

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

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

Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

<210> 2
<211> 10
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<213> Secuencia Artificial

<220>
<223> Sintético sdCDR1 -Focalización sdAbs - alfa-EGFR1

<400> 2

Gly Arg Thr Phe Ser Ser Tyr Ala Met Gly
1 5 10

<210> 3
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR2 -Focalización sdAbs - alfa-EGFR1

<400> 3

Ile Asn Trp Ser Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 4
<211> 18

<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR3 – Focalización sdAbs - alfa-EGFR1

<400> 4

Gly Tyr Gln Ile Asn Ser Gly Asn Tyr Asn Phe Lys Asp Tyr Glu Tyr
1 5 10 15

Asp Tyr

<210> 5
<211> 124
<212> PRT
<213> Secuencia Artificial

<220>
<223> Dominio de unión de antígeno sintético -Focalización sdAbs - alfa-EGFR2

<400> 5

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

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

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<220>
<223> Sintético sdCDR1 -Focalización sdAbs - alfa-EGFR2

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Gly Arg Thr Ser Arg Ser Tyr Gly Met Gly
1 5 10

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<211> 17
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR2 -Focalización sdAbs - alfa-EGFR2

<400> 7

Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 8
<211> 15
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<213> Secuencia Artificial

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<223> Sintético sdCDR3 -Focalización sdAbs - alfa-EGFR2

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Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr
1 5 10 15

<210> 9
<211> 127
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<223> Dominio de Unión de Antígeno Sintético-Focalización sdAbs - h-alfa-EGFR1

<400> 9

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

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

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

Val Ala Ile Asn Trp Ser Ser 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 Ala Gly Tyr Gln Ile Asn Ser Gly Asn Tyr Asn Phe Lys Asp Tyr

100 105 110

Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 10
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<213> Secuencia Artificial

<220>
<223> Sintético sdCDR1 -Focalización sdAbs - h-alfa-EGFR1

<400> 10

Gly Arg Thr Phe Ser Ser Tyr Ala Met Gly
1 5 10

<210> 11
<211> 16
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<213> Secuencia Artificial

<220>
<223> Sintético sdCDR2 -Focalización sdAbs - h-alfa-EGFR1

<400> 11

Ile Asn Trp Ser Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 12
<211> 18
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<213> Secuencia Artificial

<220>
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Gly Tyr Gln Ile Asn Ser Gly Asn Tyr Asn Phe Lys Asp Tyr Glu Tyr
1 5 10 15

Asp Tyr

<210> 13
<211> 124
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<220>
<223> Dominio de Unión de Antígeno Sintético-Focalización sdAbs - h-alfa-EGFR2

<400> 13

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

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

<210> 14
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<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR1 -Focalización sdAbs - h-alfa-EGFR2

<400> 14

Gly Arg Thr Ser Arg Ser Tyr Gly Met Gly
1 5 10

<210> 15
<211> 17
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR2 -Focalización sdAbs - h-alfa-EGFR2

<400> 15

Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 16
<211> 15
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR3 -Focalización sdAbs - h-alfa-EGFR2

<400> 16

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr
1 5 10 15

<210> 17
<211> 114
<212> PRT
<213> Secuencia Artificial

<220>
<223> Dominio de Unión de Antígeno Sintético-Focalización sdAbs - alfa-FOLR1
h77-2

<400> 17

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

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

Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val
35 40 45

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

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

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

Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser

<210> 18
<211> 10

<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR1 -Focalización sdAbs - alfa-FOLR1 h77-2

<400> 18

Gly Phe Thr Val Ser Asn Ser Val Met Ala
1 5 10

<210> 19
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR2 -Focalización sdAbs - alfa-FOLR1 h77-2

<400> 19

Ile Ile Asn Ser Ile Gly Ile Thr Asn Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 20
<211> 6
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<220>
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<400> 20

Asn Phe Asp Arg Ile Tyr
1 5

<210> 21
<211> 113
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<223> Dominio de Unión de Antígeno Sintético-Focalización sdAbs - alfa-FOLR1
h59.3

<400> 21

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

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

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

Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

Ser

<210> 22
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR1 -Focalización sdAbs - alfa-FOLR1 h59.3

<400> 22

Gly Asn Thr Phe Ser Ile Ser Ala Met Gly
1 5 10

<210> 23
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR2 -Focalización sdAbs - alfa-FOLR1 h59.3

<400> 23

Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 24
<211> 5
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR3 -Focalización sdAbs - alfa-FOLR1 h59.3

<400> 24

Tyr Gly Ile Asp Tyr
1 5

<210> 25
<211> 117
<212> PRT
<213> Secuencia Artificial

<220>
<223> Dominio de Unión de Antígeno Sintético-Focalización sdAbs - alfa-FOLR1
h22-4

<400> 25

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

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

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

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

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

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

Ala Asn Thr Ala Thr Trp Gly Arg Val Phe Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
        115
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<210> 26
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
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<400> 26

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Gly Thr Thr Phe Ser Arg Asp Val Met Gly
1               5                   10
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<210> 27
<211> 16
<212> PRT

<213> Secuencia Artificial

<220>
<223> Sintético sdCDR2 -Focalización sdAbs - alfa-FOLR1 h22-4

<400> 27

Ile Ile Ser Arg Gly Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 28
<211> 9
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR3 -Focalización sdAbs - alfa-FOLR1 h22-4

<400> 28

Asn Thr Ala Thr Trp Gly Arg Val Phe
1 5

<210> 29
<211> 124
<212> PRT
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<220>
<223> Dominio de Unión de Antígeno Sintético-Focalización sdAbs - alfa-B7H3
hF7

<400> 29

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

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

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

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

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

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

Ala Ala Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp
100 105 110

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

<210> 30
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR1 -Focalización sdAbs - alfa-B7H3 hF7

<400> 30

Arg Arg Thr Phe His Thr Tyr His Met Gly
1 5 10

<210> 31
<211> 17
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR2 -Focalización sdAbs - alfa-B7H3 hF7

<400> 31

Val Ile Asn Trp Ser Gly Gly Ser Thr Val Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 32
<211> 15
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR3 -Focalización sdAbs - alfa-B7H3 hF7

<400> 32

Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp Tyr
1 5 10 15

<210> 33
<211> 122
<212> PRT
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<220>
<223> Dominio de Unión de Antígeno Sintético-Focalización sdAbs - alfa-B7H3
hF12

<400> 33

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

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

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

Ala Ala Ile Asn Trp Ser Gly Gly Asn 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 Ala Gly Gly Val Leu Ala His His Asn Tyr Glu Tyr Asp Tyr Trp
100 105 110

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

<210> 34
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR1 -Focalización sdAbs - alfa-B7H3 hF12

<400> 34

Pro Arg Thr Phe Ser Thr Tyr Ser Met Ala
1 5 10

<210> 35
<211> 17
<212> PRT
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<223> Sintético sdCDR2 -Focalización sdAbs - alfa-B7H3 hF12

<400> 35

Ala Ile Asn Trp Ser Gly Gly Asn Thr Ser Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 36
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Gly Gly Val Leu Ala His His Asn Tyr Glu Tyr Asp Tyr
1 5 10

<210> 37
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<220>
<223> Dominio de Unión de Antígeno Sintético-Focalización sdAbs - alfa-EpCAM
h13

<400> 37

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
100 105 110

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

<210> 38
<211> 12
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR1 -Focalización sdAbs - alfa-EpCAM h13

<400> 38

Gly Thr Gly Ser Ile Phe Ser Ile Asn Leu Met Gly
1 5 10

<210> 39
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR2 -Focalización sdAbs - alfa-EpCAM h13

<400> 39

Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 40
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<220>
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Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr
1 5 10

<210> 41
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<220>
<223> Dominio de Unión de Antígeno Sintético-Focalización sdAbs - alfa-EpCAM
h23

<400> 41

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
100 105 110

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

<210> 42
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<220>
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<400> 42

Gly Ser Phe Ser Ala Leu Trp Ala Met Arg
1 5 10

<210> 43
<211> 15
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético sdCDR2 -Focalización sdAbs - alfa-EpCAM h23

<400> 43

Ser Ser Arg Gly Gly Thr Thr Ser Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 44
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<220>
<223> Sintético sdCDR3 -Focalización sdAbs - alfa-EpCAM h23

<400> 44

Ile Asp Gly His Leu Ala Tyr
1 5

<210> 45
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<220>
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<400> 45

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr 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

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 46
<211> 10

<212> PRT
<213> Secuencia Artificial

<220>
<223> SintéticosdCDR1 - alfa-HSA dominio de extensión de vida media

<400> 46

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser
1 5 10

<210> 47
<211> 17
<212> PRT
<213> Secuencia Artificial

<220>
<223> SintéticosdCDR2 - alfa-HSA dominio de extensión de vida media

<400> 47

Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys
1 5 10 15

Gly

<210> 48
<211> 6
<212> PRT
<213> Secuencia Artificial

<220>
<223> SintéticosdCDR3 - alfa-HSA dominio de extensión de vida media

<400> 48

Gly Gly Ser Leu Ser Val
1 5

<210> 49
<211> 109
<212> PRT
<213> Secuencia Artificial

<220>
<223> Dominio de Unión de Antígeno Sintético- alfa-CD3 scFv - Dominio alfa-CD3V(L)

<400> 49

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

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

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn
85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 50
<211> 14
<212> PRT
<213> Secuencia Artificial

<220>
<223> SintéticoaVLCDR1 - alfa CD3 scFV Dominio - alfa-CD3 V(L)

<400> 50

Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
1 5 10

<210> 51
<211> 7
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético aVLsdCDR2 - alfa CD3 scFV Dominio - alfa-CD3 V(L)

<400> 51

Gly Thr Lys Phe Leu Val Pro
1 5

<210> 52
<211> 9
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético aVLsdCDR3 - alfa CD3 scFV Dominio - alfa-CD3 V(L)

<400> 52

Thr Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 53
<211> 110
<212> PRT
<213> Secuencia Artificial

<220>
<223> Dominio de Unión de Antígeno Sintético- alfa-CD3 scFv Dominio - alfa-CD3V(Li)

<400> 53

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

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

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45

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

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly
65                  70                  75                  80

Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser
                85                  90                  95

Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110
```

<210> 54
<211> 14
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético iVLCDR1 - alfa CD3 scFV Dominio - alfa-CD3 V(Li)

<400> 54

```
Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
1               5                  10
```

<210> 55
<211> 8
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético iVLsdCDR2 - alfa CD3 scFV Dominio - alfa-CD3 V(Li)

<400> 55

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 56
<211> 9
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético iVLsdCDR3 - alfa CD3 scFV Dominio - alfa-CD3 V(Li)

<400> 56

Val Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 57
<211> 109
<212> PRT
<213> Secuencia Artificial

<220>
<223> Dominio de Unión de Antígeno Sintético- alfa-CD3 scFv Dominio - alfa-CD3V(Li2)

<400> 57

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

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

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Lys Asp Asp Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 58
<211> 14
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético iVLCDR1 - alfa CD3 scFV Dominio - alfa-CD3 V(Li2)

<400> 58

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
1 5 10

<210> 59
<211> 7
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético iVLCDR2 - alfa CD3 scFV Dominio - alfa-CD3 V(Li2)

<400> 59

Gly Thr Lys Asp Asp Ala Pro
1 5

<210> 60
<211> 9
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético iVLCDR3 - alfa CD3 scFV Dominio - alfa-CD3 V(Li2)

<400> 60

Val Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 61
<211> 125
<212> PRT
<213> Secuencia Artificial

<220>
<223> Dominio de Unión de Antígeno Sintético- alfa-CD3 scFv Dominio - alfa-CD3V(H)

<400> 61

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

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

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

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 62
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético aVHCDR1 - alfa CD3 scFV Dominio - alfa-CD3 V(H)

<400> 62

Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn
1 5 10

<210> 63
<211> 19
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético aVHsdCDR2 - alfa CD3 scFV Dominio - alfa-CD3 V(H)

<400> 63

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln
1 5 10 15

Val Lys Asp

<210> 64
<211> 14
<212> PRT

<213> Secuencia Artificial

<220>
<223> Sintético aVHsdCDR3 - alfa CD3 scFV Dominio - alfa-CD3 V(H)

<400> 64

His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
1 5 10

<210> 65
<211> 126
<212> PRT
<213> Secuencia Artificial

<220>
<223> Dominio de Unión de Antígeno Sintético- alfa-CD3 scFv Dominio - alfa-CD3V(Hi)

<400> 65

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

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

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

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
50 55 60

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
65 70 75 80

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

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
100 105 110

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 66
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético iVHsdCDR1 - alfa CD3 scFV Dominio - alfa-CD3 V(Hi)

<400> 66

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn
1 5 10

<210> 67
<211> 20
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético iVHsdCDR2 - alfa CD3 scFV Dominio - alfa-CD3 V(Hi)

<400> 67

Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp
1 5 10 15

Ser Val Lys Asp
20

<210> 68
<211> 14
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético iVHsdCDR3 - alfa CD3 scFV Dominio - alfa-CD3 V(Hi)

<400> 68

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
1 5 10

<210> 69
<211> 125
<212> PRT
<213> Secuencia Artificial

<220>
<223> Dominio de Unión de Antígeno Sintético- alfa-CD3 scFv Dominio - alfa-CD3V(Hi2)

<400> 69

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

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

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

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Ala Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 70
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético iVHsdCDR1 - alfa CD3 scFV Dominio - alfa-CD3 V(Hi2)

<400> 70

Gly Phe Thr Phe Asn Lys His Ala Met Asn
1 5 10

<210> 71
<211> 19
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético iVHsdCDR2 - alfa CD3 scFV Dominio - alfa-CD3 V(Hi2)

<400> 71

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Ala Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 72
<211> 14
<212> PRT
<213> Secuencia Artificial

<220>

<223> Sintético iVHsdCDR3 - alfa CD3 scFV Dominio - alfa-CD3 V(Hi2)

<400> 72

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
1 5 10

<210> 73
<211> 15
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Sintético - alfa-CD3 scFV - Nomal, no-plegable

<400> 73

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

<210> 74
<211> 8
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Sintético - alfa-CD3 scFV - Restringido

<400> 74

Gly Gly Gly Ser Gly Gly Gly Ser
1 5

<210> 75
<211> 8
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - MMP 2/9

<400> 75

Gly Pro Ala Gly Met Lys Gly Leu
1 5

<210> 76
<211> 15
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - MMP 2/9

<400> 76

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
1 5 10 15

<210> 77
<211> 17
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - MMP 2/9

<400> 77

Ser Gly Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Gly
1 5 10 15

Ser

<210> 78
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Meprina A/B

<400> 78

Gly Gly Gly Gly Lys Lys Leu Ala Asp Glu Pro Glu Gly Gly Gly Ser

1 5 10 15

<210> 79
<211> 8
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Meprina A/B

<400> 79

Lys Lys Leu Ala Asp Glu Pro Glu
1 5

<210> 80
<211> 13
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Meprina A/B (Variante, alta eficiencia)

<400> 80

Gly Gly Gly Lys Phe Leu Ala Asp Glu Pro Glu Gly Gly
1 5 10

<210> 81
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Catepsina S,K,L

<400> 81

Ser Gly Gly Gly Ala Arg Leu Gln Ser Ala Ala Pro Gly Gly Gly Ser
1 5 10 15

<210> 82

<211> 8
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Catepsina S,K,L

<400> 82

Ala Arg Leu Gln Ser Ala Ala Pro
1 5

<210> 83
<211> 18
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Meprina/Grancima B

<400> 83

Ser Gly Gly Gly Gly Val Tyr Ala Asp Ser Leu Glu Asp Gly Gly Gly
1 5 10 15

Gly Ser

<210> 84
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Meprina/Grancima B

<400> 84

Gly Val Tyr Ala Asp Ser Leu Glu Asp Gly
1 5 10

<210> 85
<211> 16

<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Matriptasa/apu (MS)

<400> 85

Gly Gly Gly Ser Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser
1 5 10 15

<210> 86
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Matriptasa/apu (MS)

<400> 86

Gly Leu Ser Gly Arg Ser Asp Asn His Gly
1 5 10

<210> 87
<211> 17
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Matriptasa (MV)

<400> 87

Ser Gly Gly Gly Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly Gly
1 5 10 15

Ser

<210> 88
<211> 9
<212> PRT

<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Matriptasa (MV)

<400> 88

Ser Phe Thr Arg Gln Ala Arg Val Val
1 5

<210> 89
<211> 14
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Catepsina S/MMP9/Meprina A

<400> 89

Ala Arg Leu Gln Ser Ala Ala Pro Ala Gly Leu Lys Gly Ala
1 5 10

<210> 90
<211> 13
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - MMP9 (Variante, alta eficiencia)

<400> 90

Gly Gly Pro Gly Pro Ala Gly Met His Gly Leu Pro Gly
1 5 10

<210> 91
<211> 13
<212> PRT
<213> Secuencia Artificial

<220>

<223> Vinculado Plegable Sintético - MMP9 (Variante, baja eficiencia)

<400> 91

Gly Gly Pro Gly Pro Ala Gly Met Glu Gly Leu Pro Gly
1 5 10

<210> 92
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Trombina 1

<400> 92

Gly Gly Gly Gly Leu Val Pro Arg Gly Ser Leu Gly Gly Gly Gly Ser
1 5 10 15

<210> 93
<211> 15
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Trombina 2

<400> 93

Ser Ser Gly Gly Gly Met Pro Arg Ser Phe Arg Gly Gly Gly Ser
1 5 10 15

<210> 94
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - Enteropeptidasa/Banderín

<400> 94

Gly Gly Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly Ser
1 5 10 15

<210> 95
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - KLK7-6

<400> 95

Ser Gly Gly Gly Gln Asn Pro Tyr Ser Ala Gly Arg Gly Gly Gly Ser
1 5 10 15

<210> 96
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - KLK7-13

<400> 96

Ser Gly Gly Gly Gln Asn Pro Tyr Ser Ala Gly Gly Gly Ser Gly Gly
1 5 10 15

<210> 97
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - KLK7-11

<400> 97

Ser Gly Gly Gly Arg Asn Val Tyr Ser Ala Gly Gly Gly Ser Gly Gly
1 5 10 15

<210> 98

<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - KLK7-10

<400> 98

Ser Gly Gly Gly Gln Asn Thr Trp Ser Ala Gly Lys Gly Gly Gly Ser
1 5 10 15

<210> 99
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - apu

<400> 99

Gly Gly Gly Ser His Thr Gly Arg Ser Ala Tyr Phe Gly Gly Gly Ser
1 5 10 15

<210> 100
<211> 8
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - MMP7

<400> 100

Lys Arg Ala Leu Gly Leu Pro Gly
1 5

<210> 101
<211> 24
<212> PRT
<213> Secuencia Artificial

<220>

<223> Sitio de escisión de peptidasa sintética - MMP7

<220>
<221> características_diversas
<222> (1)..(8)
<223> X puede ser Asp o Glu

<220>
<221> características_diversas
<222> (17)..(24)
<223> X puede ser Asp o Arg

<400> 101

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Pro Leu Ala Leu Trp Arg Ser
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20

<210> 102
<211> 8
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - MMP9

<400> 102

Pro Arg Ser Thr Leu Ile Ser Thr
1 5

<210> 103
<211> 5
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - MMP9

<400> 103

Leu Glu Ala Thr Ala
1 5

<210> 104
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - MMP11

<400> 104

Gly Gly Ala Ala Asn Leu Val Arg Gly Gly
1 5 10

<210> 105
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - MMP14

<400> 105

Ser Gly Arg Ile Gly Phe Leu Arg Thr Ala
1 5 10

<210> 106
<211> 6
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - MMP

<400> 106

Pro Leu Gly Leu Ala Gly
1 5

<210> 107

<211> 6
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - MMP

<220>
<221> características_diversas
<222> (6)..(6)
<223> Xaa puede ser cualquier aminoácido que se produce de forma natural

<400> 107

Pro Leu Gly Leu Ala Xaa
1 5

<210> 108
<211> 7
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - MMP

<220>
<221> características_diversas
<222> (5)..(5)
<223> X puede ser Met o Glu

<400> 108

Pro Leu Gly Cys Xaa Ala Gly
1 5

<210> 109
<211> 8
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - MMP

<400> 109

Glu Ser Pro Ala Tyr Tyr Thr Ala
1 5

<210> 110
<211> 6
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - MMP

<400> 110

Arg Leu Gln Leu Lys Leu
1 5

<210> 111
<211> 7
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - MMP

<400> 111

Arg Leu Gln Leu Lys Ala Cys
1 5

<210> 112
<211> 7
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - MMP2, MMP9, MMP14

<220>
<221> características_diversas

<222> (1)..(3)
<223> X puede ser Cys o Ile o Thr

<220>
<221> características_diversas
<222> (5)..(5)
<223> X puede ser His o On o Phe

<400> 112

Glu Pro Xaa Gly Xaa Tyr Leu
1 5

<210> 113
<211> 5
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Activador del Plasminaógeno tipo uroquinasa(apu)

<400> 113

Ser Gly Arg Ser Ala
1 5

<210> 114
<211> 4
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Activador del Plasminaógeno tipo uroquinasa (apu)

<400> 114

Asp Ala Phe Lys
1

<210> 115
<211> 5
<212> PRT

<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Activador del Plasminaógeno tipo uroquinasa (apu)

<400> 115

Gly Gly Gly Arg Arg
1 5

<210> 116
<211> 4
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética – Enzima Lisosomal

<400> 116

Gly Phe Leu Gly
1

<210> 117
<211> 4
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Enzima Lisosomal

<400> 117

Ala Leu Ala Leu
1

<210> 118
<211> 2
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Enzima Lisosomal

<400> 118

Phe Lys
1

<210> 119
<211> 3
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética – Catepsina B

<400> 119

Asn Leu Leu
1

<210> 120
<211> 6
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética – Catepsina D

<220>
<221> características_diversas
<222> (4)..(4)
<223> X puede ser Glu o Thr

<400> 120

Pro Ile Cys Xaa Phe Phe
1 5

<210> 121
<211> 8
<212> PRT

<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética – Catepsina K

<400> 121

Gly Gly Pro Arg Gly Leu Pro Gly
1 5

<210> 122
<211> 6
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Antígeno prostático específico

<400> 122

His Ser Ser Lys Leu Gln
1 5

<210> 123
<211> 7
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Antígeno prostático específico

<400> 123

His Ser Ser Lys Leu Gln Leu
1 5

<210> 124
<211> 9
<212> PRT
<213> Secuencia Artificial

<220>

<223> Sitio de escisión de peptidasa sintética - Antígeno prostático específico

<400> 124

His Ser Ser Lys Leu Gln Glu Asp Ala
1 5

<210> 125
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Proteasa del virus del herpes simple

<400> 125

Leu Val Leu Ala Ser Ser Ser Phe Gly Tyr
1 5 10

<210> 126
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Proteasa Hiv

<400> 126

Gly Val Ser Gln Asn Tyr Pro Ile Val Gly
1 5 10

<210> 127
<211> 10
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Proteasa Cmv

<400> 127

Gly Val Val Gln Ala Ser Cys Arg Leu Ala
1 5 10

<210> 128
<211> 4
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Trombina

<220>
<221> características_diversas
<222> (2)..(2)
<223> X puede ser Pro o Ile o Pro

<400> 128

Phe Xaa Arg Ser
1

<210> 129
<211> 6
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Trombina

<400> 129

Asp Pro Arg Ser Phe Leu
1 5

<210> 130
<211> 6
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Trombina

<400> 130

Pro Pro Arg Ser Phe Leu
1 5

<210> 131
<211> 4
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Caspasa-3

<400> 131

Asp Glu Val Asp
1

<210> 132
<211> 5
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Caspasa-3

<400> 132

Asp Glu Val Asp Pro
1 5

<210> 133
<211> 8
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Caspasa-3

<400> 133

Lys Gly Ser Gly Asp Val Glu Gly
1 5

<210> 134
<211> 6
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Enzima de conversión de interleucina 1-beta

<400> 134

Gly Trp Glu His Asp Gly
1 5

<210> 135
<211> 7
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Enteropeptidasa

<400> 135

Glu Asp Asp Asp Asp Lys Ala
1 5

<210> 136
<211> 9
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Fap

<400> 136

Lys Gln Glu Gln Asn Pro Gly Ser Thr
1 5

<210> 137
<211> 6

<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Calicreína 2

<400> 137

Gly Lys Ala Phe Arg Arg
1 5

<210> 138
<211> 4
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Plasmina

<400> 138

Asp Ala Phe Lys
1

<210> 139
<211> 4
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Plasmina

<400> 139

Asp Val Leu Lys
1

<210> 140
<211> 4
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Plasmina

<400> 140

Asp Ala Phe Lys
1

<210> 141
<211> 7
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sitio de escisión de peptidasa sintética - Cresta

<400> 141

Ala Leu Leu Leu Ala Leu Leu
1 5

<210> 142
<211> 121
<212> PRT
<213> Secuencia Artificial

<220>
<223> Dominio de Unión de Antígeno Sintético- alfa-HSA extensión de dominio de media vida

<400> 142

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr 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

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser His His His His His His
115 120

<210> 143
<211> 889
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro140 Formato1

<400> 143

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

