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DESCRIPCIÓN

Biomarcador para la predicción de la capacidad de respuesta a un tratamiento anti-factor de necrosis tumoral alfa (TNF)

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Campo de la invención

La invención se refiere a un método de diagnóstico de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-factor de necrosis tumoral alfa (TNF α o TNF) para evaluar la capacidad de respuesta a un tratamiento anti-TNF que comprende la detección de inmunoglobulina/s contra una o más proteínas biomarcadoras en un fluido corporal o un excremento de dicho paciente, y clasificar al individuo en una de las dos categorías basadas en la detección de dicha/s inmunoglobulina/s, en el que los individuos se clasifican como pacientes que NO responden o pacientes que responden. La invención se refiere al uso de kits de diagnóstico que comprenden dichas una o más proteínas biomarcadoras para evaluar la capacidad de respuesta a un tratamiento anti-TNF de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α .

Antecedentes

Las enfermedades reumáticas son los trastornos inflamatorios crónicos más comunes. Solo en Alemania, un millón de pacientes padecen enfermedades reumáticas mediadas inmunológicamente, entre las que se incluyen la artritis reumatoide (AR), las espondiloartropatías (SpA) y las enfermedades autoinmunes sistémicas como el lupus eritematoso sistémico (LES), mientras que otros cinco millones tienen artrosis (OA), una enfermedad principalmente degenerativa de las articulaciones, que, sin embargo, en sus fases activas también está dominada por procesos inflamatorios. La artritis reumatoide produce dolor grave, pérdida de la función y deterioro grave de la calidad de vida. Además de estas consecuencias perjudiciales para cada paciente, existe un notable impacto socio-económico que conduce a costes directos e indirectos de aproximadamente 20 billones de euros al año en Alemania. El desarrollo demográfico indica claramente que las enfermedades reumáticas aumentarán drásticamente en las próximas décadas y tendrán la misma importancia que las enfermedades cardiovasculares y que el cáncer. Ya en la actualidad, los trastornos reumáticos dominan el número de visitas de los pacientes a la consulta del médico de cabecera y son la causa principal del absentismo laboral y la invalidez prematura. En reconocimiento del tremendo impacto de las enfermedades artríticas y óseas, la Organización Mundial de la Salud ha denominado la década actual como la "década de las enfermedades óseas y articulares".

Se dispone de una variedad de tratamientos para la artritis reumatoide basados en fármacos antirreumáticos modificadores de la enfermedad convencional (DMARD), tales como el Metotrexato (MTX) y en productos biológicos tales como los inhibidores/antagonistas del TNF. Los niveles crónicamente elevados del TNF se han visto implicados como un componente patógeno en la artritis reumatoide. Los inhibidores del TNF son productos biológicos que se unen a la forma soluble y asociada a la membrana celular del TNF α y neutralizan el efecto proinflamatorio del TNF α al evitar la unión del TNF α a los receptores de la superficie celular TNF-R1/II. Los agentes biológicos inhibidores del TNF α comprenden, por ejemplo, anticuerpos terapéuticos (Adalimumab[®] e Infliximab[®]) y construcciones de receptores solubles (Etanercept[®]). Estos productos biológicos se usan actualmente para tratar la artritis reumatoide activa, reduciendo todos ellos eficazmente los signos y síntomas de la enfermedad e inhibiendo la progresión radiográfica del daño articular. Actualmente ~10 % de los pacientes de Alemania, pero hasta un 30 % de los pacientes de los países escandinavos se tratan con inhibidores del TNF α , y las cifras están en continuo crecimiento. Los anticuerpos anti-TNF α (Adalimumab[®], Humira) representan el 90 % de todos los productos biológicos en uso actual para el tratamiento de la artritis reumatoide.

Sin embargo, solo el 70 % de los pacientes con artritis reumatoide se beneficia de un tratamiento con anti-TNF α , mientras que el 30 % (~10.000 pacientes en Alemania en 2006) siguen sin responder. Un tratamiento anti-TNF α actualmente cuesta ~20.000 € en Alemania y, por lo tanto, solo en Alemania, los costes de los tratamientos infructuosos representan 200 millones de euros al año.

Junto a la artritis reumatoide, los niveles crónicamente elevados de TNF se han visto implicados como un componente patógeno en una serie de otros estados patológicos, principalmente enfermedades autoinmunes tales como la soriasis, la artritis soriásica, la espondilitis anquilosante, la enfermedad de Crohn, la colitis ulcerosa, etc.

En la actualidad, no se dispone de biomarcadores que puedan predecir el resultado de un tratamiento con agentes anti-TNF (por ejemplo, antagonistas/inhibidores del TNF) antes del tratamiento. La única reducción de todos los niveles de isotipo de los factores reumatoides durante y después del tratamiento se asocia con una respuesta positiva y el resultado del tratamiento (van Laar J. M. *Nat Clin Pract Rheumatol.* octubre de 2007; 3(10):544-5. PMID: 17726429). Sin embargo, se ha sugerido un alto nivel de factor reumatoide IgA en sueros de pacientes con artritis reumatoide para identificar un subgrupo de pacientes en riesgo de una mala respuesta clínica al tratamiento con anticuerpos anti-TNF α (Bobbio-Pallavicini F. *et al. Ann Rheum Dis.* marzo de 2007; 66(3):302-7. PMID: 17079248; Bobbio-Pallavicini F. *et al. Ann N Y Acad Sci.* agosto de 2007; 1109:287-95. PMID: 17785317; van Laar J. M. *Nat Clin Pract Rheumatol.* octubre de 2007; 3(10):544-5. PMID: 17726429). La naturaleza de los anticuerpos anti-CCP sugeridos como un predictor de la eficacia del tratamiento es controvertida (Braun-Moscovici Y *et al. J Rheumatol.*

marzo de 2006; 33(3):497-500. PMID: 16511906; Bobbio-Pallavicini F *et al.* *Ann N Y Acad Sci.* agosto de 2007; 1109:287-95. PMID: 17785317; van Laar J. M. *Nat Clin Pract Rheumatol.* octubre de 2007; 3(10):544-5. PMID: 17726429).

5 Por lo tanto, existe la necesidad en la técnica de marcadores que puedan predecir el resultado de un tratamiento anti-TNF α antes y durante el tratamiento. Es necesario estratificar a los pacientes que van a ser sometidos o están siendo sometidos a un tratamiento anti-TNF α y distinguir entre los que responden al tratamiento con anti-TNF α y los pacientes que no responden.

10 Es objeto de la presente invención un método de diagnóstico de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α para evaluar la capacidad de respuesta a un tratamiento anti-TNF antes, durante y/o después del tratamiento anti-TNF α , que comprende:

- 15 a. La detección de inmunoglobulina/s contra una o más proteínas biomarcadoras en un fluido corporal o excremento de dicho paciente, en la que uno o más biomarcadores son indicativos de la capacidad de respuesta a un tratamiento anti-TNF anterior, durante y después del tratamiento anti-TNF α .
- b. La clasificación del individuo como individuo que responde o individuo que no responde basándose en la detección de dichas inmunoglobulinas), como se define en las reivindicaciones.

20 Por lo tanto, la invención proporciona el primer marcador de tiempo que puede predecir el resultado de un tratamiento anti-TNF α antes del tratamiento además de durante y/o después del tratamiento. El tratamiento anti-TNF α puede realizarse mediante la administración de inhibidores del TNF, por ejemplo, antagonistas del TNF. Estos marcadores no están relacionados con el factor reumatoide IgA. El marcador de acuerdo con la presente invención puede ser indicativo de un individuo que responde o de un individuo que NO responde como se describirá a continuación en detalle. Se prefiere la evaluación de la capacidad de respuesta antes del tratamiento.

Es objeto de la presente invención un método de diagnóstico de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α para evaluar la capacidad de respuesta a un tratamiento anti-TNF, que comprende:

30 La detección de inmunoglobulina/s contra una o más proteínas biomarcadoras en un líquido corporal o un excremento de dicho paciente, en la que una proteína biomarcadora es un producto de expresión codificado por un gen seleccionado del grupo que comprende RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1, en la que un individuo positivo en al menos una de dichas inmunoglobulinas se clasifica como individuo que NO responde, en la que la/s inmunoglobulina/s es/son IgA.

En una realización preferida del método identificado anteriormente, el individuo se clasifica en una de dos categorías basándose en la detección de dicha/s inmunoglobulina/s, en la que un individuo positivo en al menos una de dichas inmunoglobulinas se clasifica como individuo que NO responde y, en la que un individuo negativo en cualquiera de dichas inmunoglobulinas detectadas se clasifica como individuo que responde.

En una realización preferida del método, se detectan al menos dos de las proteínas biomarcadoras del grupo de marcadores proteicos, en la que una proteína biomarcadora es un producto de expresión codificado por un gen seleccionado del grupo que comprende RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1 (conjunto de proteínas 1 = RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1). En otra realización preferida del método, se detectan al menos productos de expresión codificados por los genes RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1. En otra realización preferida, solo se detectan productos de expresión codificados por los genes RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1. En otra realización preferida, se detectan cada uno y solo los productos de expresión codificados por los genes RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1.

En otra realización preferida del método de diagnóstico de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α de acuerdo con la invención, el grupo de proteínas biomarcadoras comprende además al menos otro producto de expresión codificado por un gen seleccionado del grupo que comprende Peci, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4 (conjunto de proteínas 2), y se detecta al menos una de las proteínas de todo el grupo 1 y 2 (conjunto de proteínas 1 y 2). En una realización preferida de la invención, se detecta al menos una proteína del conjunto de proteínas 1 y además se detecta al menos una del conjunto de proteínas 2. En otra realización preferida, se detectan al menos dos de las proteínas del conjunto de proteínas 1 y además al menos una del grupo de proteínas 2. En otra realización preferida, se detectan el conjunto de proteínas 1 y el conjunto de proteínas 2.

En otra realización preferida, además de las combinaciones de proteínas marcadoras citadas anteriormente, se detecta una proteína del conjunto de proteínas 3: el conjunto de proteínas 3 comprende los productos de expresión codificados por los genes PRC1, NAT6, EEF1A1, NP_612480.1, PLXNA2, ELMO2 y NDUFS2.

En otra realización preferida de la invención, se seleccionan al menos dos proteínas marcadoras del grupo que comprende el marcador de los conjuntos de proteínas 1, 2 y 3 para el método de diagnóstico de un individuo que se

va a someter o que se está sometiendo a un tratamiento anti-TNF α con el fin de evaluar la capacidad de respuesta a un tratamiento anti-TNF antes, durante y/o después del tratamiento anti-TNF α . Esto significa que, en dicha realización, se seleccionan al menos dos marcadores del grupo que comprende al menos RAB11B, PPP2R1A, KPNB1, COG4, FDFT1 y además PECL, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4, PRC1, NAT6, EEF1AL3, NP_612480.1, PLXNA2, ELMO2 y NDUFS2.

En otra realización preferida, se seleccionan al menos tres proteínas marcadoras, más preferentemente, cuatro o cinco proteínas marcadoras.

De acuerdo con la presente invención, las proteínas biomarcadores de la presente invención pueden ser péptidos, fragmentos de proteínas, variantes de longitud completa o de corte y empalme o derivados modificados sintéticamente o versiones modificadas después de la traducción de las proteínas codificadas por los genes mencionados anteriormente. Preferentemente, dichos fragmentos de proteína tienen una longitud de más de nueve aminoácidos, más preferentemente al menos doce o más de doce aminoácidos. La modificación de las proteínas puede ser, pero sin limitación, la desiminación, desamidación y/o transglutaminación. Además, pueden ser polipéptidos artificiales que son productos de expresión derivados de fases de lectura incorrectas dentro del gen. En la Figura 122, se muestra un ejemplo de dicho producto de expresión derivado de fases de lectura incorrectas dentro del gen, que es una secuencia de proteína derivada de una fase de lectura incorrecta del gen HS6SP1. En la Figura 121, se muestra otro ejemplo que es una secuencia de proteína derivada de una fase de lectura incorrecta del gen C20orf149. Otro ejemplo más se muestra en la Figura 120, que es una secuencia de proteína derivada de una fase de lectura incorrecta del gen IRAK1.

Esto significa que cuando se menciona IRAK1 en el contexto de la presente solicitud, puede referirse a péptidos, fragmentos de proteínas, variantes de longitud completa o de corte y empalme o derivados modificados sintéticamente y/o versiones modificadas después de la traducción de IRAK1 y/o una secuencia de proteína derivada de una fase de lectura incorrecta del gen IRAK1.

Una proteína biomarcadora también engloba variantes de la misma tales como péptidos, fragmentos de proteína, polipéptidos artificiales, variantes de longitud completa o de corte y empalme, derivados modificados sintéticamente o versiones modificadas después de la traducción de las proteínas codificadas por los genes anteriormente mencionados, que se caracterizan porque estas variantes presentan esencialmente la misma capacidad de ser reconocidas por la respectiva inmunoglobulina que las proteínas biomarcadoras que son objeto de la invención.

En particular, de acuerdo con la presente invención, se engloban proteínas biomarcadoras en las que las secuencias implicadas en la unión a la respectiva inmunoglobulina presentan al menos un 80 %, preferentemente al menos un 90 %, más preferentemente al menos un 95 % de grado de identidad de secuencia en los aminoácidos con las secuencias que participan en la unión de las proteínas biomarcadoras definidas en SEQ ID NO: 59-122, así como péptidos, fragmentos de proteína, variantes de longitud completa o de corte y empalme, derivados modificados sintéticamente o versiones modificadas después de la traducción de los mismos que presentan la misma capacidad.

En el contexto de la presente invención, se define una secuencia de ADN de un gen como aquella que comprende todos los exones de un gen necesarios para representar la secuencia de codificación de proteínas (CDS) o todas las variantes de corte y empalme de la misma, así como los exones que representan la región 5' no traducida (UTR) y la UTR 3'.