```
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Pro Ala Gly Met Lys Gly Leu Gln Thr Val Val Thr Gln Glu
            260                 265                 270
```

```
Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
```

450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
500 505 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
515 520 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
530 535 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545 550 555 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp
565 570 575

Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
580 585 590

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
595 600 605

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
610 615 620

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu
625 630 635 640

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
645 650 655

Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala
660 665 670

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
675 680 685

Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp
690 695 700

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
705 710 715 720

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
725 730 735

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
740 745 750

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
755 760 765

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
770 775 780

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
785 790 795 800

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
805 810 815

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
820 825 830

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
835 840 845

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
850 855 860

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
865 870 875 880

Gln Gly Thr Leu Val Thr Val Ser Ser
885

<210> 144
<211> 890
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro140b Formato 1

<400> 144

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

```
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Lys Lys Leu Ala Asp Glu Pro Glu Gln Thr Val Val Thr Gln Glu
            260                 265                 270
```

```
Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
    450                 455                 460
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Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser Lys Lys
500 505 510

Leu Ala Asp Glu Pro Glu Gly Gly Gly Ser Gln Thr Val Val Thr Gln
515 520 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
530 535 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545 550 555 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
565 570 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
580 585 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
595 600 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
610 615 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625 630 635 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

645 650 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
660 665 670

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
675 680 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
690 695 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705 710 715 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
725 730 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
740 745 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
755 760 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
770 775 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785 790 795 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
805 810 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
820 825 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
835 840 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
850 855 860

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser
885 890

<210> 145
<211> 889
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro186 Formato2

<400> 145

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys

85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
500 505 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
515 520 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
530 535 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545 550 555 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp
565 570 575

Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
580 585 590

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
595 600 605

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
610 615 620

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu
625 630 635 640

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
645 650 655

Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala
660 665 670

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
675 680 685

Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp
690 695 700

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
705 710 715 720

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
725 730 735

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
740 745 750

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
755 760 765

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
770 775 780

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
785 790 795 800

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
805 810 815

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
820 825 830

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn

835 840 845

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
850 855 860

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
865 870 875 880

Gln Gly Thr Leu Val Thr Val Ser Ser
885

<210> 146
<211> 890
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro187 Formato 2

<400> 146

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

```
Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
```

275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser Lys Lys
500 505 510

Leu Ala Asp Glu Pro Glu Gly Gly Gly Ser Gln Thr Val Val Thr Gln
515 520 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
530 535 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545 550 555 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
565 570 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
580 585 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
595 600 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
610 615 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625 630 635 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
645 650 655

```
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
                805                 810                 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
            820                 825                 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
        835                 840                 845
```

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
850 855 860

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser
885 890

<210> 147
<211> 895
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro225 (FL aB7H3 hF7 MMP9 enlazador) Formato 2

<400> 147

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

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

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

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

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

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

```
Ala Ala Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
```

275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Arg Leu Ser Cys Ala Pro Ser Arg Arg Thr Phe His Thr Tyr His Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ala Val
420 425 430

Ile Asn Trp Ser Gly Gly Ser Thr Val Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
450 455 460

```
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala
465                 470                 475                 480

Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
            500                 505                 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
        515                 520                 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
    530                 535                 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545                 550                 555                 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp
                565                 570                 575

Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
            580                 585                 590

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
        595                 600                 605

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
    610                 615                 620

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu
625                 630                 635                 640

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
                645                 650                 655
```

```
Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala
            660                 665                 670

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
        675                 680                 685

Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp
    690                 695                 700

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
705                 710                 715                 720

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
                725                 730                 735

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
            740                 745                 750

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
        755                 760                 765

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
    770                 775                 780

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
785                 790                 795                 800

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
                805                 810                 815

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
            820                 825                 830

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
        835                 840                 845
```

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
850 855 860

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
865 870 875 880

Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 148
<211> 891
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro226 (FL aB7H3 hF12 MMP9 enlazador) Formato 2

<400> 148

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

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

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

Ala Ala Ile Asn Trp Ser Gly Gly Asn 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 Ala Gly Gly Val Leu Ala His His Asn Tyr Glu Tyr Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145                 150                 155                 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
            180                 185                 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
        195                 200                 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
                245                 250                 255

Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
            260                 265                 270

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser
```

275 280 285

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
290 295 300

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val
305 310 315 320

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
325 330 335

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
340 345 350

Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
355 360 365

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu
370 375 380

Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
385 390 395 400

Ser Cys Glu Ala Ser Pro Arg Thr Phe Ser Thr Tyr Ser Met Ala Trp
405 410 415

Phe Arg Gln Ala Pro Gly Lys Glu Arg Ser Phe Val Ala Ala Ile Asn
420 425 430

Trp Ser Gly Gly Asn Thr Ser Tyr Ala Asp Ser Val Lys Gly Arg Phe
435 440 445

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
450 455 460

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Gly Gly
465 470 475 480

Val Leu Ala His His Asn Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr
485 490 495

Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
500 505 510

Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
515 520 525

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
530 535 540

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
545 550 555 560

Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys
565 570 575

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
580 585 590

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
595 600 605

Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu
610 615 620

Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val
625 630 635 640

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser
645 650 655

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val
660 665 670

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser
675 680 685

Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp
690 695 700

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
705 710 715 720

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
725 730 735

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
740 745 750

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
755 760 765

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
770 775 780

Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
785 790 795 800

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
805 810 815

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
820 825 830

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr
835 840 845

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
850 855 860

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
865 870 875 880

Val Thr Val Ser Ser His His His His His His
885 890

<210> 149
<211> 895
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro233 (Pro186 humanizado) Formato 2

<400> 149

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala

275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
500 505 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
515 520 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
530 535 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545 550 555 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp
565 570 575

Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
580 585 590

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
595 600 605

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
610 615 620

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu
625 630 635 640

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
645 650 655

```
Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala
            660                 665                 670

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
        675                 680                 685

Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp
    690                 695                 700

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
705                 710                 715                 720

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
                725                 730                 735

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
            740                 745                 750

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
        755                 760                 765

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
    770                 775                 780

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
785                 790                 795                 800

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
                805                 810                 815

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
            820                 825                 830

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
        835                 840                 845
```

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
850 855 860

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
865 870 875 880

Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 150
<211> 875
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro311 (FL aFOLR1 h77.2 MMP9 enlazador) Formato 2

<400> 150

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

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

Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val
35 40 45

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

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

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

```
Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
        115                 120                 125

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys
    130                 135                 140

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg
145                 150                 155                 160

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys
                165                 170                 175

Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe
            180                 185                 190

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
        195                 200                 205

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala
    210                 215                 220

Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
                245                 250                 255

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
            260                 265                 270

Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
```

275 280 285

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
290 295 300

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
305 310 315 320

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
325 330 335

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
340 345 350

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser
355 360 365

Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
370 375 380

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
385 390 395 400

Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu
405 410 415

Arg Glu Phe Val Ala Ile Ile Asn Ser Ile Gly Ile Thr Asn Tyr Ala
420 425 430

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
435 440 445

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
450 455 460

Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr
465 470 475 480

Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
485 490 495

Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
500 505 510

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
515 520 525

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
530 535 540

Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys
545 550 555 560

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
565 570 575

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
580 585 590

Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu
595 600 605

Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val
610 615 620

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser
625 630 635 640

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val
645 650 655

```
Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser
            660                 665                 670

Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp
        675                 680                 685

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
    690                 695                 700

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
705                 710                 715                 720

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
                725                 730                 735

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
            740                 745                 750

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
        755                 760                 765

Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
    770                 775                 780

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
785                 790                 795                 800

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
                805                 810                 815

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr
            820                 825                 830

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
        835                 840                 845
```

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
850 855 860

Val Thr Val Ser Ser His His His His His His
865 870 875

<210> 151
<211> 873
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro312 (FL aFOLR1 h59.3 MMP9 enlazador)

<400> 151

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

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

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

Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
115 120 125

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
130 135 140

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln
145 150 155 160

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
165 170 175

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr
180 185 190

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
195 200 205

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn
210 215 220

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
225 230 235 240

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr
245 250 255

Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
260 265 270

Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr
275 280 285

Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile

290 295 300

Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly
305 310 315 320

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
325 330 335

Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp
340 345 350

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly
355 360 365

Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
370 375 380

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Pro Gly Asn Thr Phe
385 390 395 400

Ser Ile Ser Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg
405 410 415

Glu Trp Val Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp
420 425 430

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
435 440 445

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
450 455 460

Tyr Cys Lys His Tyr Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
465 470 475 480

```
Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu
                485                 490                 495

Pro Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
            500                 505                 510

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
        515                 520                 525

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
    530                 535                 540

Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr
545                 550                 555                 560

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
                565                 570                 575

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
            580                 585                 590

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
        595                 600                 605

Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
    610                 615                 620

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
625                 630                 635                 640

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
                645                 650                 655

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
            660                 665                 670
```

```
Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe
        675                 680                 685

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
    690                 695                 700

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly
705                 710                 715                 720

Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly
                725                 730                 735

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
            740                 745                 750

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
        755                 760                 765

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
    770                 775                 780

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
785                 790                 795                 800

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val
                805                 810                 815

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
            820                 825                 830

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
        835                 840                 845

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
    850                 855                 860
```

Val Ser Ser His His His His His His
865 870

<210> 152
<211> 881
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro313 (FL aFOLR1 h22.4 MMP9 enlazador) Formato 2

<400> 152

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

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

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

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

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

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

Ala Asn Thr Ala Thr Trp Gly Arg Val Phe Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
115 120 125

```
Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
    130                 135                 140

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn
145                 150                 155                 160

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
                165                 170                 175

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys
            180                 185                 190

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
        195                 200                 205

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
    210                 215                 220

Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
                245                 250                 255

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro
            260                 265                 270

Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr
        275                 280                 285

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro
    290                 295                 300

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala
```

305 310 315 320

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
325 330 335

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr
340 345 350

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
355 360 365

Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly
370 375 380

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser
385 390 395 400

Gly Thr Thr Phe Ser Arg Asp Val Met Gly Trp Tyr Arg Gln Ala Pro
405 410 415

Gly Lys Gln Arg Glu Leu Val Ala Ile Ile Ser Arg Gly Gly Ser Thr
420 425 430

Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
435 440 445

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
450 455 460

Thr Ala Val Tyr Tyr Cys Asn Ala Asn Thr Ala Thr Trp Gly Arg Val
465 470 475 480

Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro
485 490 495

```
Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr
            500                 505                 510

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
        515                 520                 525

Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
    530                 535                 540

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr
545                 550                 555                 560

Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
                565                 570                 575

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
            580                 585                 590

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
        595                 600                 605

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
    610                 615                 620

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
625                 630                 635                 640

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
                645                 650                 655

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            660                 665                 670

Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys
        675                 680                 685
```

```
Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
    690                 695                 700

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
705                 710                 715                 720

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser
                725                 730                 735

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
            740                 745                 750

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
        755                 760                 765

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
    770                 775                 780

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
785                 790                 795                 800

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
                805                 810                 815

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
            820                 825                 830

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
        835                 840                 845

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
    850                 855                 860

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His
865                 870                 875                 880
```

His

<210> 153
<211> 898
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro246 (FL haEGFR1/haEGFR2 heterólogo de COBRA con MMP9 enlazador)

<400> 153

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

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

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

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

Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
130 135 140

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
145 150 155 160

Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro
165 170 175

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
180 185 190

Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser
195 200 205

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
210 215 220

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly
225 230 235 240

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
245 250 255

Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val
260 265 270

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
275 280 285

Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
290 295 300

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly

305 310 315 320

Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
325 330 335

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
340 345 350

Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe
355 360 365

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
370 375 380

Ser Gln Val Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly
385 390 395 400

Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser
405 410 415

Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe
420 425 430

Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser
435 440 445

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
450 455 460

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr
465 470 475 480

Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr
485 490 495

```
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly
            500                 505                 510

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val
        515                 520                 525

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
    530                 535                 540

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
545                 550                 555                 560

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp
                565                 570                 575

Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser
            580                 585                 590

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
        595                 600                 605

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
    610                 615                 620

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly
625                 630                 635                 640

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
                645                 650                 655

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
            660                 665                 670

Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        675                 680                 685
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Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp
    690                 695                 700

Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
705                 710                 715                 720

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
                725                 730                 735

Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile
            740                 745                 750

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        755                 760                 765

Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
    770                 775                 780

Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala
785                 790                 795                 800

Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln
                805                 810                 815

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
            820                 825                 830

Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser
        835                 840                 845

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
    850                 855                 860

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
865                 870                 875                 880
```

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His
885 890 895

His His

<210> 154
<211> 893
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro256 (FL haEpCAM VIB13/haEGFR1 heterólogo de COBRA MMP9 enlazador)

<400> 154

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145 150 155 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
180 185 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
195 200 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225 230 235 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
245 250 255

Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
260 265 270

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser
275 280 285

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys

290 295 300

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val
305 310 315 320

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
325 330 335

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
340 345 350

Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
355 360 365

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Lys Leu
370 375 380

Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu Thr Leu
385 390 395 400

Ser Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met Gly Trp
405 410 415

Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly Ile Ser
420 425 430

Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe
435 440 445

Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn
450 455 460

Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala Ala Ala
465 470 475 480

Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp Gly Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
500 505 510

Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
515 520 525

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser
530 535 540

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
545 550 555 560

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp
565 570 575

Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
580 585 590

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
595 600 605

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
610 615 620

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
625 630 635 640

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
645 650 655

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn
660 665 670

```
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
        675                 680                 685

Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val
    690                 695                 700

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
705                 710                 715                 720

Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                725                 730                 735

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
            740                 745                 750

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        755                 760                 765

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    770                 775                 780

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
785                 790                 795                 800

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
                805                 810                 815

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
            820                 825                 830

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
        835                 840                 845

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
    850                 855                 860
```

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
865 870 875 880

Thr Leu Val Thr Val Ser Ser His His His His His His
885 890

<210> 155
<211> 885
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro420 (FL aFOLR1 h77.2/haEGFR1 heterólogo de COBRA MMP9 enlazador)

<400> 155

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

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

Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val
35 40 45

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

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

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

Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

```
Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
        115                 120                 125

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys
    130                 135                 140

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg
145                 150                 155                 160

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys
                165                 170                 175

Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe
            180                 185                 190

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
        195                 200                 205

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala
    210                 215                 220

Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
                245                 250                 255

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
            260                 265                 270

Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
        275                 280                 285

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
```

290 295 300

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
305 310 315 320

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
325 330 335

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
340 345 350

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser
355 360 365

Gly Gly Gly Ser Gln Val Lys Leu Val Glu Ser Gly Gly Gly Val Val
370 375 380

Arg Pro Gly Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr
385 390 395 400

Ser Arg Ser Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu
405 410 415

Arg Glu Phe Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr
420 425 430

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
435 440 445

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
450 455 460

Leu Tyr Tyr Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu
465 470 475 480

Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
485 490 495

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln
500 505 510

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
515 520 525

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
530 535 540

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
545 550 555 560

Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe
565 570 575

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
580 585 590

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
595 600 605

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
610 615 620

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625 630 635 640

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
645 650 655

Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
660 665 670

```
Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp
        675                 680                 685

Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg
    690                 695                 700

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr
705                 710                 715                 720

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn
                725                 730                 735

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
            740                 745                 750

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
        755                 760                 765

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu
    770                 775                 780

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp
785                 790                 795                 800

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
                805                 810                 815

Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe
            820                 825                 830

Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn
        835                 840                 845

Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly
    850                 855                 860
```

Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His
865 870 875 880

His His His His His
885

<210> 156
<211> 885
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro421 (FL haEGFR1/aFOLR1 h77.2 heterólogo de COBRA MMP9 enlazador)

<400> 156

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Asn Ser Val Met
405 410 415

Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val Ala Ile
420 425 430

Ile Asn Ser Ile Gly Ile Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg
435 440 445

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
450 455 460

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Val Cys Asn Arg Asn
465 470 475 480

```
Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
                485                 490                 495

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln
            500                 505                 510

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
        515                 520                 525

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
    530                 535                 540

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
545                 550                 555                 560

Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe
                565                 570                 575

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
            580                 585                 590

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
        595                 600                 605

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
    610                 615                 620

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
            660                 665                 670
```

```
Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp
        675                 680                 685

Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg
    690                 695                 700

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr
705                 710                 715                 720

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn
                725                 730                 735

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
            740                 745                 750

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
        755                 760                 765

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu
    770                 775                 780

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp
785                 790                 795                 800

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
                805                 810                 815

Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe
            820                 825                 830

Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn
        835                 840                 845

Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly
    850                 855                 860
```

Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His
865 870 875 880

His His His His His
885

<210> 157
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro393 (Pro186 S9 enlazador)

<400> 157

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

```
Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300
```

```
Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
    450                 455                 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465                 470                 475                 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
```

485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Ala Arg Leu Gln Ser
500 505 510

Ala Ala Pro Ala Gly Leu Lys Gly Ala Gly Gln Thr Val Val Thr Gln
515 520 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
530 535 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545 550 555 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
565 570 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
580 585 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
595 600 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
610 615 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625 630 635 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
645 650 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
660 665 670

```
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
                805                 810                 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
            820                 825                 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
        835                 840                 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
    850                 855                 860
```

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 158
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro394 (Pro186 ST14(MV) enlazador)

<400> 158

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

```
Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300
```

```
Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
    450                 455                 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465                 470                 475                 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495
```

```
Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser Phe Thr
            500                 505                 510

Arg Gln Ala Arg Val Val Gly Gly Gly Ser Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

675 680 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
690 695 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705 710 715 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
725 730 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
740 745 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
755 760 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
770 775 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785 790 795 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
805 810 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
820 825 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
835 840 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
850 855 860

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 159
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro395 (Pro186 CathS enlazador)

<400> 159

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser

115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser Ala Arg
500 505 510

Leu Gln Ser Ala Ala Pro Gly Gly Gly Ser Gln Thr Val Val Thr Gln
515 520 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
530 535 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545 550 555 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
565 570 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
580 585 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
595 600 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
610 615 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625 630 635 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
645 650 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
660 665 670

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
675 680 685

```
Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
                805                 810                 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
            820                 825                 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
        835                 840                 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
    850                 855                 860

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
```

865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 160
<211> 897
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro396 (Pro186 MMP9v enlazador)

<400> 160

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

```
Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
```

305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Ser Gly Gly Pro Gly
500 505 510

Pro Ala Gly Met His Gly Leu Pro Gly Gly Ser Gln Thr Val Val Thr
515 520 525

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
530 535 540

Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
545 550 555 560

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr
565 570 575

Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
580 585 590

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
595 600 605

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
610 615 620

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
625 630 635 640

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
645 650 655

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
660 665 670

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
675 680 685

```
Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys
    690                 695                 700

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
705                 710                 715                 720

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
                725                 730                 735

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser
            740                 745                 750

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
        755                 760                 765

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
    770                 775                 780

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
785                 790                 795                 800

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
                805                 810                 815

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
            820                 825                 830

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
        835                 840                 845

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
    850                 855                 860

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
865                 870                 875                 880
```

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His
885 890 895

His

<210> 161
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro429 (Pro186 Meprina/Grancima B enlazador)

<400> 161

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

```
Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
```

290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

```
Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Gly Val Tyr
            500                 505                 510

Ala Asp Ser Leu Glu Asp Gly Gly Gly Ser Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670
```

```
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
                805                 810                 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
            820                 825                 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
        835                 840                 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
    850                 855                 860
```

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 162
<211> 895
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro430 (Pro186 MMP9-2 enlazador)

<400> 162

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

```
Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300
```

```
Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
    450                 455                 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465                 470                 475                 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
```

485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
500 505 510

Ala Gly Leu Lys Gly Ala Pro Gly Ser Gln Thr Val Val Thr Gln Glu
515 520 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
530 535 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545 550 555 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp
565 570 575

Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
580 585 590

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
595 600 605

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
610 615 620

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu
625 630 635 640

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
645 650 655

Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala
660 665 670

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
675 680 685

Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp
690 695 700

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
705 710 715 720

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
725 730 735

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
740 745 750

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
755 760 765

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
770 775 780

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
785 790 795 800

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
805 810 815

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
820 825 830

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
835 840 845

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
850 855 860

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
865 870 875 880

Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 163
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro431 (Pro186 ST14(MS) enlazador)

<400> 163

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

```
Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
    450                 455                 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465                 470                 475                 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495
```

```
Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser Leu Ser
            500                 505                 510

Gly Arg Ser Asp Asn His Gly Gly Gly Ser Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
```

675 680 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
690 695 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705 710 715 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
725 730 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
740 745 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
755 760 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
770 775 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785 790 795 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
805 810 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
820 825 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
835 840 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
850 855 860

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 164
<211> 763
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro258 (Pro186 con un único dominio aEGFR y un dominio aHSA central)

<400> 164

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

```
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300
```

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
370 375 380

Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
385 390 395 400

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
405 410 415

Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
420 425 430

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
435 440 445

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
450 455 460

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
465 470 475 480

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
500 505 510

Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
515 520 525

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser
530 535 540

Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg
545 550 555 560

Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala
565 570 575

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
580 585 590

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr
595 600 605

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
610 615 620

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
625 630 635 640

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
645 650 655

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
660 665 670

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr

675 680 685

Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
690 695 700

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
705 710 715 720

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
725 730 735

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
740 745 750

Val Thr Val Ser Ser His His His His His His
755 760

<210> 165
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro221 - Enlazador Plegable Variante

<400> 165

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val

```
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240
```

```
Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430
```

```
Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
    450                 455                 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465                 470                 475                 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Gly Gln Asn
            500                 505                 510

Pro Tyr Ser Ala Gly Arg Gly Gly Gly Ser Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620
```

```
Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
```

805 810 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
820 825 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
835 840 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
850 855 860

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 166
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro222 - enlazador Plegable Variante

<400> 166

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val

```
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240
```

```
Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430
```

```
Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
    450                 455                 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465                 470                 475                 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Gly Gln Asn
            500                 505                 510

Pro Tyr Ser Ala Gly Gly Gly Ser Gly Gly Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620
```

```
Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
```

805 810 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
820 825 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
835 840 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
850 855 860

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 167
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro223 - enlazador Plegable Variante

<400> 167

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

```
Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430
```

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Gly Arg Asn
500 505 510

Val Tyr Ser Ala Gly Gly Gly Ser Gly Gly Gln Thr Val Val Thr Gln
515 520 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
530 535 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545 550 555 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
565 570 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
580 585 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
595 600 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
610 615 620

```
Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
```

805 810 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
820 825 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
835 840 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
850 855 860

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 168
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro224- enlazador Plegable Variante

<400> 168

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val

```
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240
```

```
Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430
```

```
Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
    450                 455                 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465                 470                 475                 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Gly Gln Asn
            500                 505                 510

Thr Trp Ser Ala Gly Lys Gly Gly Gly Ser Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620
```

```
Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
```

805 810 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
820 825 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
835 840 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
850 855 860

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 169
<211> 898
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro254- Heterólogo Formato 2

<400> 169

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser

245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val
370 375 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr Ala Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Val Ala
420 425 430

Ile Asn Trp Ser Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala
465 470 475 480

Gly Tyr Gln Ile Asn Ser Gly Asn Tyr Asn Phe Lys Asp Tyr Glu Tyr
485 490 495

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly
500 505 510

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val
515 520 525

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
530 535 540

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
545 550 555 560

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp
565 570 575

Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser
580 585 590

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
595 600 605

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
610 615 620

```
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly
625                 630                 635                 640

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
                645                 650                 655

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
            660                 665                 670

Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        675                 680                 685

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp
    690                 695                 700

Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
705                 710                 715                 720

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
                725                 730                 735

Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile
            740                 745                 750

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        755                 760                 765

Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
    770                 775                 780

Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala
785                 790                 795                 800

Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln
                805                 810                 815
```

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
820 825 830

Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser
835 840 845

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
850 855 860

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
865 870 875 880

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His
885 890 895

His His

<210> 170
<211> 893
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro255- Heterólogo Formato 2

<400> 170

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240
```

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
405 410 415

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

420 425 430

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
450 455 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465 470 475 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
500 505 510

Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
515 520 525

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser
530 535 540

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
545 550 555 560

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp
565 570 575

Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
580 585 590

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
595 600 605

```
Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
    610                 615                 620

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
625                 630                 635                 640

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
                645                 650                 655

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn
            660                 665                 670

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
        675                 680                 685

Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val
    690                 695                 700

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
705                 710                 715                 720

Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                725                 730                 735

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
            740                 745                 750

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        755                 760                 765

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    770                 775                 780

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
785                 790                 795                 800
```

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
805 810 815

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
820 825 830

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
835 840 845

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
850 855 860

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
865 870 875 880

Thr Leu Val Thr Val Ser Ser His His His His His His
885 890

<210> 171
<211> 902
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro262

<400> 171

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240
```

```
Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            260                 265                 270

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
        275                 280                 285

Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly
    290                 295                 300

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
305                 310                 315                 320

Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe
                325                 330                 335

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
            340                 345                 350

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn
        355                 360                 365

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Ser Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser
385                 390                 395                 400

Val Gln Thr Gly Gly Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg
                405                 410                 415

Thr Ser Arg Ser Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys
            420                 425                 430
```

Glu Arg Glu Phe Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly
435 440 445

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
450 455 460

Lys Asn Thr Val Asp Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
465 470 475 480

Ala Ile Tyr Tyr Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr
485 490 495

Leu Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
500 505 510

Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
515 520 525

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
530 535 540

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly
545 550 555 560

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
565 570 575

Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg
580 585 590

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

Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser

610 615 620

Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
625 630 635 640

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
645 650 655

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
660 665 670

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly
675 680 685

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys
690 695 700

Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
705 710 715 720

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
725 730 735

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
740 745 750

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
755 760 765

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
770 775 780

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg
785 790 795 800

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser
805 810 815

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile
820 825 830

Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg
835 840 845

Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met
850 855 860

Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly
865 870 875 880

Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
885 890 895

His His His His His His
900

<210> 172
<211> 766
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro356 – Formato 4

<400> 172

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

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

Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val

35 40 45

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

Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
130 135 140

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
145 150 155 160

Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro
165 170 175

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
180 185 190

Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser
195 200 205

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
210 215 220

```
Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly
225                 230                 235                 240

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
                245                 250                 255

Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val
            260                 265                 270

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
        275                 280                 285

Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
    290                 295                 300

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
305                 310                 315                 320

Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
                325                 330                 335

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
            340                 345                 350

Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe
        355                 360                 365

Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gly Gly Pro Gly Pro Ala
    370                 375                 380

Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly
385                 390                 395                 400

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
                405                 410                 415
```

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
420 425 430

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
435 440 445

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
450 455 460

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
465 470 475 480

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
485 490 495

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
500 505 510

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
515 520 525

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
530 535 540

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
545 550 555 560

Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly
565 570 575

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
580 585 590

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
595 600 605

```
Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
    610                 615                 620

Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
625                 630                 635                 640

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys
                645                 650                 655

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg
            660                 665                 670

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys
        675                 680                 685

Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg
    690                 695                 700

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met
705                 710                 715                 720

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
                725                 730                 735

Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln
            740                 745                 750

Gly Thr Leu Val Thr Val Ser Ser His His His His His His
        755                 760                 765
```

<210> 173
<211> 763
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro359 – Formato 4

<400> 173

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

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

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

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

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

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

Ala Ala Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175
```

```
Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
```

355 360 365

Thr Lys Leu Thr Val Leu Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
370 375 380

Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
385 390 395 400

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
405 410 415

Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
420 425 430

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
435 440 445

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
450 455 460

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
465 470 475 480

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
500 505 510

Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
515 520 525

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser
530 535 540

Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg
545 550 555 560

Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala
565 570 575

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
580 585 590

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr
595 600 605

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
610 615 620

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
625 630 635 640

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
645 650 655

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
660 665 670

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr
675 680 685

Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
690 695 700

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
705 710 715 720

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
725 730 735

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
740 745 750

Val Thr Val Ser Ser His His His His His His
755 760

<210> 174
<211> 752
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro364 – Formato 4

<400> 174

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

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

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

Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
115 120 125

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
130 135 140

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln
145 150 155 160

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
165 170 175

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr
180 185 190

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
195 200 205

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn
210 215 220

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
225 230 235 240

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr
245 250 255

Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
260 265 270

Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr
275 280 285

Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile
290 295 300

```
Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly
305                 310                 315                 320

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
                325                 330                 335

Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp
            340                 345                 350

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gly Gly Pro Gly
        355                 360                 365

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu
    370                 375                 380

Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys
385                 390                 395                 400

Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg
                405                 410                 415

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser
            420                 425                 430

Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile
        435                 440                 445

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

Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu
465                 470                 475                 480

Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
                485                 490                 495
```

Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu
500 505 510

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr
515 520 525

Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro
530 535 540

Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp
545 550 555 560

Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
565 570 575

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
580 585 590

Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
595 600 605

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
610 615 620

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
625 630 635 640

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
645 650 655

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
660 665 670

Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys

675 680 685

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
690 695 700

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
705 710 715 720

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
725 730 735

Gly Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
740 745 750

<210> 175
<211> 753
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro388 – Formato 4

<400> 175

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

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

Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val
35 40 45

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

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

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

Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
        115                 120                 125

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys
    130                 135                 140

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg
145                 150                 155                 160

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys
                165                 170                 175

Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe
            180                 185                 190

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
        195                 200                 205

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala
    210                 215                 220

Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
                245                 250                 255

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
```

260 265 270

Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
275 280 285

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
290 295 300

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
305 310 315 320

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
325 330 335

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
340 345 350

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gly Gly Pro
355 360 365

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val
370 375 380

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser
385 390 395 400

Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val
405 410 415

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly
420 425 430

Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr
435 440 445

```
Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
    450                 455                 460

Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser
465                 470                 475                 480

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
                485                 490                 495

Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
            500                 505                 510

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser
        515                 520                 525

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
    530                 535                 540

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp
545                 550                 555                 560

Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
                565                 570                 575

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
            580                 585                 590

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
        595                 600                 605

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
    610                 615                 620

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
625                 630                 635                 640
```

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn
645 650 655

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
660 665 670

Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val
675 680 685

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
690 695 700

Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
705 710 715 720

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
725 730 735

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His
740 745 750

His

<210> 176
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro432- Heterólogo – Formato 2

<400> 176

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

```
Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser
            20                  25                  30

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145                 150                 155                 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
            180                 185                 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
        195                 200                 205
```

```
Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
                245                 250                 255

Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
            260                 265                 270

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser
        275                 280                 285

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
    290                 295                 300

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val
305                 310                 315                 320

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
                325                 330                 335

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
            340                 345                 350

Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
        355                 360                 365

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
    370                 375                 380

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
385                 390                 395                 400
```

Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr Ala Met Gly Trp
405 410 415

Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Val Ala Ile Asn
420 425 430

Trp Ser Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe
435 440 445

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
450 455 460

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Gly Tyr
465 470 475 480

Gln Ile Asn Ser Gly Asn Tyr Asn Phe Lys Asp Tyr Glu Tyr Asp Tyr
485 490 495

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly
500 505 510

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln
515 520 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
530 535 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545 550 555 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
565 570 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu

580 585 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
595 600 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
610 615 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625 630 635 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
645 650 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
660 665 670

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
675 680 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
690 695 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705 710 715 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
725 730 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
740 745 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
755 760 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
770 775 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785 790 795 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
805 810 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
820 825 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
835 840 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
850 855 860

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 177
<211> 636
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro448- Focalización Dual Hemis Formato 3

<400> 177

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

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

Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val
35 40 45

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

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

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

Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Lys Leu Val
115 120 125

Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu Thr Leu Ser
130 135 140

Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met Gly Trp Phe
145 150 155 160

Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly Ile Ser Trp
165 170 175

Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
180 185 190

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
195 200 205

```
Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala Ala Ala Gly
    210                 215                 220

Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
                245                 250                 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
            260                 265                 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
        275                 280                 285

Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
    290                 295                 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305                 310                 315                 320

Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
                325                 330                 335

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
            340                 345                 350

Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
        355                 360                 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly
    370                 375                 380

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val
385                 390                 395                 400
```

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp
435 440 445

Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser
450 455 460

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
465 470 475 480

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
485 490 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly
500 505 510

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
515 520 525

Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
530 535 540

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
545 550 555 560

Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala
565 570 575

Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr

580 585 590

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
595 600 605

Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
610 615 620

Leu Val Thr Val Ser Ser His His His His His His
625 630 635

<210> 178
<211> 636
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro449 Focalización Dual Hemis Formato 3

<400> 178

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

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

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

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

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys

85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

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

Glu Arg Glu Phe Val Ala Ile Ile Asn Ser Ile Gly Ile Thr Asn Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly
225 230 235 240

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
340 345 350

Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly
370 375 380

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp
435 440 445

Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser
450 455 460

```
Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
465                 470                 475                 480

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
                485                 490                 495

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly
            500                 505                 510

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
        515                 520                 525

Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    530                 535                 540

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
545                 550                 555                 560

Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala
                565                 570                 575

Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
            580                 585                 590

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
        595                 600                 605

Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
    610                 615                 620

Leu Val Thr Val Ser Ser His His His His His His
625                 630                 635
```

<210> 179
<211> 636

<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro450 Focalización Dual Hemis Formato 3

<400> 179

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

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

Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val
35 40 45

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

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

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

Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Lys Leu Val
115 120 125

Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu Thr Leu Ser
130 135 140

Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met Gly Trp Phe
145 150 155 160

```
Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly Ile Ser Trp
                165                 170                 175

Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
            180                 185                 190

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
        195                 200                 205

Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala Ala Ala Gly
    210                 215                 220

Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
                245                 250                 255

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
            260                 265                 270

Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly
        275                 280                 285

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
    290                 295                 300

Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe
305                 310                 315                 320

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
                325                 330                 335

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn
```

340 345 350

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gly Gly
355 360 365

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu
370 375 380

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
385 390 395 400

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
405 410 415

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
420 425 430

Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys
435 440 445

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
450 455 460

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
465 470 475 480

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
485 490 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
500 505 510

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
515 520 525

Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
530 535 540

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
545 550 555 560

Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala
565 570 575

Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
580 585 590

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
595 600 605

Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
610 615 620

Leu Val Thr Val Ser Ser His His His His His His
625 630 635

<210> 180
<211> 636
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro451 Focalización Dual Hemis Formato 3

<400> 180

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

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

Glu Arg Glu Phe Val Ala Ile Ile Asn Ser Ile Gly Ile Thr Asn Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

```
Val Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
                245                 250                 255

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
            260                 265                 270

Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly
        275                 280                 285

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
    290                 295                 300

Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe
305                 310                 315                 320

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
                325                 330                 335

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn
            340                 345                 350

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gly Gly
        355                 360                 365

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu
    370                 375                 380

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
385                 390                 395                 400

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
                405                 410                 415
```

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
420 425 430

Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys
435 440 445

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
450 455 460

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
465 470 475 480

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
485 490 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
500 505 510

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
515 520 525

Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
530 535 540

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
545 550 555 560

Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala
565 570 575

Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
580 585 590

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val

595 600 605

Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
610 615 620

Leu Val Thr Val Ser Ser His His His His His His
625 630 635

<210> 181
<211> 893
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro479- Heterólogo – Formato 2

<400> 181

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

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

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

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

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

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

Ala Ala Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Arg Leu Ser Cys Glu Ala Ser Pro Arg Thr Phe Ser Thr Tyr Ser Met
405 410 415

Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Ser Phe Val Ala Ala
420 425 430

Ile Asn Trp Ser Gly Gly Asn Thr Ser Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala
465 470 475 480

Gly Gly Val Leu Ala His His Asn Tyr Glu Tyr Asp Tyr Trp Gly Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
500 505 510

Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
515 520 525

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser
530 535 540

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
545 550 555 560

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp
565 570 575

Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
580 585 590

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
595 600 605

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
610 615 620

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
625 630 635 640

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
645 650 655

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn
660 665 670

```
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
        675                 680                 685

Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val
    690                 695                 700

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
705                 710                 715                 720

Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                725                 730                 735

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
            740                 745                 750

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        755                 760                 765

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    770                 775                 780

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
785                 790                 795                 800

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
                805                 810                 815

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
            820                 825                 830

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
        835                 840                 845

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
    850                 855                 860
```

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
865 870 875 880

Thr Leu Val Thr Val Ser Ser His His His His His His
885 890

<210> 182
<211> 893
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro480- Heterólogo – Formato 2

<400> 182

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

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

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

Ala Ala Ile Asn Trp Ser Gly Gly Asn 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 Ala Gly Gly Val Leu Ala His His Asn Tyr Glu Tyr Asp Tyr Trp
100 105 110

```
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145                 150                 155                 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
            180                 185                 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
        195                 200                 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
                245                 250                 255

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
            260                 265                 270

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser
        275                 280                 285

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
    290                 295                 300
```

```
Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val
305                 310                 315                 320

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
                325                 330                 335

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
            340                 345                 350

Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
        355                 360                 365

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu
    370                 375                 380

Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
385                 390                 395                 400

Ser Cys Ala Pro Ser Arg Arg Thr Phe His Thr Tyr His Met Gly Trp
                405                 410                 415

Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ala Val Ile Asn
            420                 425                 430

Trp Ser Gly Gly Ser Thr Val Tyr Ala Asp Ser Val Lys Gly Arg Phe
        435                 440                 445

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
    450                 455                 460

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Gly Gly
465                 470                 475                 480

Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp Tyr Trp Gly Gln
```

485 490 495

Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
500 505 510

Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
515 520 525

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser
530 535 540

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
545 550 555 560

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp
565 570 575

Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
580 585 590

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
595 600 605

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
610 615 620

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
625 630 635 640

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
645 650 655

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn
660 665 670

```
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
        675                 680                 685

Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val
    690                 695                 700

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
705                 710                 715                 720

Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                725                 730                 735

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
            740                 745                 750

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        755                 760                 765

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    770                 775                 780

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
785                 790                 795                 800

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
                805                 810                 815

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
            820                 825                 830

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
        835                 840                 845

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
    850                 855                 860
```

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
865 870 875 880

Thr Leu Val Thr Val Ser Ser His His His His His His
885 890

<210> 183
<211> 893
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro495 - Formato 2

<400> 183

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

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

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

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

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

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

Ala Ala Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp
100 105 110

```
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300
```

```
Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Ser Cys Ala Pro Ser Arg Arg Thr Phe His Thr Tyr His Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ala Val
            420                 425                 430

Ile Asn Trp Ser Gly Gly Ser Thr Val Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
    450                 455                 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala
465                 470                 475                 480

Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp Tyr Trp
                485                 490                 495
```

```
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
            500                 505                 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
        515                 520                 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
    530                 535                 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545                 550                 555                 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Asp
                565                 570                 575

Asp Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
            580                 585                 590

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
        595                 600                 605

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
    610                 615                 620

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val
625                 630                 635                 640

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
                645                 650                 655

Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys His Ala Met
            660                 665                 670

Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg
```

675 680 685

Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Ala Tyr Ala Asp Ser Val
690 695 700