De acuerdo con la presente invención, se engloban todas las secuencias de ADN que codifican las proteínas biomarcadoras mencionadas anteriormente.

En particular, de acuerdo con la presente invención, además, se engloban secuencias de ADN que presentan, en referencia a la secuencia que codifica un tramo que participa en la región de unión, al menos un 80 %, preferentemente al menos un 90 %, más preferentemente al menos un 95 % de grado de identidad de secuencia en el ácido nucleico con las secuencias de ADN que codifican un tramo que participa en la región de unión definida en SEQ ID NO: 1-58, así como fragmentos de la misma que codifican los biomarcadores de acuerdo con la presente invención.

Las definiciones mencionadas anteriormente para proteínas biomarcadoras y para genes que codifican dichas proteínas biomarcadoras se aplican a cada realización individual de la presente invención, a cualquier método específico, kit, etc.

La determinación del porcentaje de identidad entre dos secuencias se realiza usando el algoritmo matemático de Karlin y Altschul (1993) *Proc. Natl. Acad. Sci. EE.UU.*, 90: 5873-5877. Dicho algoritmo se incorpora a los programas BLASTN y BLASTP de Altschul *et al.* (1990) *J. Mol. Biol.* 215: 403-410. Las búsquedas de nucleótidos BLAST se pueden realizar con el programa BLASTN, puntuación = 100, longitud de palabra = 12, para obtener secuencias de nucleótidos homólogas a los ácidos nucleicos que codifican la variante de polipéptido. Las búsquedas de proteínas BLAST se realizan con el programa BLASTP, puntuación = 50, longitud de palabra = 3, para obtener secuencias de aminoácidos homólogas a la variante de polipéptido, respectivamente. Para obtener alineamientos vacíos con fines

comparativos, se utiliza Gapped BLAST según lo descrito en Altschul *et al.* (1997) *Nucleic Acids Res.* 25: 3389-3402. Cuando se utilizan los programas BLAST y Gapped BLAST, se usan los parámetros por defecto de los respectivos programas.

- 5 La/s inmunoglobulina/s que se va/n a detectar es/son IgA. La/s inmunoglobulina/s que se va/n a detectar no está/n relacionada/s con el factor reumatoide IgA.

En otra realización preferida, se pueden usar subconjuntos de proteínas biomarcadoras para evaluar la capacidad de respuesta a un tratamiento anti-TNF antes, durante y/o después del tratamiento anti-TNF α .

- 10 El respectivo conjunto de proteínas no solo puede predecir la capacidad de respuesta antes, sino también durante el tratamiento. Por lo tanto, un ensayo de diagnóstico basado en una o más proteínas del conjunto ayudará al médico a tomar las decisiones sobre el tratamiento y la identificación de individuos que responden y que no responden al tratamiento anti-TNF a priori.

- 15 El fluido corporal y/o el excremento del individuo que se va a evaluar se pueden seleccionar de un grupo que comprende: sangre, saliva, lágrimas, líquido sinovial y líquido espinal, plasma, orina y heces.

- 20 Un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α puede padecer condiciones autoinmunes tales como la enfermedad de Crohn, colitis ulcerosa, soriasis, artritis soriásica, espondilitis anquilosante, espondiloartropatías, artritis reumatoide, etc.

El método de la invención es especialmente adecuado para individuos que padecen artritis reumatoide.

- 25 Es objeto de la presente invención además el uso de un kit para diagnosticar a un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α con el fin de evaluar la respuesta a un tratamiento anti-TNF que comprende una o más proteínas biomarcadoras, en el que una proteína biomarcadora es un producto de expresión codificado por un gen seleccionado del grupo que comprende RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1. En una realización preferida, el kit comprende al menos aquellas proteínas codificadas por un gen seleccionado del grupo que comprende RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1.

- 35 En una realización preferida del uso del kit, se detectan al menos dos de las proteínas biomarcadoras del grupo de marcadores proteicos, en el que una proteína biomarcadora es un producto de expresión codificado por un gen seleccionado del grupo que comprende RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1 (conjunto de proteínas 1 = RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1). En otra realización preferida del kit, se detecta al menos un producto de expresión codificado por los genes RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1. En otra realización preferida, solo se detectan productos de expresión codificados por los genes RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1. En otra realización preferida, se detectan cada uno y solo los productos de expresión codificados por los genes RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1.

- 40 En otra realización preferida del uso del kit de diagnóstico de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α de acuerdo con la invención, el grupo de proteínas biomarcadoras comprende además al menos otro producto de expresión codificado por un gen seleccionado del grupo que comprende Peci, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4 (conjunto de proteínas 2), y se detecta al menos una de las proteínas de todo el grupo 1 y 2 (conjunto de proteínas 1 y 2). En una realización preferida de la invención, se detecta al menos una proteína del conjunto de proteínas 1 y además se detecta al menos una del conjunto de proteínas 2. En otra realización preferida, se detectan al menos dos de las proteínas del conjunto de proteínas 1 y además al menos una del conjunto de proteínas 2. En otra realización preferida, se detectan el conjunto de proteínas 1 y el conjunto de proteínas 2.

- 50 En otra realización preferida, además de las combinaciones de proteínas marcadoras citadas anteriormente, se detecta una proteína del conjunto de proteínas 3: el conjunto de proteínas 3 comprende los productos de expresión codificados por los genes PRC1, NAT6, EEF1A13, NP_612480.1, PLXNA2, ELMO2 y NDUFS2.

- 55 En otra realización preferida del uso de la kit, el grupo de proteínas biomarcadoras comprende además al menos un producto de expresión codificado por los genes Peci, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4, PRC1, NAT6, EEF1A13, NP_612480.1, PLXNA2, ELMO2 y NDUFS2.

- 60 Otra realización preferida de la invención es el uso de un kit de diagnóstico de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α para evaluar la capacidad de respuesta a un tratamiento anti-TNF que comprende al menos dos proteínas biomarcadoras, en el que una proteína biomarcadora es un producto de expresión codificado por un gen seleccionado del grupo que comprende al menos RAB11B, PPP2R1A, KPNB1, COG4, FDFT1 y además Peci, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4, PRC1, NAT6, EEF1A13, NP_612480.1, PLXNA2, ELMO2 y NDUFS2.

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En otra realización de la invención, el uso del kit y el método de acuerdo con la presente invención pueden comprender además uno o más marcadores de diagnóstico conocidos, por ejemplo, para trastornos autoinmunes. En una realización preferida, el kit también puede comprender otros marcadores de diagnóstico conocidos para la artritis reumatoide.

5 Las proteínas, los conjuntos/kits de proteínas se pueden realizar en diferentes tipos de ensayos conocidos por los expertos en la materia.

10 Las inmunoglobulinas que se van a detectar están en o se aíslan de fluidos corporales y excrementos tales como sangre, saliva, lágrimas, líquido sinovial y espinal, plasma, orina y heces, etc.

El ensayo de diagnóstico puede ser de cualquier tipo aplicado en el campo del diagnóstico, incluyendo, pero sin limitación, métodos de ensayo basados en:

- 15
- reacciones enzimáticas;
 - luminiscencia;
 - fluorescencia;
 - compuestos radioquímicos.

20 Los métodos de detección preferidos comprenden ensayo de tira reactiva, radioinmunoensayo, inmunoensayo de quimioluminiscencia y fluorescencia, ensayo de inmunotransferencia, inmunoensayo ligado a enzimas (ELISA), matrices de perlas basadas en Luminex y ensayo de micromatrices de proteínas.

25 Los tipos de ensayos además pueden estar basados en placas de microvaloración, basados en microplacas, basados en perlas, en los que las proteínas biomarcadoras se pueden unir a la superficie o estar en solución.

Los ensayos pueden ser ensayos homogéneos o heterogéneos, ensayos de tipo sándwich, ensayos competitivos y no competitivos ("The Immunoassay Handbook", Ed. David Wild, Elsevier LTD, Oxford; 3ª ed. (mayo de 2005), ISBN-13: 978-0080445267; Hultschig C. *et al.*, *Curr Opin Chem Biol.*, febrero de 2006; 10(1):4-10. PMID: 16376134).

30 El tratamiento anti-TNF α se realiza mediante la administración de un inhibidor de TNF a un individuo que lo necesite. Los inhibidores de TNF son compuestos biológicos que se unen a la forma de TNF α soluble y asociada a la membrana celular, y neutralizan el efecto proinflamatorio de TNF evitando la unión de TNF α a los receptores de superficie celular TNF-RI/II. Los inhibidores de TNF pueden ser anticuerpos anti-TNF α o moléculas receptoras, pero también de otros tipos. Lo esencial de un inhibidor de TNF de acuerdo con la presente invención es la capacidad de capturar el TNF antes de que se una al receptor de TNF en las células.

35 También es objeto de la presente invención el uso de las proteínas biomarcadoras y/o conjuntos de proteínas y los kits que comprenden estas proteínas biomarcadoras y/o conjuntos de proteínas de acuerdo con la presente invención para evaluar la capacidad de respuesta a un tratamiento anti-TNF α de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α .

Descripción de las figuras

45 La Figura 1 muestra la SEQ ID NO: 1, que es una secuencia de ADN del gen RAB11B (Tabla 1, n.º 1).
La Figura 2 muestra la SEQ ID NO: 2, que es una secuencia de ADN del gen PPP2R1A (Tabla 1, n.º 2).
La Figura 3 muestra la SEQ ID NO: 3, que es una secuencia de ADN del gen PPP2R1A (Tabla 1, n.º 2).
La Figura 4 muestra la SEQ ID NO: 4, que es una secuencia de ADN del gen KPNB1 (Tabla 1, n.º 3).
La Figura 5 muestra la SEQ ID NO: 5, que es una secuencia de ADN del gen COG4 (Tabla 1, n.º 4).
50 La Figura 6 muestra la SEQ ID NO: 6, que es una secuencia de ADN del gen COG4 (Tabla 1, n.º 4).
La Figura 7 muestra la SEQ ID NO: 7, que es una secuencia de ADN del gen COG4 (Tabla 1, n.º 4).
La Figura 8 muestra la SEQ ID NO: 8, que es una secuencia de ADN del gen COG4 (Tabla 1, n.º 4).
La Figura 9 muestra la SEQ ID NO: 9, que es una secuencia de ADN del gen FDFT1 (Tabla 1, n.º 5).
La Figura 10 muestra la SEQ ID NO: 10, que es una secuencia de ADN del gen PECL (Tabla 1, n.º 6).
55 La Figura 11 muestra la SEQ ID NO: 11, que es una secuencia de ADN del gen PECL (Tabla 1, n.º 6).
La Figura 12 muestra la SEQ ID NO: 12, que es una secuencia de ADN del gen PECL (Tabla 1, n.º 6).
La Figura 13 muestra la SEQ ID NO: 13, que es una secuencia de ADN del gen PECL (Tabla 1, n.º 6).
La Figura 14 muestra la SEQ ID NO: 14, que es una secuencia de ADN del gen PECL (Tabla 1, n.º 6).
La Figura 15 muestra la SEQ ID NO: 15, que es una secuencia de ADN del gen CTNND2 (Tabla 1, n.º 7).
60 La Figura 16 muestra la SEQ ID NO: 16, que es una secuencia de ADN del gen CTNND2 (Tabla 1, n.º 7).
La Figura 17 muestra la SEQ ID NO: 17, que es una secuencia de ADN del gen NSMCE1 (Tabla 1, n.º 8).
La Figura 18 muestra la SEQ ID NO: 18, que es una secuencia de ADN del gen NSMCE1 (Tabla 1, n.º 8).
La Figura 19 muestra la SEQ ID NO: 19, que es una secuencia de ADN del gen NSMCE1 (Tabla 1, n.º 8).
La Figura 20 muestra la SEQ ID NO: 20, que es una secuencia de ADN del gen KTELC1 (Tabla 1, n.º 9).
65 La Figura 21 muestra la SEQ ID NO: 21, que es una secuencia de ADN del gen HS6ST1 (Tabla 1, n.º 10).
La Figura 22 muestra la SEQ ID NO: 22, que es una secuencia de ADN del gen ARMC6 (Tabla 1, n.º 11).