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
705 710 715 720

Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
725 730 735

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
740 745 750

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
755 760 765

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
770 775 780

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
785 790 795 800

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
805 810 815

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
820 825 830

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
835 840 845

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
850 855 860

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
865 870 875 880

Thr Leu Val Thr Val Ser Ser His His His His His His
885 890

<210> 184
<211> 15
<212> PRT
<213> Secuencia Artificial

<220>
<223> Vinculado Plegable Sintético - MMP9-2

<400> 184

Ser Gly Gly Pro Gly Pro Ala Gly Leu Lys Gly Ala Pro Gly Ser
1 5 10 15

<210> 185
<211> 887
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro141

<400> 185

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255
```

```
Ser Gly Pro Ala Gly Met Lys Gly Leu Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
```

435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
500 505 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
515 520 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
530 535 540

Ser Ser Thr Gly Ala Val Thr Ser Gly His Tyr Pro Asn Trp Val Gln
545 550 555 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Ser Asn
565 570 575

Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
580 585 590

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
595 600 605

Tyr Tyr Cys Val Leu Trp Gly Ser Arg Arg Trp Val Phe Gly Gly Gly
610 615 620

```
Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val
625                 630                 635                 640

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
                645                 650                 655

Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Ser Ala Met
            660                 665                 670

Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg
        675                 680                 685

Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Ala Tyr Ala Asp Ser Val
    690                 695                 700

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
705                 710                 715                 720

Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                725                 730                 735

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Thr Phe Trp Ala Tyr
            740                 745                 750

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        755                 760                 765

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    770                 775                 780

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
785                 790                 795                 800

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
                805                 810                 815
```

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
820 825 830

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
835 840 845

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
850 855 860

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
865 870 875 880

Thr Leu Val Thr Val Ser Ser
885

<210> 186
<211> 903
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro160

<400> 186

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255
```

```
Ser Gly Gly Pro Ala Gly Met Lys Gly Leu Gly Gln Thr Val Val Thr
            260                 265                 270

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
        275                 280                 285

Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
    290                 295                 300

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr
305                 310                 315                 320

Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
                325                 330                 335

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
            340                 345                 350

Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
        355                 360                 365

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
    370                 375                 380

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
385                 390                 395                 400

Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr
                405                 410                 415

Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
            420                 425                 430

Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val
        435                 440                 445
```

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
450 455 460

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
465 470 475 480

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
485 490 495

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro
500 505 510

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr
515 520 525

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
530 535 540

Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly His Tyr Pro Asn Trp
545 550 555 560

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr
565 570 575

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

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
595 600 605

Ala Glu Tyr Tyr Cys Val Leu Trp Gly Ser Arg Arg Trp Val Phe Gly
610 615 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser

625 630 635 640

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
645 650 655

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
660 665 670

Ser Gly Phe Thr Phe Asn Lys Ser Ala Met Asn Trp Val Arg Gln Ala
675 680 685

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
690 695 700

Asn Tyr Ala Thr Ala Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
705 710 715 720

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
725 730 735

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
740 745 750

Gly Asn Ser Tyr Ile Thr Phe Trp Ala Tyr Trp Gly Gln Gly Thr Leu
755 760 765

Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly
770 775 780

Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
785 790 795 800

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
805 810 815

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
820 825 830

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
835 840 845

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
850 855 860

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
865 870 875 880

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
885 890 895

Thr Leu Val Thr Val Ser Ser
900

<210> 187
<211> 899
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro161

<400> 187

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

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

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

Leu Val Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser

```
    50                  55                  60

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145                 150                 155                 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
            180                 185                 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
        195                 200                 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240
```

```
Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
                245                 250                 255

Gly Pro Ala Gly Met Lys Gly Leu Gly Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385                 390                 395                 400

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
                405                 410                 415

Leu Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
            420                 425                 430
```

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
450 455 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465 470 475 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
500 505 510

Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
515 520 525

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser
530 535 540

Thr Gly Ala Val Thr Ser Gly His Tyr Pro Asn Trp Val Gln Gln Lys
545 550 555 560

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Ser Asn Lys His
565 570 575

Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
580 585 590

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
595 600 605

Cys Val Leu Trp Gly Ser Arg Arg Trp Val Phe Gly Gly Gly Thr Lys
610 615 620

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
625 630 635 640

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
645 650 655

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
660 665 670

Phe Asn Lys Ser Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
675 680 685

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
690 695 700

Ala Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
705 710 715 720

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
725 730 735

Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr
740 745 750

Ile Thr Phe Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
755 760 765

Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
770 775 780

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
785 790 795 800

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe

805 810 815

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
820 825 830

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val
835 840 845

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
850 855 860

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
865 870 875 880

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
885 890 895

Val Ser Ser

<210> 188
<211> 901
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro162

<400> 188

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145                 150                 155                 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
            180                 185                 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
        195                 200                 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
```

225 230 235 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
245 250 255

Val Tyr Ala Asp Ser Leu Glu Asp Gly Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
405 410 415

```
Leu Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
            420                 425                 430

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
        435                 440                 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
    450                 455                 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465                 470                 475                 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln
                485                 490                 495

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Val Tyr Ala Asp
            500                 505                 510

Ser Leu Glu Asp Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
        515                 520                 525

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
    530                 535                 540

Ser Thr Gly Ala Val Thr Ser Gly His Tyr Pro Asn Trp Val Gln Gln
545                 550                 555                 560

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Ser Asn Lys
                565                 570                 575

His Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
            580                 585                 590

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
        595                 600                 605
```

```
Tyr Cys Val Leu Trp Gly Ser Arg Arg Trp Val Phe Gly Gly Gly Thr
    610                 615                 620

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
625                 630                 635                 640

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
                645                 650                 655

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
            660                 665                 670

Thr Phe Asn Lys Ser Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
        675                 680                 685

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala
    690                 695                 700

Thr Ala Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp
705                 710                 715                 720

Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu
                725                 730                 735

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser
            740                 745                 750

Tyr Ile Thr Phe Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
        755                 760                 765

Ser Ser Gly Gly Gly Ser Val Tyr Ala Asp Ser Leu Glu Asp Gly Gly
    770                 775                 780

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
785                 790                 795                 800
```

Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
805 810 815

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
820 825 830

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
835 840 845

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr
850 855 860

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
865 870 875 880

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
885 890 895

Val Thr Val Ser Ser
900

<210> 189
<211> 901
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro189

<400> 189

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145 150 155 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
180 185 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
195 200 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
210 215 220

```
Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
                245                 250                 255

Ala Arg Leu Gln Ser Ala Ala Pro Gly Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385                 390                 395                 400

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
```

405 410 415

Leu Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
420 425 430

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
450 455 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465 470 475 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Ala Arg Leu Gln
500 505 510

Ser Ala Ala Pro Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
515 520 525

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
530 535 540

Ser Thr Gly Ala Val Thr Ser Gly His Tyr Pro Asn Trp Val Gln Gln
545 550 555 560

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Ser Asn Lys
565 570 575

His Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
580 585 590

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
595 600 605

Tyr Cys Val Leu Trp Gly Ser Arg Arg Trp Val Phe Gly Gly Gly Thr
610 615 620

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
625 630 635 640

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
645 650 655

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
660 665 670

Thr Phe Asn Lys Ser Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
675 680 685

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala
690 695 700

Thr Ala Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp
705 710 715 720

Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu
725 730 735

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser
740 745 750

Tyr Ile Thr Phe Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
755 760 765

Ser Ser Gly Gly Gly Ser Ala Arg Leu Gln Ser Ala Ala Pro Gly Gly
770 775 780

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
785 790 795 800

Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
805 810 815

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
820 825 830

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
835 840 845

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr
850 855 860

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
865 870 875 880

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
885 890 895

Val Thr Val Ser Ser
900

<210> 190
<211> 901
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro164

<400> 190

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145 150 155 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
180 185 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
195 200 205

```
Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
                245                 250                 255

Lys Lys Leu Ala Asp Glu Pro Glu Gly Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385                 390                 395                 400
```

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
405 410 415

Leu Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
420 425 430

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
450 455 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465 470 475 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Lys Lys Leu Ala
500 505 510

Asp Glu Pro Glu Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
515 520 525

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
530 535 540

Ser Thr Gly Ala Val Thr Ser Gly His Tyr Pro Asn Trp Val Gln Gln
545 550 555 560

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Ser Asn Lys
565 570 575

His Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

580 585 590

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
595 600 605

Tyr Cys Val Leu Trp Gly Ser Arg Arg Trp Val Phe Gly Gly Gly Thr
610 615 620

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
625 630 635 640

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
645 650 655

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
660 665 670

Thr Phe Asn Lys Ser Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
675 680 685

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala
690 695 700

Thr Ala Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp
705 710 715 720

Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu
725 730 735

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser
740 745 750

Tyr Ile Thr Phe Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
755 760 765

Ser Ser Gly Gly Gly Ser Lys Lys Leu Ala Asp Glu Pro Glu Gly Gly
770 775 780

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
785 790 795 800

Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
805 810 815

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
820 825 830

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
835 840 845

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr
850 855 860

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
865 870 875 880

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
885 890 895

Val Thr Val Ser Ser
900

<210> 191
<211> 901
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro 191

<400> 191

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145 150 155 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
180 185 190

```
Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
        195                 200                 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
                245                 250                 255

Leu Ser Gly Arg Ser Asp Asn His Gly Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380
```

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
405 410 415

Leu Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
420 425 430

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
450 455 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465 470 475 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Leu Ser Gly Arg
500 505 510

Ser Asp Asn His Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
515 520 525

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
530 535 540

Ser Thr Gly Ala Val Thr Ser Gly His Tyr Pro Asn Trp Val Gln Gln
545 550 555 560

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Ser Asn Lys
565 570 575

```
His Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
            580                 585                 590

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
        595                 600                 605

Tyr Cys Val Leu Trp Gly Ser Arg Arg Trp Val Phe Gly Gly Gly Thr
    610                 615                 620

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
625                 630                 635                 640

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
                645                 650                 655

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
            660                 665                 670

Thr Phe Asn Lys Ser Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
        675                 680                 685

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala
    690                 695                 700

Thr Ala Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp
705                 710                 715                 720

Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu
                725                 730                 735

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser
            740                 745                 750

Tyr Ile Thr Phe Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
```

755 760 765

Ser Ser Gly Gly Gly Ser Leu Ser Gly Arg Ser Asp Asn His Gly Gly
770 775 780

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
785 790 795 800

Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
805 810 815

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
820 825 830

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
835 840 845

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr
850 855 860

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
865 870 875 880

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
885 890 895

Val Thr Val Ser Ser
900

<210> 192
<211> 901
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro166

<400> 192

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145                 150                 155                 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
```

180 185 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
195 200 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225 230 235 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser
245 250 255

Phe Thr Arg Gln Ala Arg Val Val Gly Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

```
Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385                 390                 395                 400

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
                405                 410                 415

Leu Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
            420                 425                 430

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
        435                 440                 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
    450                 455                 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465                 470                 475                 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln
                485                 490                 495

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Phe Thr Arg Gln
            500                 505                 510

Ala Arg Val Val Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
        515                 520                 525

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
    530                 535                 540

Ser Thr Gly Ala Val Thr Ser Gly His Tyr Pro Asn Trp Val Gln Gln
545                 550                 555                 560
```

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Ser Asn Lys
565 570 575

His Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
580 585 590

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
595 600 605

Tyr Cys Val Leu Trp Gly Ser Arg Arg Trp Val Phe Gly Gly Gly Thr
610 615 620

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
625 630 635 640

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
645 650 655

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
660 665 670

Thr Phe Asn Lys Ser Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
675 680 685

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala
690 695 700

Thr Ala Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp
705 710 715 720

Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu
725 730 735

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser
740 745 750

Tyr Ile Thr Phe Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
755 760 765

Ser Ser Gly Gly Gly Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly
770 775 780

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
785 790 795 800

Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
805 810 815

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
820 825 830

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
835 840 845

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr
850 855 860

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
865 870 875 880

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
885 890 895

Val Thr Val Ser Ser
900

<210> 193
<211> 901
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro169

<400> 193

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145                 150                 155                 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175
```

```
Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
            180                 185                 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
        195                 200                 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
                245                 250                 255

Gly Pro Ala Gly Met Lys Gly Leu Gly Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
```

355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
405 410 415

Leu Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
420 425 430

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
450 455 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465 470 475 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
500 505 510

Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
515 520 525

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser
530 535 540

```
Thr Gly Ala Val Thr Ser Gly His Tyr Pro Asn Trp Val Gln Gln Lys
545                 550                 555                 560

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp
                565                 570                 575

Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
            580                 585                 590

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
        595                 600                 605

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
    610                 615                 620

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
625                 630                 635                 640

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
                645                 650                 655

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
            660                 665                 670

Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
        675                 680                 685

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp
    690                 695                 700

Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg
705                 710                 715                 720

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr
                725                 730                 735
```

```
Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn
            740                 745                 750

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
        755                 760                 765

Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro
    770                 775                 780

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
785                 790                 795                 800

Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
                805                 810                 815

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
            820                 825                 830

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
        835                 840                 845

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr
    850                 855                 860

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
865                 870                 875                 880

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
                885                 890                 895

Val Thr Val Ser Ser
            900
```

<210> 194
<211> 903

<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro170

<400> 194

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145                 150                 155                 160
```

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
180 185 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
195 200 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225 230 235 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
245 250 255

Val Tyr Ala Asp Ser Leu Glu Asp Gly Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
405 410 415

Leu Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
420 425 430

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
450 455 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465 470 475 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Val Tyr Ala Asp
500 505 510

Ser Leu Glu Asp Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
515 520 525

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

530 535 540

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
545 550 555 560

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp
565 570 575

Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
580 585 590

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
595 600 605

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
610 615 620

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
625 630 635 640

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
645 650 655

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
660 665 670

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly
675 680 685

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys
690 695 700

Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
705 710 715 720

```
Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
                725                 730                 735

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
            740                 745                 750

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
        755                 760                 765

Thr Val Ser Ser Gly Gly Gly Ser Val Tyr Ala Asp Ser Leu Glu Asp
    770                 775                 780

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
785                 790                 795                 800

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
                805                 810                 815

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
            820                 825                 830

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
        835                 840                 845

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
    850                 855                 860

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
865                 870                 875                 880

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
                885                 890                 895

Thr Leu Val Thr Val Ser Ser
            900
```

<210> 195
<211> 903
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro171

<400> 195

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145 150 155 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
180 185 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
195 200 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225 230 235 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
245 250 255

Ala Arg Leu Gln Ser Ala Ala Pro Gly Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
405 410 415

Leu Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
420 425 430

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
450 455 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465 470 475 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Ala Arg Leu Gln
500 505 510

Ser Ala Ala Pro Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
515 520 525

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
530 535 540

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
545 550 555 560

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp
565 570 575

Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
580 585 590

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
595 600 605

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
610 615 620

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
625 630 635 640

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
645 650 655

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
660 665 670

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly
675 680 685

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys
690 695 700

Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser

705 710 715 720

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
725 730 735

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
740 745 750

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
755 760 765

Thr Val Ser Ser Gly Gly Gly Ser Ala Arg Leu Gln Ser Ala Ala Pro
770 775 780

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
785 790 795 800

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
805 810 815

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
820 825 830

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
835 840 845

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
850 855 860

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
865 870 875 880

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
885 890 895

Thr Leu Val Thr Val Ser Ser
900

<210> 196
<211> 903
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro172

<400> 196

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro

130 135 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145 150 155 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
180 185 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
195 200 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225 230 235 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
245 250 255

Lys Lys Leu Ala Asp Glu Pro Glu Gly Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
405 410 415

Leu Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
420 425 430

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
450 455 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465 470 475 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Lys Lys Leu Ala
500 505 510

```
Asp Glu Pro Glu Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
        515                 520                 525

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
    530                 535                 540

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
545                 550                 555                 560

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp
                565                 570                 575

Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
            580                 585                 590

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
        595                 600                 605

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
    610                 615                 620

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
625                 630                 635                 640

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
                645                 650                 655

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
            660                 665                 670

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly
        675                 680                 685

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys
    690                 695                 700
```

```
Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
705                 710                 715                 720

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
                725                 730                 735

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
            740                 745                 750

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
        755                 760                 765

Thr Val Ser Ser Gly Gly Gly Ser Lys Lys Leu Ala Asp Glu Pro Glu
    770                 775                 780

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
785                 790                 795                 800

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
                805                 810                 815

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
            820                 825                 830

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
        835                 840                 845

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
    850                 855                 860

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
865                 870                 875                 880

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
```

885 890 895

Thr Leu Val Thr Val Ser Ser
900

<210> 197
<211> 903
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro173

<400> 197

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
115 120 125

```
Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145                 150                 155                 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
            180                 185                 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
        195                 200                 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
                245                 250                 255

Leu Ser Gly Arg Ser Asp Asn His Gly Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
```

305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
405 410 415

Leu Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
420 425 430

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
450 455 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465 470 475 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Leu Ser Gly Arg
500 505 510

Ser Asp Asn His Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
515 520 525

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
530 535 540

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
545 550 555 560

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp
565 570 575

Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
580 585 590

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
595 600 605

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
610 615 620

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
625 630 635 640

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
645 650 655

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
660 665 670

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly
675 680 685

```
Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys
    690                 695                 700

Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
705                 710                 715                 720

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
                725                 730                 735

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
            740                 745                 750

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
        755                 760                 765

Thr Val Ser Ser Gly Gly Gly Ser Leu Ser Gly Arg Ser Asp Asn His
    770                 775                 780

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
785                 790                 795                 800

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
                805                 810                 815

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
            820                 825                 830

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
        835                 840                 845

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
    850                 855                 860

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
865                 870                 875                 880
```

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
885 890 895

Thr Leu Val Thr Val Ser Ser
900

<210> 198
<211> 903
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro174

<400> 198

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

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

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
100 105 110

```
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145                 150                 155                 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
            180                 185                 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
        195                 200                 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser
                245                 250                 255

Phe Thr Arg Gln Ala Arg Val Val Gly Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300
```

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn
405 410 415

Leu Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
420 425 430

Ala Arg Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
450 455 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
465 470 475 480

Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln

485 490 495

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Phe Thr Arg Gln
500 505 510

Ala Arg Val Val Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
515 520 525

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
530 535 540

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
545 550 555 560

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp
565 570 575

Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
580 585 590

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
595 600 605

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
610 615 620

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
625 630 635 640

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
645 650 655

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
660 665 670

```
Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly
        675                 680                 685

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys
    690                 695                 700

Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
705                 710                 715                 720

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
                725                 730                 735

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
            740                 745                 750

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
        755                 760                 765

Thr Val Ser Ser Gly Gly Gly Ser Phe Thr Arg Gln Ala Arg Val Val
    770                 775                 780

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
785                 790                 795                 800

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
                805                 810                 815

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
            820                 825                 830

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
        835                 840                 845

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
    850                 855                 860
```

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
865 870 875 880

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
885 890 895

Thr Leu Val Thr Val Ser Ser
900

<210> 199
<211> 888
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro176

<400> 199

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

```
Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Pro Ala Gly Met Lys Gly Leu Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285
```

```
Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
    450                 455                 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465                 470                 475                 480
```

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
500 505 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
515 520 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
530 535 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545 550 555 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Asp
565 570 575

Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
580 585 590

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
595 600 605

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
610 615 620

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val
625 630 635 640

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
645 650 655

Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met

660 665 670

Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg
675 680 685

Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser
690 695 700

Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala
705 710 715 720

Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
725 730 735

Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala
740 745 750

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
755 760 765

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
770 775 780

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
785 790 795 800

Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
805 810 815

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
820 825 830

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
835 840 845

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
850 855 860

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
865 870 875 880

Gly Thr Leu Val Thr Val Ser Ser
885

<210> 200
<211> 892
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro178

<400> 200

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp

100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Lys Lys Leu Ala Asp Glu Pro Glu Gly Gln Thr Val Val Thr
260 265 270

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
275 280 285

```
Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
    290                 295                 300

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr
305                 310                 315                 320

Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
                325                 330                 335

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
            340                 345                 350

Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
        355                 360                 365

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
    370                 375                 380

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
385                 390                 395                 400

Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr
                405                 410                 415

Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
            420                 425                 430

Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val
        435                 440                 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
    450                 455                 460

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
465                 470                 475                 480
```

```
Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
                485                 490                 495

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
            500                 505                 510

Lys Lys Leu Ala Asp Glu Pro Glu Gly Gly Gly Ser Gln Thr Val Val
        515                 520                 525

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
    530                 535                 540

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
545                 550                 555                 560

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp
                565                 570                 575

Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser
            580                 585                 590

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
        595                 600                 605

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
    610                 615                 620

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly
625                 630                 635                 640

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
                645                 650                 655

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
            660                 665                 670
```

```
Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        675                 680                 685

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp
    690                 695                 700

Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
705                 710                 715                 720

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
                725                 730                 735

Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile
            740                 745                 750

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        755                 760                 765

Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
    770                 775                 780

Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala
785                 790                 795                 800

Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln
                805                 810                 815

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
            820                 825                 830

Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser
        835                 840                 845

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
```

850 855 860

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
865 870 875 880

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
885 890

<210> 201
<211> 894
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro179

<400> 201

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

```
Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Ser Lys Lys Leu Ala Asp Glu Pro Glu Gly Ser Gln Thr Val
            260                 265                 270

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
        275                 280                 285

Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
```

290 295 300

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
305 310 315 320

Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser
325 330 335

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
340 345 350

Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val
355 360 365

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly
370 375 380

Gly Ser Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr
385 390 395 400

Gly Gly Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg
405 410 415

Ser Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu
420 425 430

Phe Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp
435 440 445

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
450 455 460

Val Asp Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr
465 470 475 480

Tyr Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu
485 490 495

Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly
500 505 510

Gly Ser Lys Lys Leu Ala Asp Glu Pro Glu Gly Gly Gly Ser Gln Thr
515 520 525

Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
530 535 540

Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr
545 550 555 560

Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile
565 570 575

Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser
580 585 590

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
595 600 605

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg
610 615 620

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser
625 630 635 640

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
645 650 655

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
660 665 670

```
Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
        675                 680                 685

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp
    690                 695                 700

Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp
705                 710                 715                 720

Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu
                725                 730                 735

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser
            740                 745                 750

Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
        755                 760                 765

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val
    770                 775                 780

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser
785                 790                 795                 800

Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val
                805                 810                 815

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly
            820                 825                 830

Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr
        835                 840                 845

Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
    850                 855                 860
```

Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser
865 870 875 880

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
885 890

<210> 202
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro180

<400> 202

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

```
Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Ser Lys Lys Leu Ala Asp Glu Pro Glu Gly Gly Ser Gln
            260                 265                 270

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
        275                 280                 285

Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
    290                 295                 300
```

```
Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
305                 310                 315                 320

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
                325                 330                 335

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
            340                 345                 350

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
        355                 360                 365

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Ser Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val
385                 390                 395                 400

Gln Thr Gly Gly Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr
                405                 410                 415

Ser Arg Ser Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu
            420                 425                 430

Arg Glu Phe Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr
        435                 440                 445

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
    450                 455                 460

Asn Thr Val Asp Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
465                 470                 475                 480

Ile Tyr Tyr Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu
```

485 490 495

Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
500 505 510

Gly Gly Gly Ser Lys Lys Leu Ala Asp Glu Pro Glu Gly Gly Gly Ser
515 520 525

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
530 535 540

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly
545 550 555 560

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
565 570 575

Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg
580 585 590

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

Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser
610 615 620

Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
625 630 635 640

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
645 650 655

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
660 665 670

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly
675 680 685

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys
690 695 700

Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
705 710 715 720

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
725 730 735

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
740 745 750

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
755 760 765

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
770 775 780

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg
785 790 795 800

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser
805 810 815

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile
820 825 830

Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg
835 840 845

Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met
850 855 860

Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly
865 870 875 880

Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
885 890 895

<210> 203
<211> 898
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro181

<400> 203

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Lys Lys Leu Ala Asp Glu Pro Glu Gly Gly Gly
260 265 270

Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
275 280 285

Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser
290 295 300

```
Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg
305                 310                 315                 320

Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg
                325                 330                 335

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly
            340                 345                 350

Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser
        355                 360                 365

Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
    370                 375                 380

Gly Ser Gly Gly Gly Ser Gln Val Lys Leu Glu Glu Ser Gly Gly Gly
385                 390                 395                 400

Ser Val Gln Thr Gly Gly Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly
                405                 410                 415

Arg Thr Ser Arg Ser Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly
            420                 425                 430

Lys Glu Arg Glu Phe Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr
        435                 440                 445

Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
    450                 455                 460

Ala Lys Asn Thr Val Asp Leu Gln Met Asn Ser Leu Lys Pro Glu Asp
465                 470                 475                 480

Thr Ala Ile Tyr Tyr Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly
                485                 490                 495
```

```
Thr Leu Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
            500                 505                 510

Ser Ser Gly Gly Gly Ser Lys Lys Leu Ala Asp Glu Pro Glu Gly Gly
        515                 520                 525

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro
    530                 535                 540

Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr
545                 550                 555                 560

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro
                565                 570                 575

Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro
            580                 585                 590

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

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
    610                 615                 620

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
625                 630                 635                 640

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
                645                 650                 655

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
            660                 665                 670

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
```

675 680 685

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp
690 695 700

Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr
705 710 715 720

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
725 730 735

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
740 745 750

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
755 760 765

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu
770 775 780

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser
785 790 795 800

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly
805 810 815

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
820 825 830

Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys
835 840 845

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu
850 855 860

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr
865 870 875 880

Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val
885 890 895

Ser Ser

<210> 204
<211> 891
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro182

<400> 204

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp

100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Pro Ala Gly Met Lys Gly Leu Gly Gln Thr Val Val Thr
260 265 270

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
275 280 285

```
Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
    290                 295                 300

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr
305                 310                 315                 320

Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
                325                 330                 335

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
            340                 345                 350

Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
        355                 360                 365

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
    370                 375                 380

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
385                 390                 395                 400

Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr
                405                 410                 415

Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
            420                 425                 430

Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val
        435                 440                 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
    450                 455                 460

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
465                 470                 475                 480
```

```
Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
                485                 490                 495

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro
            500                 505                 510

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr
        515                 520                 525

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
    530                 535                 540

Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
545                 550                 555                 560

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr
                565                 570                 575

Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
            580                 585                 590

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
        595                 600                 605

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
    610                 615                 620

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
625                 630                 635                 640

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
                645                 650                 655

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
            660                 665                 670
```

```
Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        675                 680                 685

Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys
    690                 695                 700

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
705                 710                 715                 720

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
                725                 730                 735

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser
            740                 745                 750

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
        755                 760                 765

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
    770                 775                 780

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
785                 790                 795                 800

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
                805                 810                 815

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
            820                 825                 830

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
        835                 840                 845

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
```

850 855 860

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
865 870 875 880

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
885 890

<210> 205
<211> 893
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro183

<400> 205

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Ser Gly Pro Ala Gly Met Lys Gly Leu Gly Ser Gln Thr Val
260 265 270

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
275 280 285

Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro

290 295 300

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
305 310 315 320

Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser
325 330 335

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
340 345 350

Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val
355 360 365

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly
370 375 380

Gly Ser Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr
385 390 395 400

Gly Gly Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg
405 410 415

Ser Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu
420 425 430

Phe Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp
435 440 445

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
450 455 460

Val Asp Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr
465 470 475 480

Tyr Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu
485 490 495

Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly
500 505 510

Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val
515 520 525

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
530 535 540

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
545 550 555 560

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
565 570 575

Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly
580 585 590

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
595 600 605

Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp
610 615 620

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly
625 630 635 640

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
645 650 655

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
660 665 670

```
Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        675                 680                 685

Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp
    690                 695                 700

Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
705                 710                 715                 720

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
                725                 730                 735

Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr
            740                 745                 750

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        755                 760                 765

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
    770                 775                 780

Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys
785                 790                 795                 800

Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg
                805                 810                 815

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser
            820                 825                 830

Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile
        835                 840                 845

Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu
    850                 855                 860
```

Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu
865 870 875 880

Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
885 890

<210> 206
<211> 895
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro184

<400> 206

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

```
Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Ser Gly Pro Ala Gly Met Lys Gly Leu Gly Gly Ser Gln
            260                 265                 270

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
        275                 280                 285

Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
    290                 295                 300
```

```
Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
305                 310                 315                 320

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
                325                 330                 335

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
            340                 345                 350

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
        355                 360                 365

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser
    370                 375                 380

Gly Gly Gly Ser Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val
385                 390                 395                 400

Gln Thr Gly Gly Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr
                405                 410                 415

Ser Arg Ser Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu
            420                 425                 430

Arg Glu Phe Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr
        435                 440                 445

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
    450                 455                 460

Asn Thr Val Asp Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
465                 470                 475                 480

Ile Tyr Tyr Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu
```

485 490 495

Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
500 505 510

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln
515 520 525

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
530 535 540

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
545 550 555 560

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
565 570 575

Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe
580 585 590

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
595 600 605

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
610 615 620

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
625 630 635 640

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
645 650 655

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
660 665 670

```
Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
        675                 680                 685

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp
    690                 695                 700

Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg
705                 710                 715                 720

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr
                725                 730                 735

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn
            740                 745                 750

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
        755                 760                 765

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
    770                 775                 780

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu
785                 790                 795                 800

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp
                805                 810                 815

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
            820                 825                 830

Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe
        835                 840                 845

Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn
    850                 855                 860
```

Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly
865 870 875 880

Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
885 890 895

<210> 207
<211> 897
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro185

<400> 207

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

```
Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Pro Ala Gly Met Lys Gly Leu Gly Gly Gly
            260                 265                 270

Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
        275                 280                 285

Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser
    290                 295                 300
```

```
Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg
305                 310                 315                 320

Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg
                325                 330                 335

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly
            340                 345                 350

Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser
        355                 360                 365

Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
    370                 375                 380

Gly Ser Gly Gly Gly Ser Gln Val Lys Leu Glu Glu Ser Gly Gly Gly
385                 390                 395                 400

Ser Val Gln Thr Gly Gly Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly
                405                 410                 415

Arg Thr Ser Arg Ser Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly
            420                 425                 430

Lys Glu Arg Glu Phe Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr
        435                 440                 445

Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
    450                 455                 460

Ala Lys Asn Thr Val Asp Leu Gln Met Asn Ser Leu Lys Pro Glu Asp
465                 470                 475                 480

Thr Ala Ile Tyr Tyr Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly
                485                 490                 495
```

```
Thr Leu Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
            500                 505                 510

Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
        515                 520                 525

Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
    530                 535                 540

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser
545                 550                 555                 560

Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg
                565                 570                 575

Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala
            580                 585                 590

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

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr
    610                 615                 620

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
625                 630                 635                 640

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
                645                 650                 655

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
            660                 665                 670

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
```

675 680 685

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr
690 695 700

Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
705 710 715 720

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
725 730 735

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
740 745 750

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
755 760 765

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val
770 775 780

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu
785 790 795 800

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met
805 810 815

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser
820 825 830

Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly
835 840 845

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln
850 855 860

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile
865 870 875 880

Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser
885 890 895

Ser

<210> 208
<211> 889
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro188

<400> 208

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp

```
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Pro Ala Gly Met Lys Gly Leu Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285
```

```
Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
    450                 455                 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465                 470                 475                 480
```

```
Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
            500                 505                 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
        515                 520                 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
    530                 535                 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545                 550                 555                 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Asp
                565                 570                 575

Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
            580                 585                 590

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
        595                 600                 605

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
    610                 615                 620

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu
625                 630                 635                 640

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
                645                 650                 655

Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala
            660                 665                 670
```

```
Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
        675                 680                 685

Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp
    690                 695                 700

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
705                 710                 715                 720

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
                725                 730                 735

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
            740                 745                 750

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
        755                 760                 765

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
    770                 775                 780

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
785                 790                 795                 800

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
                805                 810                 815

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
            820                 825                 830

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
        835                 840                 845

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
```

850 855 860

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
865 870 875 880

Gln Gly Thr Leu Val Thr Val Ser Ser
885

<210> 209
<211> 897
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro189

<400> 209

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

```
Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
```

290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

```
Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
            500                 505                 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
        515                 520                 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
    530                 535                 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545                 550                 555                 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp
                565                 570                 575

Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
            580                 585                 590

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
        595                 600                 605

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
    610                 615                 620

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly
625                 630                 635                 640

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
                645                 650                 655

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
            660                 665                 670
```

```
Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
        675                 680                 685

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr
    690                 695                 700

Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
705                 710                 715                 720

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
                725                 730                 735

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
            740                 745                 750

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
        755                 760                 765

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val
    770                 775                 780

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu
785                 790                 795                 800

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met
                805                 810                 815

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser
            820                 825                 830

Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly
        835                 840                 845

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln
    850                 855                 860
```

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile
865 870 875 880

Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser
885 890 895

Ser

<210> 210
<211> 898
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro190

<400> 210

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

```
Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285
```

```
Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
    450                 455                 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
```

465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser Lys Lys
500 505 510

Leu Ala Asp Glu Pro Glu Gly Gly Gly Ser Gln Thr Val Val Thr Gln
515 520 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
530 535 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545 550 555 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
565 570 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
580 585 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
595 600 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
610 615 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625 630 635 640

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
645 650 655

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
660 665 670

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
675 680 685

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp
690 695 700

Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr
705 710 715 720

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
725 730 735

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
740 745 750

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
755 760 765

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu
770 775 780

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser
785 790 795 800

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly
805 810 815

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
820 825 830

Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys
835 840 845

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu
850 855 860

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr
865 870 875 880

Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val
885 890 895

Ser Ser

<210> 211
<211> 903
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro191

<400> 211

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

```
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270
```

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
500 505 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
515 520 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
530 535 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545 550 555 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp
565 570 575

Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
580 585 590

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
595 600 605

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
610 615 620

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly
625 630 635 640

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly

645 650 655

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
660 665 670

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
675 680 685

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr
690 695 700

Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
705 710 715 720

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
725 730 735

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
740 745 750

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
755 760 765

Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly
770 775 780

Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
785 790 795 800

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
805 810 815

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
820 825 830

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
835 840 845

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
850 855 860

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
865 870 875 880

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
885 890 895

Thr Leu Val Thr Val Ser Ser
900

<210> 212
<211> 905
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro192

<400> 212

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp

65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

```
Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385                 390                 395                 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
                405                 410                 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
            420                 425                 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
        435                 440                 445
```

```
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
    450                 455                 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465                 470                 475                 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser Lys Lys
            500                 505                 510

Leu Ala Asp Glu Pro Glu Gly Gly Gly Ser Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640
```

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
645 650 655

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
660 665 670

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
675 680 685

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp
690 695 700

Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr
705 710 715 720

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
725 730 735

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
740 745 750

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
755 760 765

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Lys Lys Leu Ala Asp Glu
770 775 780

Pro Glu Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
785 790 795 800

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
805 810 815

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly

820 825 830

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
835 840 845

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
850 855 860

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
865 870 875 880

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
885 890 895

Gln Gly Thr Leu Val Thr Val Ser Ser
900 905

<210> 213
<211> 763
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro193

<400> 213

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
```

245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
370 375 380

Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
385 390 395 400

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
405 410 415

Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
420 425 430

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp
435 440 445

Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg
450 455 460

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr
465 470 475 480

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn
485 490 495

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
500 505 510

Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr
515 520 525

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
530 535 540

Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
545 550 555 560

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr
565 570 575

Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
580 585 590

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
595 600 605

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
610 615 620

Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gly Gly Pro Gly Pro Ala
625 630 635 640

Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly
645 650 655

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
660 665 670

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
675 680 685

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
690 695 700

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
705 710 715 720

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
725 730 735

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
740 745 750

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
755 760

<210> 214
<211> 892
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro195

<400> 214

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1               5                  10                  15

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

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

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

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

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

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

Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    130                 135                 140

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
145                 150                 155                 160

Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro
                165                 170                 175

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
            180                 185                 190
```

Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser
195 200 205

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
210 215 220

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly
225 230 235 240

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
245 250 255

Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val
260 265 270

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
275 280 285

Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
290 295 300

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
305 310 315 320

Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
325 330 335

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
340 345 350

Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe
355 360 365

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
370 375 380

```
Ser Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly
385                 390                 395                 400

Gly Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser
                405                 410                 415

Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe
            420                 425                 430

Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser
        435                 440                 445

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val
    450                 455                 460

Asp Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr
465                 470                 475                 480

Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr
                485                 490                 495

Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly
            500                 505                 510

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val
        515                 520                 525

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
    530                 535                 540

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
545                 550                 555                 560

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp
```

565 570 575

Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser
580 585 590

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
595 600 605

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
610 615 620

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly
625 630 635 640

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
645 650 655

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
660 665 670

Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
675 680 685

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp
690 695 700

Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
705 710 715 720

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
725 730 735

Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile
740 745 750

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
755 760 765

Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
770 775 780

Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala
785 790 795 800

Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln
805 810 815

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
820 825 830

Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser
835 840 845

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
850 855 860

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
865 870 875 880

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
885 890

<210> 215
<211> 889
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro196

<400> 215

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly

1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
130 135 140

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala
145 150 155 160

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr
180 185 190

```
Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
        195                 200                 205

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu
    210                 215                 220

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
225                 230                 235                 240

Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380
```

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
500 505 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
515 520 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
530 535 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545 550 555 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp
565 570 575

```
Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
            580                 585                 590

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
        595                 600                 605

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
    610                 615                 620

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu
625                 630                 635                 640

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
                645                 650                 655

Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala
            660                 665                 670

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
        675                 680                 685

Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp
    690                 695                 700

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
705                 710                 715                 720

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
                725                 730                 735

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
            740                 745                 750

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
```

755 760 765

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
770 775 780

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
785 790 795 800

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
805 810 815

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
820 825 830

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
835 840 845

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
850 855 860

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
865 870 875 880

Gln Gly Thr Leu Val Thr Val Ser Ser
885

<210> 216
<211> 888
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro197

<400> 216

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp

195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
500 505 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser
515 520 525

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
530 535 540

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
545 550 555 560

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
565 570 575

Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe
580 585 590

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
595 600 605

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly
610 615 620

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

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
645 650 655

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
660 665 670

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
675 680 685

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
690 695 700

Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe
705 710 715 720

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
725 730 735

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
740 745 750

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
755 760 765

```
Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
    770                 775                 780

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
785                 790                 795                 800

Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
                805                 810                 815

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
            820                 825                 830

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
        835                 840                 845

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
    850                 855                 860

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
865                 870                 875                 880

Gly Thr Leu Val Thr Val Ser Ser
                885
```

<210> 217
<211> 888
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro198

<400> 217

```
Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1               5                   10                  15
```

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
130 135 140

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala
145 150 155 160

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr
180 185 190

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
195 200 205

```
Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu
    210                 215                 220

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
225                 230                 235                 240

Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
            260                 265                 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln
        275                 280                 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
    290                 295                 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr
305                 310                 315                 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
                325                 330                 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn
            340                 345                 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
        355                 360                 365

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
```

385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
500 505 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser
515 520 525

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
530 535 540

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
545 550 555 560

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
565 570 575

```
Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe
            580                 585                 590

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
        595                 600                 605

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly
    610                 615                 620

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

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
                645                 650                 655

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
            660                 665                 670

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
        675                 680                 685

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
    690                 695                 700

Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe
705                 710                 715                 720

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
                725                 730                 735

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
            740                 745                 750

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
        755                 760                 765
```

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
770 775 780

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
785 790 795 800

Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
805 810 815

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
820 825 830

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
835 840 845

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
850 855 860

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
865 870 875 880

Gly Thr Leu Val Thr Val Ser Ser
885

<210> 218
<211> 885
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro199

<400> 218

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

```
Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser
            20                  25                  30

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145                 150                 155                 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
            180                 185                 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
        195                 200                 205
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Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
                245                 250                 255

Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
            260                 265                 270

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser
        275                 280                 285

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
    290                 295                 300

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val
305                 310                 315                 320

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
                325                 330                 335

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
            340                 345                 350

Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
        355                 360                 365

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu
    370                 375                 380

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Thr Leu
385                 390                 395                 400
```

Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn Leu Met
405 410 415

Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val Ala Arg
420 425 430

Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys Gly Arg
435 440 445

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
450 455 460

Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn Leu Leu
465 470 475 480

Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln Gly Thr
485 490 495

Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
500 505 510

Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
515 520 525

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
530 535 540

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
545 550 555 560

Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys
565 570 575

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala

580 585 590

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
595 600 605

Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu
610 615 620

Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val
625 630 635 640

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser
645 650 655

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val
660 665 670

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser
675 680 685

Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp
690 695 700

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
705 710 715 720

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
725 730 735

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
740 745 750

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
755 760 765

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
770 775 780

Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
785 790 795 800

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
805 810 815

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
820 825 830

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr
835 840 845

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
850 855 860

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
865 870 875 880

Val Thr Val Ser Ser
885

<210> 219
<211> 886
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro200

<400> 219

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

Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser

20 25 30

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

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

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

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

Cys Asn Leu Leu Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145 150 155 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
180 185 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
195 200 205

```
Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
                245                 250                 255

Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
            260                 265                 270

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser
        275                 280                 285

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
    290                 295                 300

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val
305                 310                 315                 320

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
                325                 330                 335

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
            340                 345                 350

Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
        355                 360                 365

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu
    370                 375                 380

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Thr Leu
385                 390                 395                 400
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Ser Cys Ala Ala Ser Gly Thr Gly Ser Ile Phe Ser Ile Asn Leu Met
405 410 415

Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val Ala Arg
420 425 430

Ile Thr Ser Gly Asp Ser Thr Val Tyr Ala Asp Ser Val Lys Gly Arg
435 440 445

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
450 455 460

Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn Leu Leu
465 470 475 480

Leu Arg Ser Ser Pro Gly Ala Thr Thr Pro Tyr Trp Gly Gln Gly Thr
485 490 495

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Lys Lys Leu Ala Asp Glu
500 505 510

Pro Glu Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu
515 520 525

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr
530 535 540

Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro
545 550 555 560

Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp
565 570 575

Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
580 585 590

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
595 600 605

Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
610 615 620

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
625 630 635 640

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
645 650 655

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
660 665 670

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
675 680 685

Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys
690 695 700

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
705 710 715 720

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
725 730 735

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
740 745 750

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
755 760 765

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln

770 775 780

Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
785 790 795 800

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
805 810 815

Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala
820 825 830

Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
835 840 845

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
850 855 860

Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
865 870 875 880

Leu Val Thr Val Ser Ser
885

<210> 220
<211> 903
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro189 (Pro186 con enlazador largo entre dominios de acD3 inactivados)

<400> 220

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr

20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
500 505 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
515 520 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
530 535 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545 550 555 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp
565 570 575

Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
580 585 590

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
595 600 605

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
610 615 620

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly
625 630 635 640

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
645 650 655

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
660 665 670

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
675 680 685

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr
690 695 700

Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
705 710 715 720

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
725 730 735

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
740 745 750

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
755 760 765

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val

770 775 780

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu
785 790 795 800

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met
805 810 815

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser
820 825 830

Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly
835 840 845

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln
850 855 860

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile
865 870 875 880

Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser
885 890 895

Ser His His His His His His
900

<210> 221
<211> 636
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro206 (Dominio activo Pro186+ aHSA)

<400> 221

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly

1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

```
Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
    370                 375                 380
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Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
500 505 510

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
515 520 525

Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
530 535 540

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
545 550 555 560

Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala
565 570 575

Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
580 585 590

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
595 600 605

Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
610 615 620

Leu Val Thr Val Ser Ser His His His His His His
625 630 635

<210> 222
<211> 513
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro227 (Pro22 aB7H3 hF7)