- [illegible]

La Figura 90 muestra la SEQ ID NO: 90, que es una secuencia proteica del gen EDC4 (Tabla 1, n.º 15).
 La Figura 91 muestra la SEQ ID NO: 91, que es una secuencia proteica del gen PRC1 (Tabla 1, n.º 16).
 La Figura 92 muestra la SEQ ID NO: 92, que es una secuencia proteica del gen PRC1 (Tabla 1, n.º 16).
 La Figura 93 muestra la SEQ ID NO: 93, que es una secuencia proteica del gen PRC1 (Tabla 1, n.º 16).
 5 La Figura 94 muestra la SEQ ID NO: 94, que es una secuencia proteica del gen NAT6 (Tabla 1, n.º 17).
 La Figura 95 muestra la SEQ ID NO: 95, que es una secuencia proteica del gen NAT6 (Tabla 1, n.º 17).
 La Figura 96 muestra la SEQ ID NO: 96, que es una secuencia proteica del gen NAT6 (Tabla 1, n.º 17).
 La Figura 97 muestra la SEQ ID NO: 97, que es una secuencia proteica del gen EEF1AL3 (Tabla 1, n.º 18).
 La Figura 98 muestra la SEQ ID NO: 98, que es una secuencia proteica del gen NP_612480.1 (Tabla 1, n.º 19).
 10 La Figura 99 muestra la SEQ ID NO: 99, que es una secuencia proteica del gen PLXNA2 (Tabla 1, n.º 20).
 La Figura 100 muestra la SEQ ID NO: 100, que es una secuencia proteica del gen PLXNA2 (Tabla 1, n.º 20).
 La Figura 101 muestra la SEQ ID NO: 101, que es una secuencia proteica del gen ELM02 (Tabla 1, n.º 21).
 La Figura 102 muestra la SEQ ID NO: 102, que es una secuencia proteica del gen ELM02 (Tabla 1, n.º 21).
 La Figura 103 muestra la SEQ ID NO: 103, que es una secuencia proteica del gen ELM02 (Tabla 1, n.º 21).
 15 La Figura 104 muestra la SEQ ID NO: 104, que es una secuencia proteica del gen ELM02 (Tabla 1, n.º 21).
 La Figura 105 muestra la SEQ ID NO: 105, que es una secuencia proteica del gen NDUFS2 (Tabla 1, n.º 22).
 La Figura 106 muestra la SEQ ID NO: 106, que es una secuencia proteica del gen NDUFS2 (Tabla 1, n.º 22).
 La Figura 107 muestra la SEQ ID NO: 107, que es una secuencia proteica del gen IRAK1 (Tabla 1, n.º 23).
 La Figura 108 muestra la SEQ ID NO: 108, que es una secuencia proteica del gen IRAK1 (Tabla 1, n.º 23).
 20 La Figura 109 muestra la SEQ ID NO: 109, que es una secuencia proteica del gen IRAK1 (Tabla 1, n.º 23).
 La Figura 110 muestra la SEQ ID NO: 110, que es una secuencia proteica del gen IRAK1 (Tabla 1, n.º 23).
 La Figura 111 muestra la SEQ ID NO: 111, que es una secuencia proteica del gen IRAK1 (Tabla 1, n.º 23).
 La Figura 112 muestra la SEQ ID NO: 112, que es una secuencia proteica del gen C20orf49 (Tabla 1, n.º 24).
 La Figura 113 muestra la SEQ ID NO: 113, que es una secuencia proteica del gen C20orf49 (Tabla 1, n.º 24).
 25 La Figura 114 muestra la SEQ ID NO: 114, que es una secuencia proteica del gen C20orf49 (Tabla 1, n.º 24).
 La Figura 115 muestra la SEQ ID NO: 115, que es una secuencia proteica del gen PCS2L (Tabla 1, n.º 25).
 La Figura 116 muestra la SEQ ID NO: 116, que es una secuencia proteica del gen PCS2L (Tabla 1, n.º 25).
 La Figura 117 muestra la SEQ ID NO: 117, que es una secuencia proteica del gen PPIA (Tabla 1, n.º 26).
 La Figura 118 muestra la SEQ ID NO: 118, que es una secuencia proteica derivada de una fase de lectura incorrecta
 30 del gen HS6ST1 (Tabla 1, n.º 10).
 La Figura 119 muestra la SEQ ID NO: 119, que es una secuencia proteica derivada de una fase de lectura incorrecta
 del gen IRAK1 (Tabla 1, n.º 23).
 La Figura 120 muestra la SEQ ID NO: 120, que es una secuencia proteica derivada de una fase de lectura incorrecta
 del gen C20orf49 (Tabla 1, n.º 24).
 35 La Figura 121 muestra la SEQ ID NO: 121, que es una secuencia proteica derivada de una fase de lectura incorrecta
 del gen C20orf49 (Tabla 1, n.º 24).
 La Figura 122 muestra la SEQ ID NO: 122, que es una secuencia proteica derivada de una fase de lectura incorrecta
 del gen HS6SP1 (Tabla 1, n.º 10).

40 Ejemplos

El conjunto de proteínas que son objeto de la presente invención se ha encontrado realizando experimentos de selección de suero en macromatrices de proteínas. Las macromatrices de proteínas consisten en > 38.000 clones de
 45 *E. coli* individuales que expresan fragmentos de genes humanos clonados de una genoteca de ADNc de cerebro fetal. Estos fragmentos pueden ser proteínas de longitud completa y fragmentos de las mismas, así como péptidos artificiales resultantes de productos de traducción en la fase de lectura incorrecta. La tecnología para la selección se desarrolló en el MPI de Genética Molecular y constituye el estado de la técnica; Busow K, *et al. Nucleic Acids Res.* 1 de noviembre de 1998; 26(21):5007-8. PMID: 9776767; Biissow K, *et al. Genomics*, 1 de abril de 2000; 65(1):1-8. PMID: 10777659) y se ha aplicado desde entonces en múltiples publicaciones científicas (por ejemplo, Horn S., *et al. Proteomics*, enero de 2006; 6(2):605-13. PMID: 16419013; Lueking A., *et al. Mol Cell Proteomics*, septiembre de 2005; 4(9):1382-90. PMID: 15939964). La única modificación del método descrito en el documento original es la incubación con el suero del paciente y el uso de anticuerpos secundarios específicos dirigidos contra diferentes isotipos de inmunoglobulinas tales como IgG, IgA, IgM e IgD como se describe a continuación:

Se diluyó el suero del paciente a 1:40 en tampón de bloqueo (3 % de leche en polvo/TBST) y se incubó durante una
 55 noche a temperatura ambiente, se mantuvo en movimiento lento en un agitador orbital. Tras la incubación, se lavan los filtros 3 veces durante 20 min cada vez en TBST, seguido de una segunda incubación durante 1 h a temperatura ambiente con anticuerpo secundario anti-IgG humana o anti-IgA humana (ratón) conjugado con fosfatasa alcalina, 1:1000 en tampón de bloqueo. Las señales positivas de la macromatriz (filtro de PVDF) se registraron como se describe y se correlacionaron con los clones originales de *E. coli* almacenados en placas de microvaloración de 384 pocillos. Se secuenciaron los clones de *E. coli* correspondientes a las señales de la macromatriz para obtener información de la inserción y, por lo tanto, del fragmento génico del que el suero de paciente reconoce el producto de traducción. Estos fragmentos pueden ser proteínas de longitud completa y fragmentos de los mismos, así como péptidos artificiales procedentes de productos de traducción fuera de la fase.

65 Las macromatrices de proteínas se seleccionaron con grupos de pacientes que respondieron y pacientes que no respondieron al tratamiento anti-TNF α (Adalimumab[®]; Humira) antes y después del tratamiento. Las pacientes que

respondieron y los pacientes que no respondieron se clasificaron de acuerdo con la respuesta clínica evaluada después de 1 año (o en abandono) de acuerdo con los criterios de la Liga Europea contra el Reumatismo usando la puntuación de la actividad de la enfermedad modificada que incluía 28 articulaciones (DAS 28). La puntuación DAS28 y los criterios de respuesta de la Liga Europea contra el Reumatismo (EULAR) se usan ampliamente para registrar la actividad de la enfermedad y la respuesta terapéutica en pacientes con AR (Van Gestel A. M. *et al.*, *Arthritis Rheum* 1996; 39:34-40. PMID.

El DAS28 se desarrolló y se validó para pacientes con AR, y además de la actividad de la enfermedad, también refleja la satisfacción del paciente con una exactitud razonable. Este índice compuesto comprende 4 artículos, en concreto, recuento de articulaciones tumefactas (SJC), recuento de articulaciones sensibles (TJC), una escala analógica visual (VAS) de la evaluación del paciente de la salud general (GH) y velocidad de sedimentación eritrocítica (ESR; primera hora), que también forman parte de los criterios de respuesta del American College of Rheumatology (ACR).

Descripción de los sueros de pacientes usados:

Se compararon los valores de DAS28 de 2 cohortes de pacientes con AR que comprendían 3 pacientes cada una, y se usaron sueros de estos pacientes antes y después del tratamiento para la selección de las macromatrices de proteínas. La cohorte 1 de AR (AR1) consistía en pacientes que respondieron al tratamiento y la cohorte 2 de AR (AR2) consistía en pacientes de la misma edad y el mismo sexo observados durante el mismo período que no respondieron al tratamiento. La ponderación de los artículos, la carga factorial y la consistencia interna se evaluaron mediante análisis factorial, análisis del componente principal y cálculo del alfa de Cronbach. El intervalo de las puntuaciones de DAS28 en el grupo de pacientes que respondieron inicialmente antes del tratamiento fue de 4,4 a 6 con un valor medio de 4,83, y en el grupo de pacientes que no respondieron, de 4,1 a 8,6 con un valor medio de 6,2. El paciente que respondió tuvo un cambio medio de 2,36 durante el tratamiento, mientras que no hubo un cambio medio en el DAS28 en el grupo de pacientes que no respondió.

La Tabla 1 (que consiste en la Tabla 1 A y la Tabla 1 B) muestra una lista resumida de genes cuyos productos de expresión representan proteínas biomarcadoras y péptidos artificiales resultantes de productos de traducción en la fase de lectura incorrecta que resultaron predecir la capacidad de respuesta al tratamiento con anticuerpos anti-TNF α (Adalimumab; Humira) de los grupos de pacientes descritos anteriormente que se habían sometido a un tratamiento anti-TNF α .

TABLA 1 A: Lista de genes candidatos que codifican un conjunto de biomarcadores detectado por inmunoglobulinas de pacientes que NO RESPONDEN al tratamiento de inhibidor del TNF

N.º	Importancia	Desplazamiento de fase	Identificador de gen de ENSEMBL	Símbolo de gen de HGNC	Descripción del gen e identificadores alternativos
1	1: Alta	0	ENSG00000185236	RAB11B	Proteína relacionada con Ras Rab-11B (proteína de unión a GTP YPT3). [Fuente: Uniprot/SWISSPROT; Cuenta: Q159071]
2	1: Alta	0	ENSG00000105568	PPP2R1A	Isoforma alfa de la subunidad A reguladora de 65 kDa de la fosfatasa de la proteína serina/treonina 2A (PP2A, subunidad A, isoforma alfa de PR65) (PP2A, subunidad A, isoforma alfa de R1) (proteína de 61 kDa asociada al antígeno tumoral en medio). [Fuente: Uniprot/SWISSPROT; Cuenta: P30153]
3	1: Alta	0	ENSG00000108424	KPNB1	Subunidad beta-1 de Importina (subunidad beta-1 de karioferina) (factor nuclear P97) (Importina 90). [Fuente: Uniprot/SWISSPROT; Cuenta: Q14974]
4	1: Alta	0	ENSG00000103051	COG4	Componente 4 del complejo de Golgi oligomérico conservado. [Fuente: Uniprot/SWISSPROT; Cuenta: Q9H9E3]
5	1: Alta	0	ENSG00000079459	FDFT1	Escualeno sintetasa (EC 2.5.1.21) (SQS) (SS) (Farnesil-difosfato farnesiltransferasa) (FPP: FPP farnesiltransferasa). [Fuente: Uniprot/SWISSPROT; Cuenta: P37268]
6	2: Media	0	ENSG00000198721	PECI	3,2-trans-enoil-CoA isomerasa peroxisomal (EC 5.3.3.8) (Dodecenil-CoA isomerasa) (Delta(3),delta(2)-enoil-CoA isomerasa) (D3,D2-enoil-CoA isomerasa) (proteína 1 relacionada con DBI) (DRS-1) (antígeno 88 asociado con carcinoma hepatocelular) (antígeno de carcinoma renal)
7	2: Media	0	ENSG00000169862	CTNND2	Catenina delta-2 (Delta-catenina) (proteína de repetición de ARM relacionada con placofilina neuronal) (NPRAP) (Neurojüngina) (GT24). [Fuente: Uniprot/SWISSPROT; Cuenta: Q9UQB3] cromosoma_NCB136:5:11024952-11957110:-1
8	2: Media	0	ENSG00000169189	NSMCE1	Homólogo de elemento no SMC 1 (Fuente: RefSeq peptide; Cuenta: NP 659547) cromosoma_NCB136:16:27143817-27187586:-1
9	2: Media	0	ENSG00000163389	KTELC1	Precursor de proteína que contiene el motivo KTEL 1 (proteína de 46 kDa de tipo CAP10) (proteína relacionada con los síndromes mielodisplásicos). [Fuente: Uniprot/SWISSPROT; Cuenta: Q8NBL1]
10	2: Media	-1	ENSG00000136720	HS6ST1	Heparán-sulfato 6-O-sulfotransferasa 1 (EC 2.8.2.-) (HS6ST-1) [Fuente: Uniprot/SWISSPROT; Cuenta: O602431]
11	2: Media	0	ENSG00000105676	ARMC6	Proteína 6 que contiene repetición de Armadillo. [Fuente: Uniprot/SWISSPROT; Cuenta: Q6NXX6] cromosoma_NCB136:19:19005538-19029985:1
12	2: Media	0	ENSG00000101158	TH1L	Factor de elongación negativo C/D (NELF-C/D) (proteína de tipo TH1). [Fuente: Uniprot/SWISSPROT; Cuenta: Q8IXH71]
13	2: Media	0	ENSG00000092010	PSME1	Subunidad 1 del complejo activador proteosómico (subunidad 28-alfa del activador proteosómico) (PA28alfa) (PA28a) (Activador de la subunidad 1 de la proteasa multicatalítica) (subunidad alfa del complejo regulador 11S) (REG-alfa) (Proteína I-5111 regulada positivamente por interferón gamma) (IGUP I-51)