<400> 222

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

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

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

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

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

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

Ala Ala Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
    130                 135                 140

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
145                 150                 155                 160

Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys
                165                 170                 175

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala
            180                 185                 190

Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp
        195                 200                 205

Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu
    210                 215                 220

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser
225                 230                 235                 240

Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
                245                 250                 255

Ser Ser Gly Gly Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly
            260                 265                 270
```

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro
275 280 285

Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr
290 295 300

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro
305 310 315 320

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala
325 330 335

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
340 345 350

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr
355 360 365

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
385 390 395 400

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
405 410 415

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
420 425 430

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
435 440 445

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

450 455 460

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
465 470 475 480

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
485 490 495

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His
500 505 510

His

<210> 223
<211> 511
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro228 (Pro22 aB7H3 hF12)

<400> 223

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

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

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

Ala Ala Ile Asn Trp Ser Gly Gly Asn 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 Ala Gly Gly Val Leu Ala His His Asn Tyr Glu Tyr Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
    130                 135                 140

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
145                 150                 155                 160

Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
                165                 170                 175

Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr
            180                 185                 190

Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
        195                 200                 205

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
    210                 215                 220

Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile
225                 230                 235                 240

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
                245                 250                 255

Gly Gly Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly Ser
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260 265 270

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
275 280 285

Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly
290 295 300

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
305 310 315 320

Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe
325 330 335

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
340 345 350

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn
355 360 365

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
385 390 395 400

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
405 410 415

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
420 425 430

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
435 440 445

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
450 455 460

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
465 470 475 480

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
485 490 495

Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
500 505 510

<210> 224
<211> 512
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro244 (Pro51 aB7H3 hF7)

<400> 224

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

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

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

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

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

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

85 90 95

Ala Ala Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
130 135 140

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
145 150 155 160

Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys
165 170 175

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala
180 185 190

Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp
195 200 205

Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu
210 215 220

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser
225 230 235 240

Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
245 250 255

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
260 265 270

Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
275 280 285

Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser
290 295 300

Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg
305 310 315 320

Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg
325 330 335

Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly
340 345 350

Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser
355 360 365

Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
385 390 395 400

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
405 410 415

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
420 425 430

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
435 440 445

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
450 455 460

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
465 470 475 480

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

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
500 505 510

<210> 225
<211> 510
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro245 (Pro51 aB7H3 hF12)

<400> 225

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

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

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

Ala Ala Ile Asn Trp Ser Gly Gly Asn 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

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Ala Ala Gly Gly Val Leu Ala His His Asn Tyr Glu Tyr Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
    130                 135                 140

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
145                 150                 155                 160

Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
                165                 170                 175

Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr
            180                 185                 190

Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
        195                 200                 205

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
    210                 215                 220

Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile
225                 230                 235                 240

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
                245                 250                 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
            260                 265                 270

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
        275                 280                 285
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Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
    290                 295                 300

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
305                 310                 315                 320

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
                325                 330                 335

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
            340                 345                 350

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
        355                 360                 365

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
385                 390                 395                 400

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                405                 410                 415

Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
            420                 425                 430

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
        435                 440                 445

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    450                 455                 460

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
465                 470                 475                 480
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Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
485 490 495

Gly Thr Leu Val Thr Val Ser Ser His His His His His His
500 505 510

<210> 226
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro247 (Pro186 humanizado con enlazador de Meprina)

<400> 226

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala
465 470 475 480

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Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Lys Lys
            500                 505                 510

Leu Ala Asp Glu Pro Glu Gly Gly Gly Ser Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670
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Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
                805                 810                 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
            820                 825                 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
        835                 840                 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
    850                 855                 860
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Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 227
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro248 (Pro186 humanizado con enlazador CathS)

<400> 227

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala
465 470 475 480

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Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Ala Arg
            500                 505                 510

Leu Gln Ser Ala Ala Pro Gly Gly Gly Ser Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670
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Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
                805                 810                 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
            820                 825                 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
        835                 840                 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
    850                 855                 860
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Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 228
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro249 (Pro186 humanizado con enlazador de Meprina/Grancima B)

<400> 228

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala
465 470 475 480

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Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Val Tyr
            500                 505                 510

Ala Asp Ser Leu Glu Asp Gly Gly Gly Ser Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670
```

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Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
                805                 810                 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
            820                 825                 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
        835                 840                 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
    850                 855                 860
```

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 229
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro250 (Pro186 humanizado con S9 - enlazador CathS/MMP9)

<400> 229

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala
465 470 475 480

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Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ala Arg Leu Gln Ser
            500                 505                 510

Ala Ala Pro Ala Gly Leu Lys Gly Ala Gly Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670
```

```
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
                805                 810                 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
            820                 825                 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
        835                 840                 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
    850                 855                 860
```

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 230
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro251 (Pro186 humanizado con enlazador ST14(MS)

<400> 230

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala
465 470 475 480

```
Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Leu Ser
            500                 505                 510

Gly Arg Ser Asp Asn His Gly Gly Gly Ser Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670
```

```
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705                 710                 715                 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
                725                 730                 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
            740                 745                 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        755                 760                 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    770                 775                 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785                 790                 795                 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
                805                 810                 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
            820                 825                 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
        835                 840                 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
    850                 855                 860
```

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 231
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro252 (Pro186 humanizado con enlazador ST14(MV)

<400> 231

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

```
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
```

290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala
465 470 475 480

```
Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Phe Thr
            500                 505                 510

Arg Gln Ala Arg Val Val Gly Gly Gly Ser Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670
```

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
675 680 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
690 695 700

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705 710 715 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
725 730 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
740 745 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
755 760 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
770 775 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785 790 795 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
805 810 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
820 825 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
835 840 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
850 855 860

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 232
<211> 897
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro253 (Pro18 humanizado 6 con MMP9v enlazador)

<400> 232

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala
465 470 475 480

```
Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Gly Gly Pro Gly
            500                 505                 510

Pro Ala Gly Met His Gly Leu Pro Gly Gly Ser Gln Thr Val Val Thr
        515                 520                 525

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
    530                 535                 540

Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
545                 550                 555                 560

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr
                565                 570                 575

Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
            580                 585                 590

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
        595                 600                 605

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
    610                 615                 620

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
625                 630                 635                 640

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
                645                 650                 655

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
            660                 665                 670
```

```
Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        675                 680                 685

Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys
    690                 695                 700

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
705                 710                 715                 720

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
                725                 730                 735

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser
            740                 745                 750

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
        755                 760                 765

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
    770                 775                 780

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
785                 790                 795                 800

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
                805                 810                 815

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
            820                 825                 830

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
        835                 840                 845

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
    850                 855                 860
```

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
865 870 875 880

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His
885 890 895

His

<210> 233
<211> 902
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro261 (Pro186 humanizado con un enlazador acD3 de largo dominio activo)

<400> 233

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

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

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

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

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

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

```
Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            260                 265                 270

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
```

275 280 285

Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly
290 295 300

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
305 310 315 320

Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe
325 330 335

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
340 345 350

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn
355 360 365

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
370 375 380

Ser Gly Gly Gly Ser Gln Val Lys Leu Val Glu Ser Gly Gly Gly Val
385 390 395 400

Val Arg Pro Gly Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Arg
405 410 415

Thr Ser Arg Ser Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys
420 425 430

Glu Arg Glu Phe Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly
435 440 445

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
450 455 460

```
Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
465                 470                 475                 480

Ala Leu Tyr Tyr Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr
                485                 490                 495

Leu Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
            500                 505                 510

Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
        515                 520                 525

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
    530                 535                 540

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly
545                 550                 555                 560

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
                565                 570                 575

Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg
            580                 585                 590

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

Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser
    610                 615                 620

Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
625                 630                 635                 640

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
                645                 650                 655
```

```
Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
            660                 665                 670

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly
        675                 680                 685

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys
    690                 695                 700

Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
705                 710                 715                 720

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
                725                 730                 735

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
            740                 745                 750

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
        755                 760                 765

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
    770                 775                 780

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg
785                 790                 795                 800

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser
                805                 810                 815

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile
            820                 825                 830

Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg
        835                 840                 845
```

Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met
850 855 860

Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly
865 870 875 880

Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
885 890 895

His His His His His His
900

<210> 234
<211> 901
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro294 (enlazador FL haEGFR2 MMP9)

<400> 234

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

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

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

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

Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
    130                 135                 140

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
145                 150                 155                 160

Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro
                165                 170                 175

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
            180                 185                 190

Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser
        195                 200                 205

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
    210                 215                 220

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly
225                 230                 235                 240

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
                245                 250                 255

Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val
            260                 265                 270
```

```
Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
        275                 280                 285

Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
    290                 295                 300

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
305                 310                 315                 320

Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
                325                 330                 335

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
            340                 345                 350

Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe
        355                 360                 365

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
    370                 375                 380

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
385                 390                 395                 400

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser
                405                 410                 415

Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe
            420                 425                 430

Val Val Ala Ile Asn Trp Ser Ser Gly Ser Thr Tyr Tyr Ala Asp Ser
        435                 440                 445

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
```

450 455 460

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
465 470 475 480

Cys Ala Ala Gly Tyr Gln Ile Asn Ser Gly Asn Tyr Asn Phe Lys Asp
485 490 495

Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
500 505 510

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln
515 520 525

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
530 535 540

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
545 550 555 560

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
565 570 575

Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe
580 585 590

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
595 600 605

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
610 615 620

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
625 630 635 640

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
645 650 655

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
660 665 670

Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
675 680 685

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp
690 695 700

Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg
705 710 715 720

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr
725 730 735

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn
740 745 750

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
755 760 765

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
770 775 780

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu
785 790 795 800

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp
805 810 815

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
820 825 830

Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe
835 840 845

Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn
850 855 860

Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly
865 870 875 880

Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His
885 890 895

His His His His His
900

<210> 235
<211> 895
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro295 (enlazador FL aB7H3 hF7 NC)

<400> 235

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

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

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

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

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

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

Ala Ala Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255
```

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Arg Leu Ser Cys Ala Pro Ser Arg Arg Thr Phe His Thr Tyr His Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ala Val
420 425 430

Ile Asn Trp Ser Gly Gly Ser Thr Val Tyr Ala Asp Ser Val Lys Gly
435 440 445

```
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
    450                 455                 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala
465                 470                 475                 480

Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp Tyr Trp
                485                 490                 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
            500                 505                 510

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
        515                 520                 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
    530                 535                 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545                 550                 555                 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp
                565                 570                 575

Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
            580                 585                 590

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
        595                 600                 605

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
    610                 615                 620

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu
```

625 630 635 640

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
645 650 655

Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala
660 665 670

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
675 680 685

Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp
690 695 700

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
705 710 715 720

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
725 730 735

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
740 745 750

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
755 760 765

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
770 775 780

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
785 790 795 800

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
805 810 815

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
820 825 830

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
835 840 845

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
850 855 860

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
865 870 875 880

Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 236
<211> 891
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro296 (enlazador FL aB7H3 hF12 NC)

<400> 236

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

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

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

Ala Ala Ile Asn Trp Ser Gly Gly Asn 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 Ala Gly Gly Val Leu Ala His His Asn Tyr Glu Tyr Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145                 150                 155                 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
            180                 185                 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
        195                 200                 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
    210                 215                 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225                 230                 235                 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
                245                 250                 255
```

```
Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
            260                 265                 270

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser
        275                 280                 285

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
    290                 295                 300

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val
305                 310                 315                 320

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
                325                 330                 335

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
            340                 345                 350

Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
        355                 360                 365

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu
    370                 375                 380

Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
385                 390                 395                 400

Ser Cys Glu Ala Ser Pro Arg Thr Phe Ser Thr Tyr Ser Met Ala Trp
                405                 410                 415

Phe Arg Gln Ala Pro Gly Lys Glu Arg Ser Phe Val Ala Ala Ile Asn
            420                 425                 430

Trp Ser Gly Gly Asn Thr Ser Tyr Ala Asp Ser Val Lys Gly Arg Phe
        435                 440                 445
```

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
450 455 460

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Gly Gly
465 470 475 480

Val Leu Ala His His Asn Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr
485 490 495

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
500 505 510

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
515 520 525

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
530 535 540

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
545 550 555 560

Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys
565 570 575

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
580 585 590

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
595 600 605

Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu
610 615 620

Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val

625 630 635 640

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser
645 650 655

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val
660 665 670

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser
675 680 685

Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp
690 695 700

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
705 710 715 720

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
725 730 735

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
740 745 750

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
755 760 765

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
770 775 780

Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
785 790 795 800

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
805 810 815

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
820 825 830

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr
835 840 845

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
850 855 860

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
865 870 875 880

Val Thr Val Ser Ser His His His His His His
885 890

<210> 237
<211> 876
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro297 (enlazador FL aFOLR1 h77-2 KLK7.6)

<400> 237

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

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

Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val
35 40 45

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

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

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

Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
        115                 120                 125

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys
    130                 135                 140

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg
145                 150                 155                 160

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys
                165                 170                 175

Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe
            180                 185                 190

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
        195                 200                 205

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala
    210                 215                 220

Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
                245                 250                 255
```

```
Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
            260                 265                 270

Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
        275                 280                 285

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
    290                 295                 300

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
305                 310                 315                 320

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
                325                 330                 335

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
            340                 345                 350

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser
        355                 360                 365

Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    370                 375                 380

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
385                 390                 395                 400

Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu
                405                 410                 415

Arg Glu Phe Val Ala Ile Ile Asn Ser Ile Gly Ile Thr Asn Tyr Ala
            420                 425                 430

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
        435                 440                 445
```

```
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
    450                 455                 460

Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr
465                 470                 475                 480

Leu Val Thr Val Ser Ser Ser Gly Gly Gly Gln Asn Pro Tyr Ser Ala
                485                 490                 495

Gly Arg Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu
            500                 505                 510

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr
        515                 520                 525

Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro
    530                 535                 540

Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp
545                 550                 555                 560

Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
                565                 570                 575

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
            580                 585                 590

Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
        595                 600                 605

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
    610                 615                 620

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
```

625 630 635 640

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
645 650 655

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
660 665 670

Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys
675 680 685

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
690 695 700

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
705 710 715 720

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
725 730 735

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
740 745 750

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
755 760 765

Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
770 775 780

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
785 790 795 800

Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala
805 810 815

Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
820 825 830

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
835 840 845

Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
850 855 860

Leu Val Thr Val Ser Ser His His His His His His
865 870 875

<210> 238
<211> 876
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro298 (enlazador FL aFOLR1 h77-2 KLK7.11)

<400> 238

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

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

Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val
35 40 45

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

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

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

Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
        115                 120                 125

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys
    130                 135                 140

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg
145                 150                 155                 160

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys
                165                 170                 175

Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe
            180                 185                 190

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
        195                 200                 205

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala
    210                 215                 220

Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
                245                 250                 255

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
            260                 265                 270
```

```
Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
        275                 280                 285

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
    290                 295                 300

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
305                 310                 315                 320

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
                325                 330                 335

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
            340                 345                 350

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser
        355                 360                 365

Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    370                 375                 380

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
385                 390                 395                 400

Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu
                405                 410                 415

Arg Glu Phe Val Ala Ile Ile Asn Ser Ile Gly Ile Thr Asn Tyr Ala
            420                 425                 430

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
        435                 440                 445

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
    450                 455                 460
```

Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr
465 470 475 480

Leu Val Thr Val Ser Ser Ser Gly Gly Gly Arg Asn Val Tyr Ser Ala
485 490 495

Gly Gly Gly Ser Gly Gly Gln Thr Val Val Thr Gln Glu Pro Ser Leu
500 505 510

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr
515 520 525

Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro
530 535 540

Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp
545 550 555 560

Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
565 570 575

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
580 585 590

Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
595 600 605

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
610 615 620

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
625 630 635 640

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

645 650 655

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
660 665 670

Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys
675 680 685

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
690 695 700

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
705 710 715 720

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
725 730 735

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
740 745 750

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
755 760 765

Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
770 775 780

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
785 790 795 800

Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala
805 810 815

Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
820 825 830

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
835 840 845

Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
850 855 860

Leu Val Thr Val Ser Ser His His His His His His
865 870 875

<210> 239
<211> 876
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - enlazador Pro299 (FL aFOLR1 h77-2 NC)

<400> 239

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

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

Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val
35 40 45

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

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

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

```
Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
        115                 120                 125

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys
    130                 135                 140

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg
145                 150                 155                 160

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys
                165                 170                 175

Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe
            180                 185                 190

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
        195                 200                 205

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala
    210                 215                 220

Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
                245                 250                 255

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
            260                 265                 270

Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
        275                 280                 285
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Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
    290                 295                 300

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
305                 310                 315                 320

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
                325                 330                 335

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
            340                 345                 350

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser
        355                 360                 365

Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    370                 375                 380

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
385                 390                 395                 400

Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu
                405                 410                 415

Arg Glu Phe Val Ala Ile Ile Asn Ser Ile Gly Ile Thr Asn Tyr Ala
            420                 425                 430

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
        435                 440                 445

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
    450                 455                 460

Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr
465                 470                 475                 480
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Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
485 490 495

Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu
500 505 510

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr
515 520 525

Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro
530 535 540

Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp
545 550 555 560

Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
565 570 575

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
580 585 590

Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
595 600 605

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
610 615 620

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
625 630 635 640

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
645 650 655

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

660 665 670

Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys
675 680 685

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
690 695 700

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
705 710 715 720

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
725 730 735

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
740 745 750

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
755 760 765

Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
770 775 780

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
785 790 795 800

Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala
805 810 815

Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
820 825 830

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
835 840 845

Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
850 855 860

Leu Val Thr Val Ser Ser His His His His His His
865 870 875

<210> 240
<211> 502
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro300 (Pro51 aFOLR1 h77-2)

<400> 240

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

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

Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val
35 40 45

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

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

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

Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val

115 120 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser
130 135 140

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val
145 150 155 160

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser
165 170 175

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg
180 185 190

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met
195 200 205

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
210 215 220

Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln
225 230 235 240

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
245 250 255

Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
260 265 270

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser
275 280 285

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
290 295 300

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val
305 310 315 320

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
325 330 335

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
340 345 350

Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
355 360 365

Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
370 375 380

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg
385 390 395 400

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser
405 410 415

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile
420 425 430

Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg
435 440 445

Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met
450 455 460

Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly
465 470 475 480

Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
485 490 495

His His His His His His
500

<210> 241
<211> 874
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro301 (enlazador FL aFOLR1 h59.3 KLK7.6)

<400> 241

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

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

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

Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
115 120 125

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Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
    130                 135                 140

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln
145                 150                 155                 160

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
                165                 170                 175

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr
            180                 185                 190

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
        195                 200                 205

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn
    210                 215                 220

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
225                 230                 235                 240

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr
                245                 250                 255

Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
            260                 265                 270

Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr
        275                 280                 285

Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile
    290                 295                 300

Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly
305                 310                 315                 320
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Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
325 330 335

Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp
340 345 350

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly
355 360 365

Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
370 375 380

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Pro Gly Asn Thr Phe
385 390 395 400

Ser Ile Ser Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg
405 410 415

Glu Trp Val Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp
420 425 430

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
435 440 445

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
450 455 460

Tyr Cys Lys His Tyr Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
465 470 475 480

Thr Val Ser Ser Ser Gly Gly Gly Gln Asn Pro Tyr Ser Ala Gly Arg
485 490 495

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

500 505 510

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
515 520 525

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
530 535 540

Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly
545 550 555 560

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
565 570 575

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
580 585 590

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
595 600 605

Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
610 615 620

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys
625 630 635 640

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg
645 650 655

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys
660 665 670

Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg
675 680 685

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met
690 695 700

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
705 710 715 720

Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln
725 730 735

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
755 760 765

Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys
770 775 780

Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
785 790 795 800

Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser
805 810 815

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu
820 825 830

Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr
835 840 845

Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val
850 855 860

Thr Val Ser Ser His His His His His His
865 870

<210> 242
<211> 874
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro302 (enlazador FL aFOLR1 h59.3 KLK7.11)

<400> 242

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

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

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

Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
115 120 125

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
130 135 140

```
Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln
145                 150                 155                 160

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
                165                 170                 175

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr
            180                 185                 190

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
        195                 200                 205

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn
    210                 215                 220

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
225                 230                 235                 240

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr
                245                 250                 255

Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
            260                 265                 270

Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr
        275                 280                 285

Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile
    290                 295                 300

Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly
305                 310                 315                 320

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
                325                 330                 335
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Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp
            340                 345                 350

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly
        355                 360                 365

Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
    370                 375                 380

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Pro Gly Asn Thr Phe
385                 390                 395                 400

Ser Ile Ser Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg
                405                 410                 415

Glu Trp Val Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp
            420                 425                 430

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
        435                 440                 445

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
    450                 455                 460

Tyr Cys Lys His Tyr Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
465                 470                 475                 480

Thr Val Ser Ser Ser Gly Gly Gly Arg Asn Val Tyr Ser Ala Gly Gly
                485                 490                 495

Gly Ser Gly Gly Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
            500                 505                 510

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
```

515 520 525

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
530 535 540

Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly
545 550 555 560

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
565 570 575

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
580 585 590

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
595 600 605

Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
610 615 620

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys
625 630 635 640

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg
645 650 655

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys
660 665 670

Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg
675 680 685

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met
690 695 700

```
Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
705                 710                 715                 720

Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln
                725                 730                 735

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
            740                 745                 750

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
        755                 760                 765

Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys
    770                 775                 780

Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
785                 790                 795                 800

Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser
                805                 810                 815

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu
            820                 825                 830

Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr
        835                 840                 845

Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val
    850                 855                 860

Thr Val Ser Ser His His His His His His
865                 870
```

<210> 243
<211> 874
<212> PRT

<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro303 (enlazador FL aFOLR1 h59.3 NC)