14	2: Media	0	ENSG00000063660	GPC1	Precursor de glipicano-1 [Fuente: Uniprot/SWISSPROT; Cuenta: P35052]
15	2: Media	0	ENSG00000038358	EDC4	Autoantígeno RCD8 [Fuente: RefSeq peptide; Cuenta: NP_055144] cromosoma_NCB136:16:66464500-66475906:1
16	3: Baja	0	ENSG000000198901	PRC1	Regulador proteico de la citocinesis 1. [Fuente: Uniprot/SWISSPROT; Cuenta: O43663] cromosoma_NCB136:15:89310279-89338808:-1
17	3: Baja	0	ENSG000000186792	NAT6	Precursor de la hialuronidasa-3 (EC 3.2.1.35) (Hial-3) (Hialuronoglucosaminidasa-3) (LUCA-3). [Fuente: Uniprot/SWISSPROT; Cuenta: O43820] cromosoma_NCB136:3:50300178-50311903:-1
18	3: Baja	0	ENSG000000185637	EEF1A1L3	Alfa 1 del factor 1 de elongación de la traducción eucariota (Fragmento). [Fuente: Uniprot/SPTREMBL; Cuenta: Q5JR01] cromosoma_NCB136:9:134884631-134886374:1
19	3: Baja	0	ENSG000000168005	NP_612480.1	cromosoma_NCB136:11:63337436-63351727:1
20	3: Baja	0	ENSG000000076356	PLXNA2	Precursor de la plexina-A2 (Receptor de semaforina OCT). [Fuente: Uniprot/SWISSPROT; Cuenta: O75051] cromosoma_NCB136:1:206262210-206484288:-1
21	3: Baja	0	ENSG000000062598	ELM02	Proteína de envoltura y motilidad celular 2 (homólogo A de CED-12) (hCED-12A). [Fuente: Uniprot/SWISSPROT; Cuenta: Q96JU3] cromosoma_NCB136:20:44428096-44468678:-1
22	3: Baja	0	ENSG000000158864	NDUFS2	Subunidad de 49 kDa de NADH-ubiquinona oxidoreductasa, precursor mitocondrial (EC 1.6.5.3) (EC 1.6.99.3) (Complejo I-49KD) (CI-49KD). [Fuente: Uniprot/SWISSPROT; Cuenta: O75306]

TABLA 1B: Lista de genes candidatos que codifican un conjunto de biomarcadores detectado por inmunoglobulinas de pacientes que RESPONDEN al tratamiento de inhibidor del TNF

N.º	Importancia	Desplazamiento de fase	Identificador de gen de ENSEMBL	Símbolo de gen de HGNC	Descripción del gen e identificadores alternativos
23	1: Alta	-1	ENSG000000184216	IRAK1	Quinasa 1 asociada al receptor de la interleucina 1 (EC 2.7.11.1) (IRAK-1). Fuente: Uniprot/SWISSPROT; Cuenta: P51617.1
24	1: Alta	-1	ENSG000000125534	C20orf149	Proteína de UPF0362 C20orf149. [Fuente: Uniprot/SWISSPROT; Cuenta: G9H3Y8]
25	2: Media	0	ENSG000000105443	PSCD2L	Citohesina-2 (agente de apertura del sitio de unión al nucleótido ARF) (proteína ARNO) (factor de intercambio ARF). [Fuente: Uniprot/SWISSPROT; Cuenta: Q99418] cromosoma_NCB136:19:53664424-53674457:1
26	3: Baja	0	ENSG000000198618	PPIA	Peptidil-proil <i>cis-trans</i> isomerasa A (EC 5.2.1.8) (PPIasa A) (Rotamasa A) (Ciclofilina A) (proteína de unión a ciclosporina A). [Fuente: Uniprot/SWISSPROT; Cuenta: P62937] cromosoma_NCB136:21:19151917-19152651:1

Listado de secuencias

	<110> Max-Planck-Gesellschaft zur Förderung der Wissenschaften eV	
5	<120> Biomarcador para la predicción de la capacidad de respuesta a un tratamiento anti-factor de necrosis tumoral alfa (TNF)	
	<130> N3102 PCT BLN	
10	<150> EP 07 11 9810.5 <151> 31-10-2007	
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	atcgagagcc gcgctgcccc cgacgagtcc ccggggaaca acgtggtgga catcagcgtg	600
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	<213> Humano	
30	<400> 2	

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<213> Humano

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 Lys Val Lys Glu Phe Cys Glu Asn Leu Ser Ala Asp Cys Arg Glu Asn
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 325 330 335

ES 2 671 895 T3

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His Arg Met Thr Thr Leu Phe Cys Ile Asn Val Leu Ser Glu Val Cys
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Gly Gln Asp Ile Thr Thr Lys His Met Leu Pro Thr Val Leu Arg Met
515 520 525

Ala Gly Asp Pro Val Ala Asn Val Arg Phe Asn Val Ala Lys Ser Leu
530 535 540

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

Lys Pro Ile Leu Glu Lys Leu Thr Gln Asp Gln Asp Val Asp Val Lys
565 570 575

Tyr Phe Ala Gln Glu Ala Leu Thr Val Leu Ser Leu Ala
580 585

<210> 61
<211> 509
<212> PRT
<213> Humana

<400> 61

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Met Arg Thr Phe Ser Phe Ala Ser Thr Ala Ser Arg Ser Cys Pro Pro
1      5      10      15

Ser Pro Trp Pro Leu Gly Leu Lys Gly Pro Glu Val Ser Phe Cys Leu
20      25      30

Ser Leu Gln Ile Pro Ser Met Met Lys Met Arg Ser Ser Trp Pro Trp
35      40      45

Gln Asn Ser Trp Glu Pro Ser Leu Pro Trp Trp Glu Ala Gln Ser Thr
50      55      60

Cys Thr Ala Cys Cys Leu Phe Ser Val Cys Tyr Pro Arg Val Ser Ser
65      70      75      80

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

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

Ala Lys Val Leu Glu Leu Asp Asn Val Lys Ser Glu Ile Ile Pro Met
115     120     125

Phe Ser Asn Leu Ala Ser Asp Glu Gln Asp Ser Val Arg Leu Leu Ala
130     135     140

Val Glu Ala Cys Val Asn Ile Ala Gln Leu Leu Pro Gln Glu Asp Leu
145     150     155     160

Glu Ala Leu Val Met Pro Thr Leu Arg Gln Ala Ala Glu Asp Lys Ser
165     170     175

Trp Arg Val Arg Tyr Met Val Ala Asp Lys Phe Thr Glu Leu Gln Lys
180     185     190

Ala Val Gly Pro Glu Ile Thr Lys Thr Asp Leu Val Pro Ala Phe Gln
195     200     205

Asn Leu Met Lys Asp Cys Glu Ala Glu Val Arg Ala Ala Ala Ser His
210     215     220

Lys Val Lys Glu Phe Cys Glu Asn Leu Ser Ala Asp Cys Arg Glu Asn
225     230     235     240

Val Ile Met Ser Gln Ile Leu Pro Cys Ile Lys Glu Leu Val Ser Asp
245     250     255

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Ala Asn Gln His Val Lys Ser Ala Leu Ala Ser Val Ile Met Gly Leu
260 265 270

Ser Pro Ile Leu Gly Lys Asp Asn Thr Ile Glu His Leu Leu Pro Leu
275 280 285

Phe Leu Ala Gln Leu Lys Asp Glu Cys Pro Glu Val Arg Leu Asn Ile
290 295 300

Ile Ser Asn Leu Asp Cys Val Asn Glu Val Ile Gly Ile Arg Gln Leu
305 310 315 320

Ser Gln Ser Leu Leu Pro Ala Ile Val Glu Leu Ala Glu Asp Ala Lys
325 330 335

Trp Arg Val Arg Leu Ala Ile Ile Glu Tyr Met Pro Leu Leu Ala Gly
340 345 350

Gln Leu Gly Val Glu Phe Phe Asp Glu Lys Leu Asn Ser Leu Cys Met
355 360 365

Ala Trp Leu Val Asp His Val Tyr Ala Ile Arg Glu Ala Ala Thr Ser
370 375 380

Asn Leu Lys Lys Leu Val Glu Lys Phe Gly Lys Glu Trp Ala His Ala
385 390 395 400

Thr Ile Ile Pro Lys Val Leu Ala Met Ser Gly Asp Pro Asn Tyr Leu
405 410 415

His Arg Met Thr Thr Leu Phe Cys Ile Asn Val Leu Ser Glu Val Cys
420 425 430

Gly Gln Asp Ile Thr Thr Lys His Met Leu Pro Thr Val Leu Arg Met
435 440 445

Ala Gly Asp Pro Val Ala Asn Val Arg Phe Asn Val Ala Lys Ser Leu
450 455 460

Gln Lys Ile Gly Pro Ile Leu Asp Asn Ser Thr Leu Gln Ser Glu Val
465 470 475 480

Lys Pro Ile Leu Glu Lys Leu Thr Gln Asp Gln Asp Val Asp Val Lys
485 490 495

Tyr Phe Ala Gln Glu Ala Leu Thr Val Leu Ser Leu Ala
500 505

<210> 62
<211> 876
<212> PRT
<213> Humana

<400> 62

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

Glu Leu Glu Ala Ala Gln Lys Phe Leu Glu Arg Ala Ala Val Glu Asn
20           25           30

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

Asn Ser Gln Val Ala Arg Val Ala Ala Gly Leu Gln Ile Lys Asn Ser
50           55           60

Leu Thr Ser Lys Asp Pro Asp Ile Lys Ala Gln Tyr Gln Gln Arg Trp
65           70           75           80

Leu Ala Ile Asp Ala Asn Ala Arg Arg Glu Val Lys Asn Tyr Val Leu
85           90           95

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

Val Ala Gly Ile Ala Cys Ala Glu Ile Pro Val Asn Gln Trp Pro Glu
115          120          125

Leu Ile Pro Gln Leu Val Ala Asn Val Thr Asn Pro Asn Ser Thr Glu
130          135          140

His Met Lys Glu Ser Thr Leu Glu Ala Ile Gly Tyr Ile Cys Gln Asp
145          150          155          160

Ile Asp Pro Glu Gln Leu Gln Asp Lys Ser Asn Glu Ile Leu Thr Ala
165          170          175

Ile Ile Gln Gly Met Arg Lys Glu Glu Pro Ser Asn Asn Val Lys Leu
180          185          190

Ala Ala Thr Asn Ala Leu Leu Asn Ser Leu Glu Phe Thr Lys Ala Asn
195          200          205

Phe Asp Lys Glu Ser Glu Arg His Phe Ile Met Gln Val Val Cys Glu
210          215          220

Ala Thr Gln Cys Pro Asp Thr Arg Val Arg Val Ala Ala Leu Gln Asn
225          230          235          240

Leu Val Lys Ile Met Ser Leu Tyr Tyr Gln Tyr Met Glu Thr Tyr Met
245          250          255

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Gly Pro Ala Leu Phe Ala Ile Thr Ile Glu Ala Met Lys Ser Asp Ile
 260 265 270
 Asp Glu Val Ala Leu Gln Gly Ile Glu Phe Trp Ser Asn Val Cys Asp
 275 280 285
 Glu Glu Met Asp Leu Ala Ile Glu Ala Ser Glu Ala Ala Glu Gln Gly
 290 295 300
 Arg Pro Pro Glu His Thr Ser Lys Phe Tyr Ala Lys Gly Ala Leu Gln
 305 310 315 320
 Tyr Leu Val Pro Ile Leu Thr Gln Thr Leu Thr Lys Gln Asp Glu Asn
 325 330 335
 Asp Asp Asp Asp Asp Trp Asn Pro Cys Lys Ala Ala Gly Val Cys Leu
 340 345 350
 Met Leu Leu Ala Thr Cys Cys Glu Asp Asp Ile Val Pro His Val Leu
 355 360 365
 Pro Phe Ile Lys Glu His Ile Lys Asn Pro Asp Trp Arg Tyr Arg Asp
 370 375 380
 Ala Ala Val Met Ala Phe Gly Cys Ile Leu Glu Gly Pro Glu Pro Ser
 385 390 395 400
 Gln Leu Lys Pro Leu Val Ile Gln Ala Met Pro Thr Leu Ile Glu Leu
 405 410 415
 Met Lys Asp Pro Ser Val Val Val Arg Asp Thr Ala Ala Trp Thr Val
 420 425 430
 Gly Arg Ile Cys Glu Leu Leu Pro Glu Ala Ala Ile Asn Asp Val Tyr
 435 440 445
 Leu Ala Pro Leu Leu Gln Cys Leu Ile Glu Gly Leu Ser Ala Glu Pro
 450 455 460
 Arg Val Ala Ser Asn Val Cys Trp Ala Phe Ser Ser Leu Ala Glu Ala
 465 470 475 480
 Ala Tyr Glu Ala Ala Asp Val Ala Asp Asp Gln Glu Glu Pro Ala Thr
 485 490 495
 Tyr Cys Leu Ser Ser Ser Phe Glu Leu Ile Val Gln Lys Leu Leu Glu
 500 505 510
 Thr Thr Asp Arg Pro Asp Gly His Gln Asn Asn Leu Arg Ser Ser Ala
 515 520 525

ES 2 671 895 T3

Tyr Glu Ser Leu Met Glu Ile Val Lys Asn Ser Ala Lys Asp Cys Tyr
 530 535 540
 Pro Ala Val Gln Lys Thr Thr Leu Val Ile Met Glu Arg Leu Gln Gln
 545 550 555 560
 Val Leu Gln Met Glu Ser His Ile Gln Ser Thr Ser Asp Arg Ile Gln
 565 570 575
 Phe Asn Asp Leu Gln Ser Leu Leu Cys Ala Thr Leu Gln Asn Val Leu
 580 585 590
 Arg Lys Val Gln His Gln Asp Ala Leu Gln Ile Ser Asp Val Val Met
 595 600 605
 Ala Ser Leu Leu Arg Met Phe Gln Ser Thr Ala Gly Ser Gly Gly Val
 610 615 620
 Gln Glu Asp Ala Leu Met Ala Val Ser Thr Leu Val Glu Val Leu Gly
 625 630 635 640
 Gly Glu Phe Leu Lys Tyr Met Glu Ala Phe Lys Pro Phe Leu Gly Ile
 645 650 655
 Gly Leu Lys Asn Tyr Ala Glu Tyr Gln Val Cys Leu Ala Ala Val Gly
 660 665 670
 Leu Val Gly Asp Leu Cys Arg Ala Leu Gln Ser Asn Ile Ile Pro Phe
 675 680 685
 Cys Asp Glu Val Met Gln Leu Leu Leu Glu Asn Leu Gly Asn Glu Asn
 690 695 700
 Val His Arg Ser Val Lys Pro Gln Ile Leu Ser Val Phe Gly Asp Ile
 705 710 715 720
 Ala Leu Ala Ile Gly Gly Glu Phe Lys Lys Tyr Leu Glu Val Val Leu
 725 730 735
 Asn Thr Leu Gln Gln Ala Ser Gln Ala Gln Val Asp Lys Ser Asp Tyr
 740 745 750
 Asp Met Val Asp Tyr Leu Asn Glu Leu Arg Glu Ser Cys Leu Glu Ala
 755 760 765
 Tyr Thr Gly Ile Val Gln Gly Leu Lys Gly Asp Gln Glu Asn Val His
 770 775 780
 Pro Asp Val Met Leu Val Gln Pro Arg Val Glu Phe Ile Leu Ser Phe
 785 790 795 800

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Ile Asp His Ile Ala Gly Asp Glu Asp His Thr Asp Gly Val Val Ala
805 810 815
Cys Ala Ala Gly Leu Ile Gly Asp Leu Cys Thr Ala Phe Gly Lys Asp
820 825 830
Val Leu Lys Leu Val Glu Ala Arg Pro Met Ile His Glu Leu Leu Thr
835 840 845
Glu Gly Arg Arg Ser Lys Thr Asn Lys Ala Lys Thr Leu Ala Thr Trp
850 855 860
Ala Thr Lys Glu Leu Arg Lys Leu Lys Asn Gln Ala
865 870 875

<210> 64
<211> 789
<212> PRT
<213> Humana

5

<400> 64

Met Gly Thr Lys Met Ala Asp Leu Asp Ser Pro Pro Lys Leu Ser Gly
1 5 10 15
Val Gln Gln Pro Ser Glu Gly Val Gly Gly Gly Arg Cys Ser Glu Ile
20 25 30
Ser Ala Glu Leu Ile Arg Ser Leu Thr Glu Leu Gln Glu Leu Glu Ala
35 40 45
Val Tyr Glu Arg Leu Cys Gly Glu Glu Lys Val Val Glu Arg Glu Leu
50 55 60
Asp Ala Leu Leu Glu Gln Gln Asn Thr Ile Glu Ser Lys Met Val Thr
65 70 75 80
Leu His Arg Met Gly Pro Asn Leu Gln Leu Ile Glu Gly Asp Ala Lys
85 90 95
Gln Leu Ala Gly Met Ile Thr Phe Thr Cys Asn Leu Ala Glu Asn Val
100 105 110
Ser Ser Lys Val Arg Gln Leu Asp Leu Ala Lys Asn Arg Leu Tyr Gln
115 120 125
Ala Ile Gln Arg Ala Asp Asp Ile Leu Asp Leu Lys Phe Cys Met Asp
130 135 140
Gly Val Gln Thr Ala Leu Arg Ser Glu Asp Tyr Glu Gln Ala Ala Ala
145 150 155 160
His Thr His Arg Tyr Leu Cys Leu Asp Lys Ser Val Ile Glu Leu Ser

10

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165										170					175				
Arg	Gln	Gly	Lys 180	Glu	Gly	Ser	Met	Ile 185	Asp	Ala	Asn	Leu	Lys 190	Leu	Leu				
Gln	Glu	Ala 195	Glu	Gln	Arg	Leu	Lys 200	Ala	Ile	Val	Ala	Glu 205	Lys	Phe	Ala				
Ile	Ala 210	Thr	Lys	Glu	Gly	Asp 215	Leu	Pro	Gln	Val	Glu 220	Arg	Phe	Phe	Lys				
Ile 225	Phe	Pro	Leu	Leu	Gly 230	Leu	His	Glu	Glu	Gly 235	Leu	Arg	Lys	Phe	Ser 240				
Glu	Tyr	Leu	Cys	Lys 245	Gln	Val	Ala	Ser	Lys 250	Ala	Glu	Glu	Asn	Leu 255	Leu				
Met	Val	Leu	Gly 260	Thr	Asp	Met	Ser	Asp 265	Arg	Arg	Ala	Ala	Val 270	Ile	Phe				
Ala	Asp	Thr 275	Leu	Thr	Leu	Leu	Phe 280	Glu	Gly	Ile	Ala	Arg 285	Ile	Val	Glu				
Thr	His 290	Gln	Pro	Ile	Val	Glu 295	Thr	Tyr	Tyr	Gly	Pro 300	Gly	Arg	Leu	Tyr				
Thr 305	Leu	Ile	Lys	Tyr	Leu 310	Gln	Val	Glu	Cys	Asp 315	Arg	Gln	Val	Glu	Lys 320				
Val	Val	Asp	Lys	Phe 325	Ile	Lys	Gln	Arg	Asp 330	Tyr	His	Gln	Gln	Phe 335	Arg				
His	Val	Gln	Asn 340	Asn	Leu	Met	Arg	Asn 345	Ser	Thr	Thr	Glu	Lys 350	Ile	Glu				
Pro	Arg	Glu 355	Leu	Asp	Pro	Ile	Leu 360	Thr	Glu	Val	Thr	Leu 365	Met	Asn	Ala				
Arg	Ser 370	Glu	Leu	Tyr	Leu	Arg 375	Phe	Leu	Lys	Lys	Arg 380	Ile	Ser	Ser	Asp				
Phe 385	Glu	Val	Gly	Asp	Ser 390	Met	Ala	Ser	Glu	Glu 395	Val	Lys	Gln	Glu	His 400				
Gln	Lys	Cys	Leu	Asp 405	Lys	Leu	Leu	Asn	Asn 410	Cys	Leu	Leu	Ser	Cys 415	Thr				
Met	Gln	Glu	Leu 420	Ile	Gly	Leu	Tyr	Val 425	Thr	Met	Glu	Glu	Tyr 430	Phe	Met				
Arg	Glu	Thr	Val	Asn	Lys	Ala	Val	Ala	Leu	Asp	Thr	Tyr	Glu	Lys	Gly				

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435 440 ----- 445
 Gln Leu Thr Ser Ser Met Val Asp Asp Val Phe Tyr Ile Val Lys Lys
 450 455 460
 Cys Ile Gly Arg Ala Leu Ser Ser Ser Ser Ile Asp Cys Leu Cys Ala
 465 470 475 480
 Met Ile Asn Leu Ala Thr Thr Glu Leu Glu Ser Asp Phe Arg Asp Val
 485 490 495
 Leu Cys Asn Lys Leu Arg Met Gly Phe Pro Ala Thr Thr Phe Gln Asp
 500 505 510
 Ile Gln Arg Gly Val Thr Ser Ala Val Asn Ile Met His Ser Ser Leu
 515 520 525
 Gln Gln Gly Lys Phe Asp Thr Lys Gly Ile Glu Ser Thr Asp Glu Ala
 530 535 540
 Lys Met Ser Phe Leu Val Thr Leu Asn Asn Val Glu Val Cys Ser Glu
 545 550 555 560
 Asn Ile Ser Thr Leu Lys Lys Thr Leu Glu Ser Asp Cys Thr Lys Leu
 565 570 575
 Phe Ser Gln Gly Ile Gly Gly Glu Gln Ala Gln Ala Lys Phe Asp Ser
 580 585 590
 Cys Leu Ser Asp Leu Ala Ala Val Ser Asn Lys Phe Arg Asp Leu Leu
 595 600 605
 Gln Glu Gly Leu Thr Glu Leu Asn Ser Thr Ala Ile Lys Pro Gln Val
 610 615 620
 Gln Pro Trp Ile Asn Ser Phe Phe Ser Val Ser His Asn Ile Glu Glu
 625 630 635 640
 Glu Glu Phe Asn Asp Tyr Glu Ala Asn Asp Pro Trp Val Gln Gln Phe
 645 650 655
 Ile Leu Asn Leu Glu Gln Gln Met Ala Glu Phe Lys Ala Ser Leu Ser
 660 665 670
 Pro Val Ile Tyr Asp Ser Leu Thr Gly Leu Met Thr Ser Leu Val Ala
 675 680 685
 Val Glu Leu Glu Lys Val Val Leu Lys Ser Thr Phe Asn Arg Leu Gly
 690 695 700
 Gly Leu Gln Phe Asp Lys Glu Leu Arg Ser Leu Ile Ala Tyr Leu Thr

ES 2 671 895 T3

705 710 715 720

Thr Val Thr Thr Trp Thr Ile Arg Asp Lys Phe Ala Arg Leu Ser Gln
725 730 735

Met Ala Thr Ile Leu Asn Leu Glu Arg Val Thr Glu Ile Leu Asp Tyr
740 745 750

Trp Gly Pro Asn Ser Gly Pro Leu Thr Trp Arg Leu Thr Pro Ala Glu
755 760 765

Val Arg Gln Val Leu Ala Leu Arg Ile Asp Phe Arg Ser Glu Asp Ile
770 775 780

Lys Arg Leu Arg Leu
785

<210> 65
<211> 785
<212> PRT
<213> Humana

<400> 65

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

Ser Glu Gly Val Gly Gly Gly Arg Cys Ser Glu Ile Ser Ala Glu Leu
20 25 30

Ile Arg Ser Leu Thr Glu Leu Gln Glu Leu Glu Ala Val Tyr Glu Arg
35 40 45

Leu Cys Gly Glu Glu Lys Val Val Glu Arg Glu Leu Asp Ala Leu Leu
50 55 60

Glu Gln Gln Asn Thr Ile Glu Ser Lys Met Val Thr Leu His Arg Met
65 70 75 80

Gly Pro Asn Leu Gln Leu Ile Glu Gly Asp Ala Lys Gln Leu Ala Gly
85 90 95

Met Ile Thr Phe Thr Cys Asn Leu Ala Glu Asn Val Ser Ser Lys Val
100 105 110

Arg Gln Leu Asp Leu Ala Lys Asn Arg Leu Tyr Gln Ala Ile Gln Arg
115 120 125

Ala Asp Asp Ile Leu Asp Leu Lys Phe Cys Met Asp Gly Val Gln Thr
130 135 140

Ala Leu Arg Ser Glu Asp Tyr Glu Gln Ala Ala Ala His Thr His Arg
145 150 155 160

ES 2 671 895 T3

Tyr Leu Cys Leu Asp Lys Ser Val Ile Glu Leu Ser Arg Gln Gly Lys
 165 170 175
 Glu Gly Ser Met Ile Asp Ala Asn Leu Lys Leu Leu Gln Glu Ala Glu
 180 185 190
 Gln Arg Leu Lys Ala Ile Val Ala Glu Lys Phe Ala Ile Ala Thr Lys
 195 200 205
 Glu Gly Asp Leu Pro Gln Val Glu Arg Phe Phe Lys Ile Phe Pro Leu
 210 215 220
 Leu Gly Leu His Glu Glu Gly Leu Arg Lys Phe Ser Glu Tyr Leu Cys
 225 230 235 240
 Lys Gln Val Ala Ser Lys Ala Glu Glu Asn Leu Leu Met Val Leu Gly
 245 250 255
 Thr Asp Met Ser Asp Arg Arg Ala Ala Val Ile Phe Ala Asp Thr Leu
 260 265 270
 Thr Leu Leu Phe Glu Gly Ile Ala Arg Ile Val Glu Thr His Gln Pro
 275 280 285
 Ile Val Glu Thr Tyr Tyr Gly Pro Gly Arg Leu Tyr Thr Leu Ile Lys
 290 295 300
 Tyr Leu Gln Val Glu Cys Asp Arg Gln Val Glu Lys Val Val Asp Lys
 305 310 315 320
 Phe Ile Lys Gln Arg Asp Tyr His Gln Gln Phe Arg His Val Gln Asn
 325 330 335
 Asn Leu Met Arg Asn Ser Thr Thr Glu Lys Ile Glu Pro Arg Glu Leu
 340 345 350
 Asp Pro Ile Leu Thr Glu Val Thr Leu Met Asn Ala Arg Ser Glu Leu
 355 360 365
 Tyr Leu Arg Phe Leu Lys Lys Arg Ile Ser Ser Asp Phe Glu Val Gly
 370 375 380
 Asp Ser Met Ala Ser Glu Glu Val Lys Gln Glu His Gln Lys Cys Leu
 385 390 395 400
 Asp Lys Leu Leu Asn Asn Cys Leu Leu Ser Cys Thr Met Gln Glu Leu
 405 410 415
 Ile Gly Leu Tyr Val Thr Met Glu Glu Tyr Phe Met Arg Glu Thr Val
 420 425 430

ES 2 671 895 T3

Asn Lys Ala Val Ala Leu Asp Thr Tyr Glu Lys Gly Gln Leu Thr Ser
 435 440 445
 Ser Met Val Asp Asp Val Phe Tyr Ile Val Lys Lys Cys Ile Gly Arg
 450 455 460
 Ala Leu Ser Ser Ser Ser Ile Asp Cys Leu Cys Ala Met Ile Asn Leu
 465 470 475 480
 Ala Thr Thr Glu Leu Glu Ser Asp Phe Arg Asp Val Leu Cys Asn Lys
 485 490 495
 Leu Arg Met Gly Phe Pro Ala Thr Thr Phe Gln Asp Ile Gln Arg Gly
 500 505 510
 Val Thr Ser Ala Val Asn Ile Met His Ser Ser Leu Gln Gln Gly Lys
 515 520 525
 Phe Asp Thr Lys Gly Ile Glu Ser Thr Asp Glu Ala Lys Met Ser Phe
 530 535 540
 Leu Val Thr Leu Asn Asn Val Glu Val Cys Ser Glu Asn Ile Ser Thr
 545 550 555 560
 Leu Lys Lys Thr Leu Glu Ser Asp Cys Thr Lys Leu Phe Ser Gln Gly
 565 570 575
 Ile Gly Gly Glu Gln Ala Gln Ala Lys Phe Asp Ser Cys Leu Ser Asp
 580 585 590
 Leu Ala Ala Val Ser Asn Lys Phe Arg Asp Leu Leu Gln Glu Gly Leu
 595 600 605
 Thr Glu Leu Asn Ser Thr Ala Ile Lys Pro Gln Val Gln Pro Trp Ile
 610 615 620
 Asn Ser Phe Phe Ser Val Ser His Asn Ile Glu Glu Glu Glu Phe Asn
 625 630 635 640
 Asp Tyr Glu Ala Asn Asp Pro Trp Val Gln Gln Phe Ile Leu Asn Leu
 645 650 655
 Glu Gln Gln Met Ala Glu Phe Lys Ala Ser Leu Ser Pro Val Ile Tyr
 660 665 670
 Asp Ser Leu Thr Gly Leu Met Thr Ser Leu Val Ala Val Glu Leu Glu
 675 680 685
 Lys Val Val Leu Lys Ser Thr Phe Asn Arg Leu Gly Gly Leu Gln Phe
 690 695 700