<400> 243

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

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

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

Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
115 120 125

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
130 135 140

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln
145 150 155 160

```
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
               165                 170                 175

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr
            180                 185                 190

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
        195                 200                 205

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn
    210                 215                 220

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
225                 230                 235                 240

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr
               245                 250                 255

Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
            260                 265                 270

Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr
        275                 280                 285

Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile
    290                 295                 300

Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly
305                 310                 315                 320

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
               325                 330                 335

Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp
            340                 345                 350
```

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly
355 360 365

Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
370 375 380

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Pro Gly Asn Thr Phe
385 390 395 400

Ser Ile Ser Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg
405 410 415

Glu Trp Val Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp
420 425 430

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
435 440 445

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
450 455 460

Tyr Cys Lys His Tyr Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
465 470 475 480

Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
485 490 495

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
500 505 510

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
515 520 525

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

530 535 540

Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly
545 550 555 560

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
565 570 575

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
580 585 590

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
595 600 605

Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
610 615 620

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys
625 630 635 640

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg
645 650 655

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys
660 665 670

Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg
675 680 685

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met
690 695 700

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
705 710 715 720

```
Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln
               725                 730                 735

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
           740                 745                 750

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
        755                 760                 765

Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys
    770                 775                 780

Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
785                 790                 795                 800

Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser
               805                 810                 815

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu
           820                 825                 830

Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr
        835                 840                 845

Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val
    850                 855                 860

Thr Val Ser Ser His His His His His His
865                 870
```

<210> 244
<211> 501
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro304 (Pro51 aFOLR1 h59.3)

<400> 244

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

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

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

Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
115 120 125

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys
130 135 140

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg
145 150 155 160

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys
165 170 175

```
Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe
            180                 185                 190

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
        195                 200                 205

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala
    210                 215                 220

Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                245                 250                 255

Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu
            260                 265                 270

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr
        275                 280                 285

Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro
    290                 295                 300

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro
305                 310                 315                 320

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
                325                 330                 335

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
            340                 345                 350

Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu
        355                 360                 365
```

```
Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
    370                 375                 380

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu
385                 390                 395                 400

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp
                405                 410                 415

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
            420                 425                 430

Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe
        435                 440                 445

Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn
    450                 455                 460

Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly
465                 470                 475                 480

Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His
                485                 490                 495

His His His His His
            500
```

<210> 245
<211> 882
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro305 (enlazador FL aFOLR1 h22.4 KLK7.6)

<400> 245

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

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

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

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

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

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

Ala Asn Thr Ala Thr Trp Gly Arg Val Phe Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
        115                 120                 125

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
    130                 135                 140

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn
145                 150                 155                 160

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
                165                 170                 175

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys
            180                 185                 190
```

```
Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
        195                 200                 205

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
    210                 215                 220

Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
                245                 250                 255

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro
            260                 265                 270

Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr
        275                 280                 285

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro
    290                 295                 300

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala
305                 310                 315                 320

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
                325                 330                 335

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr
            340                 345                 350

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly
```

370 375 380

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser
385 390 395 400

Gly Thr Thr Phe Ser Arg Asp Val Met Gly Trp Tyr Arg Gln Ala Pro
405 410 415

Gly Lys Gln Arg Glu Leu Val Ala Ile Ile Ser Arg Gly Gly Ser Thr
420 425 430

Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
435 440 445

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
450 455 460

Thr Ala Val Tyr Tyr Cys Asn Ala Asn Thr Ala Thr Trp Gly Arg Val
465 470 475 480

Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Gly
485 490 495

Arg Asn Val Tyr Ser Ala Gly Gly Gly Ser Gly Gly Gln Thr Val Val
500 505 510

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
515 520 525

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
530 535 540

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp
545 550 555 560

Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser
565 570 575

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
580 585 590

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
595 600 605

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly
610 615 620

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
625 630 635 640

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
645 650 655

Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
660 665 670

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp
675 680 685

Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
690 695 700

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
705 710 715 720

Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile
725 730 735

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
755 760 765

Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala
770 775 780

Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln
785 790 795 800

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
805 810 815

Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser
820 825 830

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
835 840 845

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
850 855 860

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His
865 870 875 880

His His

<210> 246
<211> 882
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro306 (enlazador FL aFOLR1 h22.4 KLK7.11)

<400> 246

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

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

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

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

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

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

Ala Asn Thr Ala Thr Trp Gly Arg Val Phe Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
        115                 120                 125

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
    130                 135                 140

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn
145                 150                 155                 160

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
                165                 170                 175

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys
            180                 185                 190
```

```
Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
        195                 200                 205

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
    210                 215                 220

Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
                245                 250                 255

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro
            260                 265                 270

Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr
        275                 280                 285

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro
    290                 295                 300

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala
305                 310                 315                 320

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
                325                 330                 335

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr
            340                 345                 350

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly
```

370 375 380

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser
385 390 395 400

Gly Thr Thr Phe Ser Arg Asp Val Met Gly Trp Tyr Arg Gln Ala Pro
405 410 415

Gly Lys Gln Arg Glu Leu Val Ala Ile Ile Ser Arg Gly Gly Ser Thr
420 425 430

Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
435 440 445

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
450 455 460

Thr Ala Val Tyr Tyr Cys Asn Ala Asn Thr Ala Thr Trp Gly Arg Val
465 470 475 480

Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Gly
485 490 495

Arg Asn Val Tyr Ser Ala Gly Gly Gly Ser Gly Gly Gln Thr Val Val
500 505 510

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
515 520 525

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
530 535 540

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp
545 550 555 560

Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser
565 570 575

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
580 585 590

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
595 600 605

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly
610 615 620

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
625 630 635 640

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
645 650 655

Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
660 665 670

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp
675 680 685

Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
690 695 700

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
705 710 715 720

Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile
725 730 735

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
755 760 765

Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala
770 775 780

Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln
785 790 795 800

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
805 810 815

Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser
820 825 830

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
835 840 845

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
850 855 860

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His
865 870 875 880

His His

<210> 247
<211> 882
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro307 (enlazador FL aFOLR1 h22.4 NC)

<400> 247

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

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

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

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

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

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

Ala Asn Thr Ala Thr Trp Gly Arg Val Phe Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
        115                 120                 125

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
    130                 135                 140

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn
145                 150                 155                 160

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
                165                 170                 175

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys
            180                 185                 190
```

```
Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
        195                 200                 205

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
    210                 215                 220

Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
                245                 250                 255

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro
            260                 265                 270

Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr
        275                 280                 285

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro
    290                 295                 300

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala
305                 310                 315                 320

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
                325                 330                 335

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr
            340                 345                 350

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly
```

370 375 380

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser
385 390 395 400

Gly Thr Thr Phe Ser Arg Asp Val Met Gly Trp Tyr Arg Gln Ala Pro
405 410 415

Gly Lys Gln Arg Glu Leu Val Ala Ile Ile Ser Arg Gly Gly Ser Thr
420 425 430

Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
435 440 445

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
450 455 460

Thr Ala Val Tyr Tyr Cys Asn Ala Asn Thr Ala Thr Trp Gly Arg Val
465 470 475 480

Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
485 490 495

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val
500 505 510

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
515 520 525

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
530 535 540

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp
545 550 555 560

```
Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser
                565                 570                 575

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
            580                 585                 590

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
        595                 600                 605

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
625                 630                 635                 640

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
                645                 650                 655

Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
            660                 665                 670

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp
        675                 680                 685

Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
    690                 695                 700

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
705                 710                 715                 720

Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile
                725                 730                 735

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            740                 745                 750
```

Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
755 760 765

Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala
770 775 780

Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln
785 790 795 800

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
805 810 815

Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser
820 825 830

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
835 840 845

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
850 855 860

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His
865 870 875 880

His His

<210> 248
<211> 505
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro308 (Pro51 aFOLR1 h22.4)

<400> 248

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

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

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

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

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

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

Ala Asn Thr Ala Thr Trp Gly Arg Val Phe Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val
        115                 120                 125

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
    130                 135                 140

Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile
145                 150                 155                 160

Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg
                165                 170                 175

Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val
            180                 185                 190
```

```
Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
        195                 200                 205

Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
    210                 215                 220

Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
225                 230                 235                 240

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
                245                 250                 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln
            260                 265                 270

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
        275                 280                 285

Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
    290                 295                 300

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys
305                 310                 315                 320

Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
                325                 330                 335

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
            340                 345                 350

Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
        355                 360                 365

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Ser
    370                 375                 380
```

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
385 390 395 400

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
405 410 415

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
420 425 430

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val
435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
450 455 460

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
465 470 475 480

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
485 490 495

Val Ser Ser His His His His His His
500 505

<210> 249
<211> 901
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro335 (enlazador FL aEGFR2 NC)

<400> 249

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

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

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

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

Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
130 135 140

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
145 150 155 160

Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro
165 170 175

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
180 185 190

Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser
195 200 205

```
Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
    210                 215                 220

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly
225                 230                 235                 240

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
                245                 250                 255

Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val
            260                 265                 270

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
        275                 280                 285

Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
    290                 295                 300

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
305                 310                 315                 320

Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
                325                 330                 335

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
            340                 345                 350

Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe
        355                 360                 365

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
    370                 375                 380

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
```

385 390 395 400

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser
405 410 415

Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe
420 425 430

Val Val Ala Ile Asn Trp Ser Ser Gly Ser Thr Tyr Tyr Ala Asp Ser
435 440 445

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
450 455 460

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
465 470 475 480

Cys Ala Ala Gly Tyr Gln Ile Asn Ser Gly Asn Tyr Asn Phe Lys Asp
485 490 495

Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
500 505 510

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
515 520 525

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
530 535 540

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
545 550 555 560

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
565 570 575

```
Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe
            580                 585                 590

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
        595                 600                 605

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
    610                 615                 620

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
625                 630                 635                 640

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
                645                 650                 655

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
            660                 665                 670

Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
        675                 680                 685

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp
    690                 695                 700

Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg
705                 710                 715                 720

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr
                725                 730                 735

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn
            740                 745                 750

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
        755                 760                 765
```

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
770 775 780

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu
785 790 795 800

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp
805 810 815

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
820 825 830

Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe
835 840 845

Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn
850 855 860

Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly
865 870 875 880

Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His
885 890 895

His His His His His
900

<210> 250
<211> 894
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro345 (humanizado Pro186 Vli2 Dominio MMP9 enlazador)

<400> 250

```
Gln Val Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1               5                  10                  15

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190
```

```
Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
```

370 375 380

Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
500 505 510

Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu
515 520 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
530 535 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545 550 555 560

```
Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Asp
               565                 570                 575

Asp Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
           580                 585                 590

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
       595                 600                 605

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
   610                 615                 620

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val
625                 630                 635                 640

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
               645                 650                 655

Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met
           660                 665                 670

Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg
       675                 680                 685

Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser
   690                 695                 700

Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala
705                 710                 715                 720

Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
               725                 730                 735

Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala
           740                 745                 750
```

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
755 760 765

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
770 775 780

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
785 790 795 800

Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
805 810 815

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
820 825 830

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
835 840 845

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
850 855 860

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
865 870 875 880

Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890

<210> 251
<211> 894
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro346 (humanizado Pro186 Vli2 Dominio NC enlazador)

<400> 251

```
Gln Val Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1               5                  10                  15

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190
```

```
Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
```

370 375 380

Lys Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu
385 390 395 400

Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
500 505 510

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
515 520 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
530 535 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545 550 555 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Asp
565 570 575

Asp Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
580 585 590

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
595 600 605

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
610 615 620

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val
625 630 635 640

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
645 650 655

Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met
660 665 670

Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg
675 680 685

Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser
690 695 700

Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala
705 710 715 720

Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
725 730 735

Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala
740 745 750

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
755 760 765

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
770 775 780

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
785 790 795 800

Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
805 810 815

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
820 825 830

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
835 840 845

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
850 855 860

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
865 870 875 880

Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890

<210> 252
<211> 880
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro368 (enlazador FL aFOLR1 wt22.4 MMP9)

<400> 252

```
Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1               5                  10                  15

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

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

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

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

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

Ala Asn Thr Ala Thr Trp Gly Arg Val Phe Trp Gly Gln Gly Thr Gln
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
        115                 120                 125

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
    130                 135                 140

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn
145                 150                 155                 160

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
                165                 170                 175

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys
            180                 185                 190
```

```
Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
        195                 200                 205

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
    210                 215                 220

Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
                245                 250                 255

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro
            260                 265                 270

Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr
        275                 280                 285

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro
    290                 295                 300

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala
305                 310                 315                 320

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
                325                 330                 335

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr
            340                 345                 350

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly
```

370 375 380

Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser
385 390 395 400

Gly Thr Thr Phe Ser Arg Asp Val Met Gly Trp Tyr Arg Gln Ala Pro
405 410 415

Gly Lys Gln Arg Glu Leu Val Ala Ile Ile Ser Arg Gly Gly Ser Thr
420 425 430

Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
435 440 445

Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Ala Pro Glu Asp
450 455 460

Thr Ala Val Tyr Tyr Cys Asn Ala Asn Thr Ala Thr Trp Gly Arg Val
465 470 475 480

Phe Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro
485 490 495

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr
500 505 510

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
515 520 525

Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
530 535 540

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr
545 550 555 560

Lys Asp Asp Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
565 570 575

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
580 585 590

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
595 600 605

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
610 615 620

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
625 630 635 640

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
645 650 655

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
660 665 670

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
675 680 685

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
690 695 700

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
705 710 715 720

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
725 730 735

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
740 745 750

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
755 760 765

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
770 775 780

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
785 790 795 800

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
805 810 815

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
820 825 830

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
835 840 845

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
850 855 860

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
865 870 875 880

<210> 253
<211> 881
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro369 (enlazador FL aFOLR1 wt22.4 KLK7.6)

<400> 253

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

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

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

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

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

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

Ala Asn Thr Ala Thr Trp Gly Arg Val Phe Trp Gly Gln Gly Thr Gln
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
115 120 125

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
130 135 140

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn
145 150 155 160

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
165 170 175

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys
180 185 190

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
195 200 205

```
Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
    210                 215                 220

Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
                245                 250                 255

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro
            260                 265                 270

Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr
        275                 280                 285

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro
    290                 295                 300

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala
305                 310                 315                 320

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
                325                 330                 335

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr
            340                 345                 350

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly
    370                 375                 380

Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser
```

385 390 395 400

Gly Thr Thr Phe Ser Arg Asp Val Met Gly Trp Tyr Arg Gln Ala Pro
405 410 415

Gly Lys Gln Arg Glu Leu Val Ala Ile Ile Ser Arg Gly Gly Ser Thr
420 425 430

Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
435 440 445

Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Ala Pro Glu Asp
450 455 460

Thr Ala Val Tyr Tyr Cys Asn Ala Asn Thr Ala Thr Trp Gly Arg Val
465 470 475 480

Phe Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Gly
485 490 495

Gln Asn Pro Tyr Ser Ala Gly Arg Gly Gly Gly Ser Gln Thr Val Val
500 505 510

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
515 520 525

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
530 535 540

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
545 550 555 560

Thr Lys Asp Asp Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
565 570 575

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
580 585 590

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
595 600 605

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
610 615 620

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
625 630 635 640

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
645 650 655

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
660 665 670

Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys
675 680 685

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
690 695 700

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
705 710 715 720

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser
725 730 735

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
740 745 750

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
755 760 765

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
770 775 780

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
785 790 795 800

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
805 810 815

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
820 825 830

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
835 840 845

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
850 855 860

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His
865 870 875 880

His

<210> 254
<211> 881
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro370 (enlazador FL aFOLR1 wt22.4 KLK7.11)

<400> 254

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

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

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

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

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

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

Ala Asn Thr Ala Thr Trp Gly Arg Val Phe Trp Gly Gln Gly Thr Gln
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
115 120 125

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
130 135 140

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn
145 150 155 160

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
165 170 175

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys
180 185 190

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
195 200 205

```
Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
    210                 215                 220

Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
                245                 250                 255

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro
            260                 265                 270

Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr
        275                 280                 285

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro
    290                 295                 300

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala
305                 310                 315                 320

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
                325                 330                 335

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr
            340                 345                 350

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly
    370                 375                 380

Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser
```

385 390 395 400

Gly Thr Thr Phe Ser Arg Asp Val Met Gly Trp Tyr Arg Gln Ala Pro
405 410 415

Gly Lys Gln Arg Glu Leu Val Ala Ile Ile Ser Arg Gly Gly Ser Thr
420 425 430

Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
435 440 445

Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Ala Pro Glu Asp
450 455 460

Thr Ala Val Tyr Tyr Cys Asn Ala Asn Thr Ala Thr Trp Gly Arg Val
465 470 475 480

Phe Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Gly
485 490 495

Arg Asn Val Tyr Ser Ala Gly Gly Gly Ser Gly Gly Gln Thr Val Val
500 505 510

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
515 520 525

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
530 535 540

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
545 550 555 560

Thr Lys Asp Asp Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
565 570 575

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
580 585 590

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
595 600 605

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
610 615 620

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
625 630 635 640

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
645 650 655

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
660 665 670

Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys
675 680 685

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
690 695 700

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
705 710 715 720

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser
725 730 735

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
740 745 750

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
755 760 765

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
770 775 780

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
785 790 795 800

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
805 810 815

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
820 825 830

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
835 840 845

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
850 855 860

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His
865 870 875 880

His

<210> 255
<211> 881
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro371 (enlazador FL aFOLR1 wt22.4 NC)

<400> 255

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

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

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

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

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

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

Ala Asn Thr Ala Thr Trp Gly Arg Val Phe Trp Gly Gln Gly Thr Gln
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
        115                 120                 125

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
    130                 135                 140

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn
145                 150                 155                 160

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
                165                 170                 175

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys
            180                 185                 190

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
        195                 200                 205
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Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
    210                 215                 220

Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
                245                 250                 255

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro
            260                 265                 270

Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr
        275                 280                 285

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro
    290                 295                 300

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala
305                 310                 315                 320

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
                325                 330                 335

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr
            340                 345                 350

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly
    370                 375                 380

Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser
```

385 390 395 400

Gly Thr Thr Phe Ser Arg Asp Val Met Gly Trp Tyr Arg Gln Ala Pro
405 410 415

Gly Lys Gln Arg Glu Leu Val Ala Ile Ile Ser Arg Gly Gly Ser Thr
420 425 430

Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
435 440 445

Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Ala Pro Glu Asp
450 455 460

Thr Ala Val Tyr Tyr Cys Asn Ala Asn Thr Ala Thr Trp Gly Arg Val
465 470 475 480

Phe Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
485 490 495

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val
500 505 510

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
515 520 525

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
530 535 540

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
545 550 555 560

Thr Lys Asp Asp Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
565 570 575

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
580 585 590

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
595 600 605

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
610 615 620

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
625 630 635 640

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
645 650 655

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
660 665 670

Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys
675 680 685

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
690 695 700

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
705 710 715 720

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser
725 730 735

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
740 745 750

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
755 760 765

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
770 775 780

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
785 790 795 800

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
805 810 815

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
820 825 830

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
835 840 845

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
850 855 860

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His
865 870 875 880

His

<210> 256
<211> 505
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro372 (Pro51 aFOLR1 wt22.4)

<400> 256

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

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

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

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

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

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

Ala Asn Thr Ala Thr Trp Gly Arg Val Phe Trp Gly Gln Gly Thr Gln
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val
115 120 125

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
130 135 140

Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile
145 150 155 160

Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg
165 170 175

Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val
180 185 190

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
195 200 205

```
Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
    210                 215                 220

Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
225                 230                 235                 240

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
                245                 250                 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln
            260                 265                 270

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
        275                 280                 285

Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
    290                 295                 300

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys
305                 310                 315                 320

Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
                325                 330                 335

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
            340                 345                 350

Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
        355                 360                 365

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Ser
    370                 375                 380

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
385                 390                 395                 400
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
405 410 415

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
420 425 430

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val
435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
450 455 460

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
465 470 475 480

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
485 490 495

Val Ser Ser His His His His His His
500 505

<210> 257
<211> 895
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro373 (enlazador FL aB7H3 hF7 Meprina)

<400> 257

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

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

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

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

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

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

Ala Ala Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp

210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Arg Leu Ser Cys Ala Pro Ser Arg Arg Thr Phe His Thr Tyr His Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ala Val
420 425 430

Ile Asn Trp Ser Gly Gly Ser Thr Val Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala
465 470 475 480

Gly Gly Ala Thr Thr Gln Arg Ala Thr Glu Ala Ser Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Gly Lys Lys
500 505 510

Leu Ala Asp Glu Pro Glu Gly Gly Ser Gln Thr Val Val Thr Gln Glu
515 520 525

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
530 535 540

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
545 550 555 560

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp
565 570 575

Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
580 585 590

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
595 600 605

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
610 615 620

Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu
625 630 635 640

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
645 650 655

Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala
660 665 670

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
675 680 685

Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp
690 695 700

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
705 710 715 720

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
725 730 735

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
740 745 750

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
755 760 765

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
770 775 780

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
785 790 795 800

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
805 810 815

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
820 825 830

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
835 840 845

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
850 855 860

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
865 870 875 880

Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

<210> 258
<211> 891
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro374 (enlazador FL aB7H3 hF12 Meprina)

<400> 258

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

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

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

Ala Ala Ile Asn Trp Ser Gly Gly Asn 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 Ala Gly Gly Val Leu Ala His His Asn Tyr Glu Tyr Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
145 150 155 160