ES 2 671 895 T3

Asp Lys Glu Leu Arg Ser Leu Ile Ala Tyr Leu Thr Thr Val Thr Thr
705 710 715 720

Trp Thr Ile Arg Asp Lys Phe Ala Arg Leu Ser Gln Met Ala Thr Ile
725 730 735

Leu Asn Leu Glu Arg Val Thr Glu Ile Leu Asp Tyr Trp Gly Pro Asn
740 745 750

Ser Gly Pro Leu Thr Trp Arg Leu Thr Pro Ala Glu Val Arg Gln Val
755 760 765

Leu Ala Leu Arg Ile Asp Phe Arg Ser Glu Asp Ile Lys Arg Leu Arg
770 775 780

Leu
785

<210> 66
<211> 337
<212> PRT
<213> Humana

<400> 66

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

Ser Glu Gly Val Gly Gly Gly Arg Cys Ser Glu Ile Ser Ala Glu Leu
20 25 30

Ile Arg Ser Leu Thr Glu Leu Gln Glu Leu Glu Ala Val Tyr Glu Arg
35 40 45

Leu Cys Gly Glu Glu Lys Val Val Glu Arg Glu Leu Asp Ala Leu Leu
50 55 60

Glu Gln Gln Asn Thr Ile Glu Ser Lys Met Val Thr Leu His Arg Met
65 70 75 80

Gly Pro Asn Leu Gln Leu Ile Glu Gly Asp Ala Lys Gln Leu Ala Gly
85 90 95

Met Ile Thr Phe Thr Cys Asn Leu Ala Glu Asn Val Ser Ser Lys Val
100 105 110

Arg Gln Leu Asp Leu Ala Lys Asn Arg Leu Tyr Gln Ala Ile Gln Arg
115 120 125

Ala Asp Asp Ile Leu Asp Leu Lys Phe Cys Met Asp Gly Val Gln Thr
130 135 140

ES 2 671 895 T3

Ala Leu Arg Ser Glu Asp Tyr Glu Gln Ala Ala Ala His Thr His Arg
145 150 155 160

Tyr Leu Cys Leu Asp Lys Ser Val Ile Glu Leu Ser Arg Gln Gly Lys
165 170 175

Glu Gly Ser Met Ile Asp Ala Asn Leu Lys Leu Leu Gln Glu Ala Glu
180 185 190

Gln Arg Leu Lys Ala Ile Val Ala Glu Lys Phe Ala Ile Ala Thr Lys
195 200 205

Glu Gly Asp Leu Pro Gln Val Glu Arg Phe Phe Lys Ile Phe Pro Leu
210 215 220

Leu Gly Leu His Glu Glu Gly Leu Arg Lys Phe Ser Glu Tyr Leu Cys
225 230 235 240

Lys Gln Val Ala Ser Lys Ala Glu Glu Asn Leu Leu Met Val Leu Gly
245 250 255

Thr Asp Met Ser Asp Arg Arg Ala Ala Val Ile Phe Ala Asp Thr Leu
260 265 270

Thr Leu Leu Phe Glu Gly Ile Ala Arg Ile Val Glu Thr His Gln Pro
275 280 285

Ile Val Glu Thr Tyr Tyr Gly Pro Gly Arg Leu Tyr Thr Leu Ile Lys
290 295 300

Tyr Leu Gln Val Glu Cys Asp Arg Gln Val Glu Lys Val Val Asp Lys
305 310 315 320

Phe Ile Lys Gln Arg Asp Tyr His Gln Gln Asn Phe Val Phe Ser Phe
325 330 335

Phe

<210> 67
<211> 695
<212> PRT
<213> Humana

<400> 67

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

Val Gln Gln Pro Ser Glu Gly Val Gly Gly Gly Arg Cys Ser Glu Ile
20 25 30

ES 2 671 895 T3

Ser Ala Glu Leu Ile Arg Ser Leu Thr Glu Leu Gln Glu Leu Glu Ala
 35 40 45
 Val Tyr Glu Arg Leu Cys Gly Glu Glu Lys Val Val Glu Arg Glu Leu
 50 55 60
 Asp Ala Leu Leu Glu Gln Gln Asn Thr Ile Glu Ser Lys Met Val Thr
 65 70 75 80
 Leu His Arg Met Gly Pro Asn Leu Gln Leu Ile Glu Ala Asn Leu Lys
 85 90 95
 Leu Leu Gln Glu Ala Glu Gln Arg Leu Lys Ala Ile Val Ala Glu Lys
 100 105 110
 Phe Ala Ile Ala Thr Lys Glu Gly Asp Leu Pro Gln Val Glu Arg Phe
 115 120 125
 Phe Lys Ile Phe Pro Leu Leu Gly Leu His Glu Glu Gly Leu Arg Lys
 130 135 140
 Phe Ser Glu Tyr Leu Cys Lys Gln Val Ala Ser Lys Ala Glu Glu Asn
 145 150 155 160
 Leu Leu Met Val Leu Gly Thr Asp Met Ser Asp Arg Arg Ala Ala Val
 165 170 175
 Ile Phe Ala Asp Thr Leu Thr Leu Leu Phe Glu Gly Ile Ala Arg Ile
 180 185 190
 Val Glu Thr His Gln Pro Ile Val Glu Thr Tyr Tyr Gly Pro Gly Arg
 195 200 205
 Leu Tyr Thr Leu Ile Lys Tyr Leu Gln Val Glu Cys Asp Arg Gln Val
 210 215 220
 Glu Lys Val Val Asp Lys Phe Ile Lys Gln Arg Asp Tyr His Gln Gln
 225 230 235 240
 Phe Arg His Val Gln Asn Asn Leu Met Arg Asn Ser Thr Thr Glu Lys
 245 250 255
 Ile Glu Pro Arg Glu Leu Asp Pro Ile Leu Thr Glu Val Thr Leu Met
 260 265 270
 Asn Ala Arg Ser Glu Leu Tyr Leu Arg Phe Leu Lys Lys Arg Ile Ser
 275 280 285
 Ser Asp Phe Glu Val Gly Asp Ser Met Ala Ser Glu Glu Val Lys Gln
 290 295 300

ES 2 671 895 T3

Glu His Gln Lys Cys Leu Asp Lys Leu Leu Asn Asn Cys Leu Leu Ser
 305 310 315 320
 Cys Thr Met Gln Glu Leu Ile Gly Leu Tyr Val Thr Met Glu Glu Tyr
 325 330 335
 Phe Met Arg Glu Thr Val Asn Lys Ala Val Ala Leu Asp Thr Tyr Glu
 340 345 350
 Lys Gly Gln Leu Thr Ser Ser Met Val Asp Asp Val Phe Tyr Ile Val
 355 360 365
 Lys Lys Cys Ile Gly Arg Ala Leu Ser Ser Ser Ser Ile Asp Cys Leu
 370 375 380
 Cys Ala Met Ile Asn Leu Ala Thr Thr Glu Leu Glu Ser Asp Phe Arg
 385 390 395 400
 Asp Val Leu Cys Asn Lys Leu Arg Met Gly Phe Pro Ala Thr Thr Phe
 405 410 415
 Gln Asp Ile Gln Arg Gly Val Thr Ser Ala Val Asn Ile Met His Ser
 420 425 430
 Ser Leu Gln Gln Gly Lys Phe Asp Thr Lys Gly Ile Glu Ser Thr Asp
 435 440 445
 Glu Ala Lys Met Ser Phe Leu Val Thr Leu Asn Asn Val Glu Val Cys
 450 455 460
 Ser Glu Asn Ile Ser Thr Leu Lys Lys Thr Leu Glu Ser Asp Cys Thr
 465 470 475 480
 Lys Leu Phe Ser Gln Gly Ile Gly Gly Glu Gln Ala Gln Ala Lys Phe
 485 490 495
 Asp Ser Cys Leu Ser Asp Leu Ala Ala Val Ser Asn Lys Phe Arg Asp
 500 505 510
 Leu Leu Gln Glu Gly Leu Thr Glu Leu Asn Ser Thr Ala Ile Lys Pro
 515 520 525
 Gln Val Gln Pro Trp Ile Asn Ser Phe Phe Ser Val Ser His Asn Ile
 530 535 540
 Glu Glu Glu Glu Phe Asn Asp Tyr Glu Ala Asn Asp Pro Trp Val Gln
 545 550 555 560
 Gln Phe Ile Leu Asn Leu Glu Gln Gln Met Ala Glu Phe Lys Ala Ser
 565 570 575

ES 2 671 895 T3

Leu Ser Pro Val Ile Tyr Asp Ser Leu Thr Gly Leu Met Thr Ser Leu
 580 585 590
 Val Ala Val Glu Leu Glu Lys Val Val Leu Lys Ser Thr Phe Asn Arg
 595 600 605
 Leu Gly Gly Leu Gln Phe Asp Lys Glu Leu Arg Ser Leu Ile Ala Tyr
 610 615 620
 Leu Thr Thr Val Thr Thr Trp Thr Ile Arg Asp Lys Phe Ala Arg Leu
 625 630 635 640
 Ser Gln Met Ala Thr Ile Leu Asn Leu Glu Arg Val Thr Glu Ile Leu
 645 650 655
 Asp Tyr Trp Gly Pro Asn Ser Gly Pro Leu Thr Trp Arg Leu Thr Pro
 660 665 670
 Ala Glu Val Arg Gln Val Leu Ala Leu Arg Ile Asp Phe Arg Ser Glu
 675 680 685
 Asp Ile Lys Arg Leu Arg Leu
 690 695

<210> 68
 <211> 417
 <212> PRT
 <213> Humana

<400> 68

Met Glu Phe Val Lys Cys Leu Gly His Pro Glu Glu Phe Tyr Asn Leu
 1 5 10 15
 Val Arg Phe Arg Ile Gly Gly Lys Arg Lys Val Met Pro Lys Met Asp
 20 25 30
 Gln Asp Ser Leu Ser Ser Ser Leu Lys Thr Cys Tyr Lys Tyr Leu Asn
 35 40 45
 Gln Thr Ser Arg Ser Phe Ala Ala Val Ile Gln Ala Leu Asp Gly Glu
 50 55 60
 Met Arg Asn Ala Val Cys Ile Phe Tyr Leu Val Leu Arg Ala Leu Asp
 65 70 75 80
 Thr Leu Glu Asp Asp Met Thr Ile Ser Val Glu Lys Lys Val Pro Leu
 85 90 95
 Leu His Asn Phe His Ser Phe Leu Tyr Gln Pro Asp Trp Arg Phe Met
 100 105 110
 Glu Ser Lys Glu Lys Asp Arg Gln Val Leu Glu Asp Phe Pro Thr Ile

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115	120	125		
Ser Leu Glu Phe Arg Asn Leu Ala Glu Lys Tyr Gln Thr Val Ile Ala	130	135	140	
Asp Ile Cys Arg Arg Met Gly Ile Gly Met Ala Glu Phe Leu Asp Lys	145	150	155	160
His Val Thr Ser Glu Gln Glu Trp Asp Lys Tyr Cys His Tyr Val Ala	165	170	175	
Gly Leu Val Gly Ile Gly Leu Ser Arg Leu Phe Ser Ala Ser Glu Phe	180	185	190	
Glu Asp Pro Leu Val Gly Glu Asp Thr Glu Arg Ala Asn Ser Met Gly	195	200	205	
Leu Phe Leu Gln Lys Thr Asn Ile Ile Arg Asp Tyr Leu Glu Asp Gln	210	215	220	
Gln Gly Gly Arg Glu Phe Trp Pro Gln Glu Val Trp Ser Arg Tyr Val	225	230	235	240
Lys Lys Leu Gly Asp Phe Ala Lys Pro Glu Asn Ile Asp Leu Ala Val	245	250	255	
Gln Cys Leu Asn Glu Leu Ile Thr Asn Ala Leu His His Ile Pro Asp	260	265	270	
Val Ile Thr Tyr Leu Ser Arg Leu Arg Asn Gln Ser Val Phe Asn Phe	275	280	285	
Cys Ala Ile Pro Gln Val Met Ala Ile Ala Thr Leu Ala Ala Cys Tyr	290	295	300	
Asn Asn Gln Gln Val Phe Lys Gly Ala Val Lys Ile Arg Lys Gly Gln	305	310	315	320
Ala Val Thr Leu Met Met Asp Ala Thr Asn Met Pro Ala Val Lys Ala	325	330	335	
Ile Ile Tyr Gln Tyr Met Glu Glu Ile Tyr His Arg Ile Pro Asp Ser	340	345	350	
Asp Pro Ser Ser Ser Lys Thr Arg Gln Ile Ile Ser Thr Ile Arg Thr	355	360	365	
Gln Asn Leu Pro Asn Cys Gln Leu Ile Ser Arg Ser His Tyr Ser Pro	370	375	380	
Ile Tyr Leu Ser Phe Val Met Leu Leu Ala Ala Leu Ser Trp Gln Tyr				

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385 390 395 400

Leu Thr Thr Leu Ser Gln Val Thr Glu Asp Tyr Val Gln Thr Gly Glu
405 410 415

His

<210> 69
<211> 359
<212> PRT
<213> Humana

<400> 69

Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser Met Asn Gln Val Lys
1 5 10 15

Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys Leu Lys Leu Tyr Ala
20 25 30

Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn Met Pro Lys Pro Gly
35 40 45

Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp Ala Trp Asn Ala Leu
50 55 60

Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn Tyr Val Asp Leu Val
65 70 75 80

Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser Gln Val Glu Pro Gly
85 90 95

Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu Val Val Thr Ser Glu
100 105 110

Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro Lys Lys Lys Asn Ala
115 120 125

Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg Ala Leu Lys Ala Ala
130 135 140

Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr Gly Asn Gly Asp Tyr
145 150 155 160

Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr Asp Ile Pro Pro Gly
165 170 175

Gly Val Glu Glu Lys Ala Lys Asn Asn Ala Val Leu Leu Arg Glu Phe
180 185 190

Val Gly Cys Phe Ile Asp Phe Pro Lys Pro Leu Ile Ala Val Val Asn
195 200 205

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Gly Pro Ala Val Gly Ile Ser Val Thr Leu Leu Gly Leu Phe Asp Ala
 210 215 220
 Val Tyr Ala Ser Asp Arg Ala Thr Phe His Thr Pro Phe Ser His Leu
 225 230 235 240
 Gly Gln Ser Pro Glu Gly Cys Ser Ser Tyr Thr Phe Pro Lys Ile Met
 245 250 255
 Ser Pro Ala Lys Ala Thr Glu Met Leu Ile Phe Gly Lys Lys Leu Thr
 260 265 270
 Ala Gly Glu Ala Cys Ala Gln Gly Leu Val Thr Glu Val Phe Pro Asp
 275 280 285
 Ser Thr Phe Gln Lys Glu Val Trp Thr Arg Leu Lys Ala Phe Ala Lys
 290 295 300
 Leu Pro Pro Asn Ala Leu Arg Ile Ser Lys Glu Val Ile Arg Lys Arg
 305 310 315 320
 Glu Arg Glu Lys Leu His Ala Val Asn Ala Glu Glu Cys Asn Val Leu
 325 330 335
 Gln Gly Arg Trp Leu Ser Asp Glu Cys Thr Asn Ala Val Val Asn Phe
 340 345 350
 Leu Ser Arg Lys Ser Lys Leu
 355

<210> 70
 <211> 227
 <212> PRT
 <213> Humana

<400> 70

Met Tyr His Glu Ile Met Arg Ala Leu Lys Ala Ala Ser Lys Asp Asp
 1 5 10 15
 Ser Ile Ile Thr Val Leu Thr Gly Asn Gly Asp Tyr Tyr Ser Ser Gly
 20 25 30
 Asn Asp Leu Thr Asn Phe Thr Asp Ile Pro Pro Gly Gly Val Glu Glu
 35 40 45
 Lys Ala Lys Asn Asn Ala Val Leu Leu Arg Glu Phe Val Gly Cys Phe
 50 55 60
 Ile Asp Phe Pro Lys Pro Leu Ile Ala Val Val Asn Gly Pro Ala Val
 65 70 75 80

ES 2 671 895 T3

Gly Ile Ser Val Thr Leu Leu Gly Leu Phe Asp Ala Val Tyr Ala Ser
85 90 95

Asp Arg Ala Thr Phe His Thr Pro Phe Ser His Leu Gly Gln Ser Pro
100 105 110

Glu Gly Cys Ser Ser Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys
115 120 125

Ala Thr Glu Met Leu Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala
130 135 140

Cys Ala Gln Gly Leu Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln
145 150 155 160

Lys Glu Val Trp Thr Arg Leu Lys Ala Phe Ala Lys Leu Pro Pro Asn
165 170 175

Ala Leu Arg Ile Ser Lys Glu Val Ile Arg Lys Arg Glu Arg Glu Lys
180 185 190

Leu His Ala Val Asn Ala Glu Glu Cys Asn Val Leu Gln Gly Arg Trp
195 200 205

Leu Ser Asp Glu Cys Thr Asn Ala Val Val Asn Phe Leu Ser Arg Lys
210 215 220

Ser Lys Leu
225

<210> 71
<211> 394
<212> PRT
<213> Humana

<400> 71

Met Ala Met Ala Tyr Leu Ala Trp Arg Leu Ala Arg Arg Ser Cys Pro
1 5 10 15

Ser Ser Leu Gln Val Thr Ser Phe Pro Val Val Gln Leu His Met Asn
20 25 30

Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser Met Asn
35 40 45

Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys Leu Lys
50 55 60

Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn Met Pro
65 70 75 80

ES 2 671 895 T3

Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp Ala Trp
 85 90 95
 Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn Tyr Val
 100 105 110
 Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser Gln Val
 115 120 125
 Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu Val Val
 130 135 140
 Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro Lys Lys
 145 150 155 160
 Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg Ala Leu
 165 170 175
 Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr Gly Asn
 180 185 190
 Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr Asp Ile
 195 200 205
 Pro Pro Gly Gly Val Glu Glu Lys Ala Lys Asn Asn Ala Val Leu Leu
 210 215 220
 Arg Glu Phe Val Gly Cys Phe Ile Asp Phe Pro Lys Pro Leu Ile Ala
 225 230 235 240
 Val Val Asn Gly Pro Ala Val Gly Ile Ser Val Thr Leu Leu Gly Leu
 245 250 255
 Phe Asp Ala Val Tyr Ala Ser Asp Arg Ala Thr Phe His Thr Pro Phe
 260 265 270
 Ser His Leu Gly Gln Ser Pro Glu Gly Cys Ser Ser Tyr Thr Phe Pro
 275 280 285
 Lys Ile Met Ser Pro Ala Lys Ala Thr Glu Met Leu Ile Phe Gly Lys
 290 295 300
 Lys Leu Thr Ala Gly Glu Ala Cys Ala Gln Gly Leu Val Thr Glu Val
 305 310 315 320
 Phe Pro Asp Ser Thr Phe Gln Lys Glu Val Trp Thr Arg Leu Lys Ala
 325 330 335
 Phe Ala Lys Leu Pro Pro Asn Ala Leu Arg Ile Ser Lys Glu Val Ile
 340 345 350

ES 2 671 895 T3

Arg Lys Arg Glu Arg Glu Lys Leu His Ala Val Asn Ala Glu Glu Cys
355 360 365

Asn Val Leu Gln Gly Arg Trp Leu Ser Asp Glu Cys Thr Asn Ala Val
370 375 380

Val Asn Phe Leu Ser Arg Lys Ser Lys Leu
385 390

<210> 72
<211> 364
<212> PRT
<213> Humana

5

<400> 72

Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser
1 5 10 15

Met Asn Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys
20 25 30

Leu Lys Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn
35 40 45

Met Pro Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp
50 55 60

Ala Trp Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn
65 70 75 80

Tyr Val Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser
85 90 95

Gln Val Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu
100 105 110

Val Val Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro
115 120 125

Lys Lys Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg
130 135 140

Ala Leu Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr
145 150 155 160

Gly Asn Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr
165 170 175

Asp Ile Pro Pro Gly Gly Val Glu Glu Lys Ala Lys Asn Asn Ala Val
180 185 190

Leu Leu Arg Glu Phe Val Gly Cys Phe Ile Asp Phe Pro Lys Pro Leu

10

ES 2 671 895 T3

195	200	205
Ile Ala Val Val Asn Gly Pro Ala Val Gly Ile Ser Val Thr Leu Leu 210 215 220		
Gly Leu Phe Asp Ala Val Tyr Ala Ser Asp Arg Ala Thr Phe His Thr 225 230 235 240		
Pro Phe Ser His Leu Gly Gln Ser Pro Glu Gly Cys Ser Ser Tyr Thr 245 250 255		
Phe Pro Lys Ile Met Ser Pro Ala Lys Ala Thr Glu Met Leu Ile Phe 260 265 270		
Gly Lys Lys Leu Thr Ala Gly Glu Ala Cys Ala Gln Gly Leu Val Thr 275 280 285		
Glu Val Phe Pro Asp Ser Thr Phe Gln Lys Glu Val Trp Thr Arg Leu 290 295 300		
Lys Ala Phe Ala Lys Leu Pro Pro Asn Ala Leu Arg Ile Ser Lys Glu 305 310 315 320		
Val Ile Arg Lys Arg Glu Arg Glu Lys Leu His Ala Val Asn Ala Glu 325 330 335		
Glu Cys Asn Val Leu Gln Gly Arg Trp Leu Ser Asp Glu Cys Thr Asn 340 345 350		
Ala Val Val Asn Phe Leu Ser Arg Lys Ser Lys Leu 355 360		

<210> 73
 <211> 241
 <212> PRT
 <213> Humana

<400> 73

Met Phe Asn Arg Pro Lys Lys Lys Asn Ala Ile Asn Thr Glu Met Tyr 1 5 10 15
His Glu Ile Met Arg Ala Leu Lys Ala Ala Ser Lys Asp Asp Ser Ile 20 25 30
Ile Thr Val Leu Thr Gly Asn Gly Asp Tyr Tyr Ser Ser Gly Asn Asp 35 40 45
Leu Thr Asn Phe Thr Asp Ile Pro Pro Gly Gly Val Glu Glu Lys Ala 50 55 60
Lys Asn Asn Ala Val Leu Leu Arg Glu Phe Val Gly Cys Phe Ile Asp 65 70 75 80

ES 2 671 895 T3

Phe Pro Lys Pro Leu Ile Ala Val Val Asn Gly Pro Ala Val Gly Ile
85 90 95

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

Ala Thr Phe His Thr Pro Phe Ser His Leu Gly Gln Ser Pro Glu Gly
115 120 125

Cys Ser Ser Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys Ala Thr
130 135 140

Glu Met Leu Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala Cys Ala
145 150 155 160

Gln Gly Leu Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln Lys Glu
165 170 175

Val Trp Thr Arg Leu Lys Ala Phe Ala Lys Leu Pro Pro Asn Ala Leu
180 185 190

Arg Ile Ser Lys Glu Val Ile Arg Lys Arg Glu Arg Glu Lys Leu His
195 200 205

Ala Val Asn Ala Glu Glu Cys Asn Val Leu Gln Gly Arg Trp Leu Ser
210 215 220

Asp Glu Cys Thr Asn Ala Val Val Asn Phe Leu Ser Arg Lys Ser Lys
225 230 235 240

Leu

<210> 74

<211> 1225

<212> PRT

<213> Humana

<400> 74

Met Phe Ala Arg Lys Pro Pro Gly Ala Ala Pro Leu Gly Ala Met Pro
1 5 10 15

Val Pro Asp Gln Pro Ser Ser Ala Ser Glu Lys Thr Ser Ser Leu Ser
20 25 30

Pro Gly Leu Asn Thr Ser Asn Gly Asp Gly Ser Glu Thr Glu Thr Thr
35 40 45

Ser Ala Ile Leu Ala Ser Val Lys Glu Gln Glu Leu Gln Phe Glu Arg
50 55 60

ES 2 671 895 T3

Leu Thr Arg Glu Leu Glu Ala Glu Arg Gln Ile Val Ala Ser Gln Leu
 65 70 75 80
 Glu Arg Cys Lys Leu Gly Ser Glu Thr Gly Ser Met Ser Ser Met Ser
 85 90 95
 Ser Ala Glu Glu Gln Phe Gln Trp Gln Ser Gln Asp Gly Gln Lys Asp
 100 105 110
 Ile Glu Asp Glu Leu Thr Thr Gly Leu Glu Leu Val Asp Ser Cys Ile
 115 120 125
 Arg Ser Leu Gln Glu Ser Gly Ile Leu Asp Pro Gln Asp Tyr Ser Thr
 130 135 140
 Gly Glu Arg Pro Ser Leu Leu Ser Gln Ser Ala Leu Gln Leu Asn Ser
 145 150 155 160
 Lys Pro Glu Gly Ser Phe Gln Tyr Pro Ala Ser Tyr His Ser Asn Gln
 165 170 175
 Thr Leu Ala Leu Gly Glu Thr Thr Pro Ser Gln Leu Pro Ala Arg Gly
 180 185 190
 Thr Gln Ala Arg Ala Thr Gly Gln Ser Phe Ser Gln Gly Thr Thr Ser
 195 200 205
 Arg Ala Gly His Leu Ala Gly Pro Glu Pro Ala Pro Pro Pro Pro Pro
 210 215 220
 Pro Pro Arg Glu Pro Phe Ala Pro Ser Leu Gly Ser Ala Phe His Leu
 225 230 235 240
 Pro Asp Ala Pro Pro Ala Ala Ala Ala Ala Ala Leu Tyr Tyr Ser Ser
 245 250 255
 Ser Thr Leu Pro Ala Pro Pro Arg Gly Gly Ser Pro Leu Ala Ala Pro
 260 265 270
 Gln Gly Gly Ser Pro Thr Lys Leu Gln Arg Gly Gly Ser Ala Pro Glu
 275 280 285
 Gly Ala Thr Tyr Ala Ala Pro Arg Gly Ser Ser Pro Lys Gln Ser Pro
 290 295 300
 Ser Arg Leu Ala Lys Ser Tyr Ser Thr Ser Ser Pro Ile Asn Ile Val
 305 310 315 320
 Val Ser Ser Ala Gly Leu Ser Pro Ile Arg Val Thr Ser Pro Pro Thr
 325 330 335

val Gln Ser Thr Ile Ser Ser Ser Pro Ile His Gln Leu Ser Ser Thr
 340 345 350
 Ile Gly Thr Tyr Ala Thr Leu Ser Pro Thr Lys Arg Leu Val His Ala
 355 360 365
 Ser Glu Gln Tyr Ser Lys His Ser Gln Glu Leu Tyr Ala Thr Ala Thr
 370 375 380
 Leu Gln Arg Pro Gly Ser Leu Ala Ala Gly Ser Arg Ala Ser Tyr Ser
 385 390 395 400
 Ser Gln His Gly His Leu Gly Pro Glu Leu Arg Ala Leu Gln Ser Pro
 405 410 415
 Glu His His Ile Asp Pro Ile Tyr Glu Asp Arg Val Tyr Gln Lys Pro
 420 425 430
 Pro Met Arg Ser Leu Ser Gln Ser Gln Gly Asp Pro Leu Pro Pro Ala
 435 440 445
 His Thr Gly Thr Tyr Arg Thr Ser Thr Ala Pro Ser Ser Pro Gly Val
 450 455 460
 Asp Ser Val Pro Leu Gln Arg Thr Gly Ser Gln His Gly Pro Gln Asn
 465 470 475 480
 Ala Ala Ala Ala Thr Phe Gln Arg Ala Ser Tyr Ala Ala Gly Pro Ala
 485 490 495
 Ser Asn Tyr Ala Asp Pro Tyr Arg Gln Leu Gln Tyr Cys Pro Ser Val
 500 505 510
 Glu Ser Pro Tyr Ser Lys Ser Gly Pro Ala Leu Pro Pro Glu Gly Thr
 515 520 525
 Leu Ala Arg Ser Pro Ser Ile Asp Ser Ile Gln Lys Asp Pro Arg Glu
 530 535 540
 Phe Gly Trp Arg Asp Pro Glu Leu Pro Glu Val Ile Gln Met Leu Gln
 545 550 555 560
 His Gln Phe Pro Ser Val Gln Ser Asn Ala Ala Ala Tyr Leu Gln His
 565 570 575
 Leu Cys Phe Gly Asp Asn Lys Ile Lys Ala Glu Ile Arg Arg Gln Gly
 580 585 590
 Gly Ile Gln Leu Leu Val Asp Leu Leu Asp His Arg Met Thr Glu Val
 595 600 605