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
180 185 190

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
195 200 205

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala

210 215 220

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
225 230 235 240

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
245 250 255

Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
260 265 270

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser
275 280 285

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
290 295 300

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val
305 310 315 320

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
325 330 335

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
340 345 350

Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
355 360 365

Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu
370 375 380

Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
385 390 395 400

Ser Cys Glu Ala Ser Pro Arg Thr Phe Ser Thr Tyr Ser Met Ala Trp
405 410 415

Phe Arg Gln Ala Pro Gly Lys Glu Arg Ser Phe Val Ala Ala Ile Asn
420 425 430

Trp Ser Gly Gly Asn Thr Ser Tyr Ala Asp Ser Val Lys Gly Arg Phe
435 440 445

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
450 455 460

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Gly Gly
465 470 475 480

Val Leu Ala His His Asn Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr
485 490 495

Leu Val Thr Val Ser Ser Ser Gly Gly Gly Lys Lys Leu Ala Asp Glu
500 505 510

Pro Glu Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
515 520 525

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
530 535 540

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
545 550 555 560

Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys
565 570 575

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
580 585 590

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
595 600 605

Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu
610 615 620

Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val
625 630 635 640

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser
645 650 655

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val
660 665 670

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser
675 680 685

Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp
690 695 700

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
705 710 715 720

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
725 730 735

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
740 745 750

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
755 760 765

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
770 775 780

Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
785 790 795 800

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
805 810 815

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
820 825 830

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr
835 840 845

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
850 855 860

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
865 870 875 880

Val Thr Val Ser Ser His His His His His His
885 890

<210> 259
<211> 898
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro375 (enlazador FL hEGFR1/hEGFR2 Meprina)

<400> 259

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp

210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val
370 375 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr Ala Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Val Ala
420 425 430

Ile Asn Trp Ser Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala
465 470 475 480

Gly Tyr Gln Ile Asn Ser Gly Asn Tyr Asn Phe Lys Asp Tyr Glu Tyr
485 490 495

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly
500 505 510

Gly Lys Lys Leu Ala Asp Glu Pro Glu Gly Gly Ser Gln Thr Val Val
515 520 525

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
530 535 540

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
545 550 555 560

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp
565 570 575

Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser
580 585 590

```
Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
        595                 600                 605

Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val
    610                 615                 620

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly
625                 630                 635                 640

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
                645                 650                 655

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
            660                 665                 670

Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        675                 680                 685

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp
    690                 695                 700

Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
705                 710                 715                 720

Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
                725                 730                 735

Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile
            740                 745                 750

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        755                 760                 765

Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
    770                 775                 780
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Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala
785 790 795 800

Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln
805 810 815

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
820 825 830

Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser
835 840 845

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
850 855 860

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
865 870 875 880

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His
885 890 895

His His

<210> 260
<211> 902
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro376 (enlazador Pro262 Meprina)

<400> 260

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

```
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            260                 265                 270

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
        275                 280                 285

Thr Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly
    290                 295                 300

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
305                 310                 315                 320

Leu Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe
                325                 330                 335

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
            340                 345                 350

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn
        355                 360                 365

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Ser Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser
```

385 390 395 400

Val Gln Thr Gly Gly Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg
405 410 415

Thr Ser Arg Ser Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys
420 425 430

Glu Arg Glu Phe Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly
435 440 445

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
450 455 460

Lys Asn Thr Val Asp Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
465 470 475 480

Ala Ile Tyr Tyr Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr
485 490 495

Leu Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
500 505 510

Ser Ser Gly Gly Gly Lys Lys Leu Ala Asp Glu Pro Glu Gly Gly Ser
515 520 525

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
530 535 540

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly
545 550 555 560

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
565 570 575

```
Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg
            580                 585                 590

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

Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser
    610                 615                 620

Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
625                 630                 635                 640

Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
                645                 650                 655

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
            660                 665                 670

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly
        675                 680                 685

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys
    690                 695                 700

Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
705                 710                 715                 720

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
                725                 730                 735

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
            740                 745                 750

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
        755                 760                 765
```

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
770 775 780

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg
785 790 795 800

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser
805 810 815

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile
820 825 830

Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg
835 840 845

Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met
850 855 860

Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly
865 870 875 880

Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
885 890 895

His His His His His His
900

<210> 261
<211> 877
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro390 (FL aFOLR1 h59.3 enlazador central extendido con enlazador MMP9)

<400> 261

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

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

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

Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp Ser Val Lys
    50                  55                  60

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

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

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

Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
        115                 120                 125

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
    130                 135                 140

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln
145                 150                 155                 160

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
                165                 170                 175

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr
            180                 185                 190
```

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
195 200 205

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn
210 215 220

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
225 230 235 240

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr
245 250 255

Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
260 265 270

Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr
275 280 285

Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile
290 295 300

Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly
305 310 315 320

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
325 330 335

Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp
340 345 350

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly
355 360 365

Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly

370 375 380

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Pro
385 390 395 400

Gly Asn Thr Phe Ser Ile Ser Ala Met Gly Trp Tyr Arg Gln Ala Pro
405 410 415

Gly Lys Gln Arg Glu Trp Val Ala Val Thr His Ser Asp Tyr Ser Thr
420 425 430

Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
435 440 445

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
450 455 460

Thr Ala Val Tyr Tyr Cys Lys His Tyr Gly Ile Asp Tyr Trp Gly Gln
465 470 475 480

Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
485 490 495

Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
500 505 510

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser
515 520 525

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
530 535 540

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp
545 550 555 560

Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
565 570 575

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
580 585 590

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
595 600 605

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
610 615 620

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
625 630 635 640

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn
645 650 655

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
660 665 670

Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val
675 680 685

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
690 695 700

Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
705 710 715 720

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
725 730 735

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
755 760 765

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
770 775 780

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
785 790 795 800

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
805 810 815

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
820 825 830

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
835 840 845

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
850 855 860

Thr Leu Val Thr Val Ser Ser His His His His His His
865 870 875

<210> 262
<211> 881
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro391 (FL aFOLR1 h59.3 enlazador central extendido y un enlazador MMP9 extendido)

<400> 262

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

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

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

Ala Val Thr His Ser Asp Tyr Ser Thr Asn Tyr Ala Asp Ser Val Lys
    50                  55                  60

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

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

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

Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
        115                 120                 125

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
    130                 135                 140

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln
145                 150                 155                 160

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
                165                 170                 175

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr
            180                 185                 190

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
        195                 200                 205
```

```
Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn
    210                 215                 220

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
225                 230                 235                 240

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr
                245                 250                 255

Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
            260                 265                 270

Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr
        275                 280                 285

Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile
    290                 295                 300

Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly
305                 310                 315                 320

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
                325                 330                 335

Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp
            340                 345                 350

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly
    370                 375                 380

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Pro
```

385 390 395 400

Gly Asn Thr Phe Ser Ile Ser Ala Met Gly Trp Tyr Arg Gln Ala Pro
405 410 415

Gly Lys Gln Arg Glu Trp Val Ala Val Thr His Ser Asp Tyr Ser Thr
420 425 430

Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
435 440 445

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
450 455 460

Thr Ala Val Tyr Tyr Cys Lys His Tyr Gly Ile Asp Tyr Trp Gly Gln
465 470 475 480

Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
485 490 495

Met Lys Gly Leu Pro Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr
500 505 510

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
515 520 525

Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
530 535 540

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr
545 550 555 560

Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
565 570 575

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
580 585 590

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
595 600 605

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
610 615 620

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
625 630 635 640

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
645 650 655

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
660 665 670

Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys
675 680 685

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
690 695 700

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
705 710 715 720

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser
725 730 735

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
740 745 750

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
755 760 765

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
770 775 780

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
785 790 795 800

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
805 810 815

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
820 825 830

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
835 840 845

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
850 855 860

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His
865 870 875 880

His

<210> 263
<211> 897
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro412 (Pro186 con enlazador 2aa central extendido)

<400> 263

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

```
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
        355                 360                 365

Thr Lys Leu Thr Val Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
    370                 375                 380

Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser
```

385 390 395 400

Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly
405 410 415

Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser
420 425 430

Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu
450 455 460

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
465 470 475 480

Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr
485 490 495

Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Ser Gly Gly Pro
500 505 510

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr
515 520 525

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
530 535 540

Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
545 550 555 560

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr
565 570 575

Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
580 585 590

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
595 600 605

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
610 615 620

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly
625 630 635 640

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
645 650 655

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys
660 665 670

Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
675 680 685

Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys
690 695 700

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
705 710 715 720

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
725 730 735

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser
740 745 750

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
755 760 765

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
770 775 780

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
785 790 795 800

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
805 810 815

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
820 825 830

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
835 840 845

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
850 855 860

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
865 870 875 880

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His
885 890 895

His

<210> 264
<211> 899
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro413 (Pro186 con enlazador 4aa central extendido)

<400> 264

```
Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1               5                  10                  15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190
```

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
210 215 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225 230 235 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
260 265 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
275 280 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
290 295 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305 310 315 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
385 390 395 400

Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr
405 410 415

Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
420 425 430

Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val
435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
450 455 460

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
465 470 475 480

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
485 490 495

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Ser Gly
500 505 510

Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln Thr Val
515 520 525

Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr
530 535 540

Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro
545 550 555 560

Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly
565 570 575

Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly
580 585 590

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
595 600 605

Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp
610 615 620

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly
625 630 635 640

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
645 650 655

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
660 665 670

Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
675 680 685

Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp
690 695 700

Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
705 710 715 720

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
725 730 735

Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr
740 745 750

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
755 760 765

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
770 775 780

Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys
785 790 795 800

Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg
805 810 815

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser
820 825 830

Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile
835 840 845

Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu
850 855 860

Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu
865 870 875 880

Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His
885 890 895

His His His

<210> 265
<211> 901
<212> PRT
<213> Secuencia Artificial

<220>

<223> Sintético constructor - Pro414 (Pro186 con enlazador central 6aa extendido)

<400> 265

```
Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1               5                  10                  15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    130                 135                 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175
```

```
Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
            340                 345                 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
```

355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
370 375 380

Ser Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly
385 390 395 400

Gly Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser
405 410 415

Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe
420 425 430

Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser
435 440 445

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val
450 455 460

Asp Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr
465 470 475 480

Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr
485 490 495

Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly
500 505 510

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln
515 520 525

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
530 535 540

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
545 550 555 560

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
565 570 575

Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe
580 585 590

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
595 600 605

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
610 615 620

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
625 630 635 640

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
645 650 655

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
660 665 670

Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
675 680 685

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp
690 695 700

Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg
705 710 715 720

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr
725 730 735

```
Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn
            740                 745                 750

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
        755                 760                 765

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
    770                 775                 780

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu
785                 790                 795                 800

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp
                805                 810                 815

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
            820                 825                 830

Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe
        835                 840                 845

Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn
    850                 855                 860

Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly
865                 870                 875                 880

Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His
                885                 890                 895

His His His His His
            900
```

<210> 266
<211> 903

<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro415 (Pro186 con enlazador central 8aa extendido)

<400> 266

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

```
Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
                325                 330                 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
```

340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
370 375 380

Gly Ser Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr
385 390 395 400

Gly Gly Ser Leu Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg
405 410 415

Ser Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu
420 425 430

Phe Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp
435 440 445

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
450 455 460

Val Asp Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr
465 470 475 480

Tyr Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu
485 490 495

Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly
500 505 510

Gly Gly Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
515 520 525

Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
530 535 540

Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser
545 550 555 560

Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg
565 570 575

Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala
580 585 590

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

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr
610 615 620

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
625 630 635 640

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
645 650 655

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
660 665 670

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
675 680 685

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr
690 695 700

Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
705 710 715 720

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
725 730 735

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
740 745 750

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
755 760 765

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val
770 775 780

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu
785 790 795 800

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met
805 810 815

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser
820 825 830

Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly
835 840 845

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln
850 855 860

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile
865 870 875 880

Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser
885 890 895

Ser His His His His His His
900

<210> 267
<211> 893
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro416 (Pro186 con enlazador cent2aa central acortado)

<400> 267

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

```
Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
```

325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Ser Gly Gly Gly Ser Gln Val Lys
370 375 380

Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu Arg
385 390 395 400

Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met Gly
405 410 415

Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly Ile
420 425 430

Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg
435 440 445

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln Met
450 455 460

Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala Ala
465 470 475 480

Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp Gly
485 490 495

Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Pro Gly Pro Ala Gly
500 505 510

Met Lys Gly Leu Pro Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
515 520 525

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser
530 535 540

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
545 550 555 560

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp
565 570 575

Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
580 585 590

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
595 600 605

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
610 615 620

Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
625 630 635 640

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
645 650 655

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn
660 665 670

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
675 680 685

Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val
690 695 700

```
Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
705                 710                 715                 720

Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                725                 730                 735

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
            740                 745                 750

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        755                 760                 765

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    770                 775                 780

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
785                 790                 795                 800

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
                805                 810                 815

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
            820                 825                 830

Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
        835                 840                 845

Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
    850                 855                 860

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
865                 870                 875                 880

Thr Leu Val Thr Val Ser Ser His His His His His His
                885                 890
```

<210> 268
<211> 891
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro417 (Pro186 con enlazador 4aa central acortado)

<400> 268

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

```
Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
```

325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Ser Gly Gly Gly Ser Gln Val Lys Leu
370 375 380

Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu Arg Leu
385 390 395 400

Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met Gly Trp
405 410 415

Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly Ile Ser
420 425 430

Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe
435 440 445

Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln Met Asn
450 455 460

Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala Ala Ala
465 470 475 480

Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp Gly Gln
485 490 495

Gly Thr Gln Val Thr Val Ser Ser Ser Gly Pro Gly Pro Ala Gly Met
500 505 510

Lys Gly Leu Pro Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
515 520 525

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
530 535 540

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
545 550 555 560

Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys
565 570 575

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
580 585 590

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
595 600 605

Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu
610 615 620

Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val
625 630 635 640

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser
645 650 655

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val
660 665 670

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser
675 680 685

Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp
690 695 700

```
Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
705                 710                 715                 720

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
                725                 730                 735

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
            740                 745                 750

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        755                 760                 765

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    770                 775                 780

Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
785                 790                 795                 800

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                805                 810                 815

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
            820                 825                 830

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr
        835                 840                 845

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
    850                 855                 860

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
865                 870                 875                 880

Val Thr Val Ser Ser His His His His His His
                885                 890
```

<210> 269
<211> 889
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro418 (Pro186 con enlazador 6aa central acortado)

<400> 269

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

```
Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
```

325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gln Val Lys Leu Glu
370 375 380

Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu Arg Leu Thr
385 390 395 400

Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met Gly Trp Phe
405 410 415

Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly Ile Ser Trp
420 425 430

Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
435 440 445

Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln Met Asn Ser
450 455 460

Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala Ala Ala Gly
465 470 475 480

Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly
485 490 495

Thr Gln Val Thr Val Ser Ser Gly Pro Gly Pro Ala Gly Met Lys Gly
500 505 510

Leu Pro Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
515 520 525

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
530 535 540

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
545 550 555 560

Pro Arg Gly Leu Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr
565 570 575

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
580 585 590

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
595 600 605

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
610 615 620

Leu Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
625 630 635 640

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
645 650 655

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
660 665 670

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
675 680 685

Asp Tyr Lys Asp Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe
690 695 700

```
Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
705                 710                 715                 720

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly
                725                 730                 735

Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly
            740                 745                 750

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
        755                 760                 765

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
    770                 775                 780

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
785                 790                 795                 800

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
                805                 810                 815

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val
            820                 825                 830

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
        835                 840                 845

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
    850                 855                 860

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
865                 870                 875                 880

Val Ser Ser His His His His His His
                885
```

<210> 270
<211> 885
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro420 (FL aFOLR1 h77.2/haEGFR1 heterólogo COBRA MMP9 enlazador)

<400> 270

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

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

Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val
35 40 45

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

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

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

Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu
115 120 125

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys
130 135 140

```
Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg
145                 150                 155                 160

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys
                165                 170                 175

Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe
            180                 185                 190

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
        195                 200                 205

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Ala
    210                 215                 220

Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
                245                 250                 255

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
            260                 265                 270

Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
        275                 280                 285

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
    290                 295                 300

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
305                 310                 315                 320

Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln
```

325 330 335

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
340 345 350

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser
355 360 365

Gly Gly Gly Ser Gln Val Lys Leu Val Glu Ser Gly Gly Gly Val Val
370 375 380

Arg Pro Gly Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Arg Thr
385 390 395 400

Ser Arg Ser Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu
405 410 415

Arg Glu Phe Val Ser Gly Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr
420 425 430

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
435 440 445

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
450 455 460

Leu Tyr Tyr Cys Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu
465 470 475 480

Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
485 490 495

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln
500 505 510

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
515 520 525

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
530 535 540

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
545 550 555 560

Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe
565 570 575

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
580 585 590

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
595 600 605

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
610 615 620

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625 630 635 640

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
645 650 655

Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
660 665 670

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp
675 680 685

Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg
690 695 700

```
Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr
705                 710                 715                 720

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn
                725                 730                 735

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
            740                 745                 750

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
        755                 760                 765

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu
    770                 775                 780

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp
785                 790                 795                 800

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
                805                 810                 815

Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe
            820                 825                 830

Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn
        835                 840                 845

Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly
    850                 855                 860

Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His
865                 870                 875                 880

His His His His His
                885
```

<210> 271
<211> 885
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro421 (FL haEGFR1/aFOLR1 h77.2 heterólogo COBRA MMP9 enlazador)

<400> 271

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

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

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

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

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

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

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

```
Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
```

325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
385 390 395 400

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Asn Ser Val Met
405 410 415

Ala Trp Tyr Arg Gln Thr Pro Gly Asn Glu Arg Glu Phe Val Ala Ile
420 425 430

Ile Asn Ser Ile Gly Ile Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg
435 440 445

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
450 455 460

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Val Cys Asn Arg Asn
465 470 475 480

Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
485 490 495

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gln
500 505 510

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr
515 520 525

Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
530 535 540

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
545 550 555 560

Ile Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe
565 570 575

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
580 585 590

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
595 600 605

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
610 615 620

Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625 630 635 640

Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
645 650 655

Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
660 665 670

Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp
675 680 685

Asp Asp Asp Lys Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg
690 695 700

```
Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr
705                 710                 715                 720

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn
                725                 730                 735

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
            740                 745                 750

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
        755                 760                 765

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu
    770                 775                 780

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp
785                 790                 795                 800

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
                805                 810                 815

Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe
            820                 825                 830

Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn
        835                 840                 845

Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly
    850                 855                 860

Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His
865                 870                 875                 880

His His His His His
                885
```

<210> 272
<211> 896
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético constructor - Pro429 (Pro186 Meprina/Grancima B enlazador)

<400> 272

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly
1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Ser
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

```
Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
145                 150                 155                 160

Phe Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
            180                 185                 190

Tyr Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
        195                 200                 205

Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp
    210                 215                 220

Thr Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr
225                 230                 235                 240

Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                245                 250                 255

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
            260                 265                 270

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala
        275                 280                 285

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
    290                 295                 300

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
305                 310                 315                 320

Leu Val Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
```

325 330 335

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
340 345 350

Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
355 360 365

Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser Gln Val
370 375 380

Lys Leu Glu Glu Ser Gly Gly Gly Ser Val Gln Thr Gly Gly Ser Leu
385 390 395 400

Arg Leu Thr Cys Ala Ala Ser Gly Arg Thr Ser Arg Ser Tyr Gly Met
405 410 415

Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ser Gly
420 425 430

Ile Ser Trp Arg Gly Asp Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Asp Leu Gln
450 455 460

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Ala
465 470 475 480

Ala Ala Gly Ser Ala Trp Tyr Gly Thr Leu Tyr Glu Tyr Asp Tyr Trp
485 490 495

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Gly Val Tyr
500 505 510

```
Ala Asp Ser Leu Glu Asp Gly Gly Gly Ser Gln Thr Val Val Thr Gln
        515                 520                 525

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
    530                 535                 540

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
545                 550                 555                 560

Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Asp Tyr Lys
                565                 570                 575

Asp Asp Asp Asp Lys Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            580                 585                 590

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
        595                 600                 605

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
    610                 615                 620

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly Gly Ser
625                 630                 635                 640

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
                645                 650                 655

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            660                 665                 670

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        675                 680                 685

Ala Arg Ile Arg Ser Lys Tyr Asp Tyr Lys Asp Asp Asp Asp Lys Ala
    690                 695                 700
```

Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
705 710 715 720

Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val
725 730 735

Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr
740 745 750

Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
755 760 765

Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
770 775 780

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
785 790 795 800

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
805 810 815

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
820 825 830

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
835 840 845

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
850 855 860

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
865 870 875 880

Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
885 890 895

# SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

## NIT: 800.176.089-2

## COMPROBANTE DE RECAUDO SISTEMA SIPI

**Radicado: NC2023/0011606**
**Recibo: 23-225477**
**Fecha: 03/11/2023**

**CAROLINA MERCEDES DAZA MONTALVO**
**CC: 66.783.790**
**Pago PSE No: 890324**
**CUS: 257811378**

NC Divisional de Patente/Modelo
Solicitado en Patente PCT NC2020/0004288

### Detalle del pago

| Id. | Rentístico | Concepto y Servicio | Cant. | Val. Unit. | Subtotal |
|---|---|---|---|---|---|
| 1 | 50005-01-03 | Modificaciones / Correcciones al registro Patente PCT (DESCUENTO INTERNET) | 1 | $ 196,000 | $ 196,000 |
| 2 | 50005-01-02 | Pago unitario reivindicacion adicional patente de invencion (A partir de de undï¿½cima reivindicacion) (DESCUENTO INTERNET) | 9 | $ 49,500 | $ 445,500 |
| | | TOTAL | | | $ 641,500 |



**Sede Centro: Carrera 13 No.27-00 Pisos 3,4,5 y 10 Bogotá D.C. - Colombia**
**Web: www.sic.gov.co e-mail:contactenos@sic.gov.co Conmutador:(571)5870000 Contact Center: (571)5920400**