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His Arg Ser Ala Cys Gly Ala Leu Arg Asn Leu Val Tyr Gly Lys Ala
 610 615 620
 Asn Asp Asp Asn Lys Ile Ala Leu Lys Asn Cys Gly Gly Ile Pro Ala
 625 630 635
 Leu Val Arg Leu Leu Arg Lys Thr Thr Asp Leu Glu Ile Arg Glu Leu
 645 650 655
 Val Thr Gly Val Leu Trp Asn Leu Ser Ser Cys Asp Ala Leu Lys Met
 660 665 670
 Pro Ile Ile Gln Asp Ala Leu Ala Val Leu Thr Asn Ala Val Ile Ile
 675 680 685
 Pro His Ser Gly Trp Glu Asn Ser Pro Leu Gln Asp Asp Arg Lys Ile
 690 695 700
 Gln Leu His Ser Ser Gln Val Leu Arg Asn Ala Thr Gly Cys Leu Arg
 705 710 715 720
 Asn Val Ser Ser Ala Gly Glu Glu Ala Arg Arg Arg Met Arg Glu Cys
 725 730 735
 Asp Gly Leu Thr Asp Ala Leu Leu Tyr Val Ile Gln Ser Ala Leu Gly
 740 745 750
 Ser Ser Glu Ile Asp Ser Lys Thr Val Glu Asn Cys Val Cys Ile Leu
 755 760 765
 Arg Asn Leu Ser Tyr Arg Leu Ala Ala Glu Thr Ser Gln Gly Gln His
 770 775 780
 Met Gly Thr Asp Glu Leu Asp Gly Leu Leu Cys Gly Glu Ala Asn Gly
 785 790 795 800
 Lys Asp Ala Glu Ser Ser Gly Cys Trp Gly Lys Lys Lys Lys Lys Lys
 805 810 815
 Lys Ser Gln Asp Gln Trp Asp Gly Val Gly Pro Leu Pro Asp Cys Ala
 820 825 830
 Glu Pro Pro Lys Gly Ile Gln Met Leu Trp His Pro Ser Ile Val Lys
 835 840 845
 Pro Tyr Leu Thr Leu Leu Ser Glu Cys Ser Asn Pro Asp Thr Leu Glu
 850 855 860
 Gly Ala Ala Gly Ala Leu Gln Asn Leu Ala Ala Gly Ser Trp Lys Trp
 865 870 875 880

ES 2 671 895 T3

Ser Val Tyr Ile Arg Ala Ala Val Arg Lys Glu Lys Gly Leu Pro Ile
 885 890 895
 Leu Val Glu Leu Leu Arg Ile Asp Asn Asp Arg Val Val Cys Ala Val
 900 905 910
 Ala Thr Ala Leu Arg Asn Met Ala Leu Asp Val Arg Asn Lys Glu Leu
 915 920 925
 Ile Gly Lys Tyr Ala Met Arg Asp Leu Val His Arg Leu Pro Gly Gly
 930 935 940
 Asn Asn Ser Asn Asn Thr Ala Ser Lys Ala Met Ser Asp Asp Thr Val
 945 950 955 960
 Thr Ala Val Cys Cys Thr Leu His Glu Val Ile Thr Lys Asn Met Glu
 965 970 975
 Asn Ala Lys Ala Leu Arg Asp Ala Gly Gly Ile Glu Lys Leu Val Gly
 980 985 990
 Ile Ser Lys Ser Lys Gly Asp Lys His Ser Pro Lys Val Val Lys A
 995 1000 1005
 Ala Ser Gln Val Leu Asn Ser Met Trp Gln Tyr Arg Asp Leu Arg
 1010 1015 1020
 Ser Leu Tyr Lys Lys Asp Gly Trp Ser Gln Tyr His Phe Val Ala
 1025 1030 1035
 Ser Ser Ser Thr Ile Glu Arg Asp Arg Gln Arg Pro Tyr Ser Ser
 1040 1045 1050
 Ser Arg Thr Pro Ser Ile Ser Pro Val Arg Val Ser Pro Asn Asn
 1055 1060 1065
 Arg Ser Ala Ser Ala Pro Ala Ser Pro Arg Glu Met Ile Ser Leu
 1070 1075 1080
 Lys Glu Arg Lys Thr Asp Tyr Glu Cys Thr Gly Ser Asn Ala Thr
 1085 1090 1095
 Tyr His Gly Ala Lys Gly Glu His Thr Ser Arg Lys Asp Ala Met
 1100 1105 1110
 Thr Ala Gln Asn Thr Gly Ile Ser Thr Leu Tyr Arg Asn Ser Tyr
 1115 1120 1125
 Gly Ala Pro Ala Glu Asp Ile Lys His Asn Gln Val Ser Ala Gln
 1130 1135 1140

ES 2 671 895 T3

Pro Val Pro Gln Glu Pro Ser Arg Lys Asp Tyr Glu Thr Tyr Gln
 1145 1150 1155
 Pro Phe Gln Asn Ser Thr Arg Asn Tyr Asp Glu Ser Phe Phe Glu
 1160 1165 1170
 Asp Gln Val His His Arg Pro Pro Ala Ser Glu Tyr Thr Met His
 1175 1180 1185
 Leu Gly Leu Lys Ser Thr Gly Asn Tyr Val Asp Phe Tyr Ser Ala
 1190 1195 1200
 Ala Arg Pro Tyr Ser Glu Leu Asn Tyr Glu Thr Ser His Tyr Pro
 1205 1210 1215
 Ala Ser Pro Asp Ser Trp Val
 1220 1225

<210> 75
 <211> 1167
 <212> PRT
 <213> Humana

<400> 75

Met Phe Ala Arg Lys Pro Pro Gly Ala Ala Pro Leu Gly Ala Met Pro
 1 5 10 15
 Val Pro Asp Gln Pro Ser Ser Ala Ser Glu Lys Thr Ser Ser Leu Ser
 20 25 30
 Pro Gly Leu Asn Thr Ser Asn Gly Asp Gly Ser Glu Thr Glu Thr Thr
 35 40 45
 Ser Ala Ile Leu Ala Ser Val Lys Glu Gln Glu Leu Gln Phe Glu Arg
 50 55 60
 Leu Thr Arg Glu Leu Glu Ala Glu Arg Gln Ile Val Ala Ser Gln Leu
 65 70 75 80
 Glu Arg Cys Lys Leu Gly Ser Glu Thr Gly Ser Met Ser Ser Met Ser
 85 90 95
 Ser Ala Glu Glu Gln Phe Gln Trp Gln Ser Gln Asp Gly Gln Lys Asp
 100 105 110
 Ile Glu Asp Glu Leu Thr Thr Gly Leu Glu Leu Val Asp Ser Cys Ile
 115 120 125
 Arg Ser Leu Gln Glu Ser Gly Ile Leu Asp Pro Gln Asp Tyr Ser Thr
 130 135 140

ES 2 671 895 T3

Gly Glu Arg Pro Ser Leu Leu Ser Gln Ser Ala Leu Gln Leu Asn Ser
 145 150 155 160
 Lys Pro Glu Gly Ser Phe Gln Tyr Pro Ala Ser Tyr His Ser Asn Gln
 165 170 175
 Thr Leu Ala Leu Gly Glu Thr Thr Pro Ser Gln Leu Pro Ala Arg Gly
 180 185 190
 Thr Gln Ala Arg Ala Thr Gly Gln Ser Phe Ser Gln Gly Thr Thr Ser
 195 200 205
 Arg Ala Gly His Leu Ala Gly Pro Glu Pro Ala Pro Pro Pro Pro Pro
 210 215 220
 Pro Pro Arg Glu Pro Phe Ala Pro Ser Leu Gly Ser Ala Phe His Leu
 225 230 235 240
 Pro Asp Ala Pro Pro Ala Ala Ala Ala Ala Ala Leu Tyr Tyr Ser Ser
 245 250 255
 Ser Thr Leu Pro Ala Pro Pro Arg Gly Gly Ser Pro Leu Ala Ala Pro
 260 265 270
 Gln Gly Gly Ser Pro Thr Lys Leu Gln Arg Gly Gly Ser Ala Pro Glu
 275 280 285
 Gly Ala Thr Tyr Ala Ala Pro Arg Gly Ser Ser Pro Lys Gln Ser Pro
 290 295 300
 Ser Arg Leu Ala Lys Ser Tyr Ser Thr Ser Ser Pro Ile Asn Ile Val
 305 310 315 320
 Val Ser Ser Ala Gly Leu Ser Pro Ile Arg Val Thr Ser Pro Pro Thr
 325 330 335
 Val Gln Ser Thr Ile Ser Ser Ser Pro Ile His Gln Leu Ser Ser Thr
 340 345 350
 Ile Gly Thr Tyr Ala Thr Leu Ser Pro Thr Lys Arg Leu Val His Ala
 355 360 365
 Ser Glu Gln Tyr Ser Lys His Ser Gln Glu Leu Tyr Ala Thr Ala Thr
 370 375 380
 Leu Gln Arg Pro Gly Ser Leu Ala Ala Gly Ser Arg Ala Ser Tyr Ser
 385 390 395 400
 Ser Gln His Gly His Leu Gly Pro Glu Leu Arg Ala Leu Gln Ser Pro
 405 410 415

ES 2 671 895 T3

Glu His His Ile Asp Pro Ile Tyr Glu Asp Arg Val Tyr Gln Lys Pro
 420 425 430
 Pro Met Arg Ser Leu Ser Gln Ser Gln Gly Asp Pro Leu Pro Pro Ala
 435 440 445
 His Thr Gly Thr Tyr Arg Thr Ser Thr Ala Pro Ser Ser Pro Gly Val
 450 455 460
 Asp Ser Val Pro Leu Gln Arg Thr Gly Ser Gln His Gly Pro Gln Asn
 465 470 475 480
 Ala Ala Ala Ala Thr Phe Gln Arg Ala Ser Tyr Ala Ala Gly Pro Ala
 485 490 495
 Ser Asn Tyr Ala Asp Pro Tyr Arg Gln Leu Gln Tyr Cys Pro Ser Val
 500 505 510
 Glu Ser Pro Tyr Ser Lys Ser Gly Pro Ala Leu Pro Pro Glu Gly Thr
 515 520 525
 Leu Ala Arg Ser Pro Ser Ile Asp Ser Ile Gln Lys Asp Pro Arg Glu
 530 535 540
 Phe Gly Trp Arg Asp Pro Glu Leu Pro Glu Val Ile Gln Met Leu Gln
 545 550 555 560
 His Gln Phe Pro Ser Val Gln Ser Asn Ala Ala Ala Tyr Leu Gln His
 565 570 575
 Leu Cys Phe Gly Asp Asn Lys Ile Lys Ala Glu Ile Arg Arg Gln Gly
 580 585 590
 Gly Ile Gln Leu Leu Val Asp Leu Leu Asp His Arg Met Thr Glu Val
 595 600 605
 His Arg Ser Ala Cys Gly Ala Leu Arg Asn Leu Val Tyr Gly Lys Ala
 610 615 620
 Asn Asp Asp Asn Lys Ile Ala Leu Lys Asn Cys Gly Gly Ile Pro Ala
 625 630 635 640
 Leu Val Arg Leu Leu Arg Lys Thr Thr Asp Leu Glu Ile Arg Glu Leu
 645 650 655
 Val Thr Gly Val Leu Trp Asn Leu Ser Ser Cys Asp Ala Leu Lys Met
 660 665 670
 Pro Ile Ile Gln Asp Ala Leu Ala Val Leu Thr Asn Ala Val Ile Ile
 675 680 685

ES 2 671 895 T3

Pro His Ser Gly Trp Glu Asn Ser Pro Leu Gln Asp Asp Arg Lys Ile
 690 695 700
 Gln Leu His Ser Ser Gln Val Leu Arg Asn Ala Thr Gly Cys Leu Arg
 705 710 715 720
 Asn Val Ser Ser Ala Gly Glu Glu Ala Arg Arg Arg Met Arg Glu Cys
 725 730 735
 Asp Gly Leu Thr Asp Ala Leu Leu Tyr Val Ile Gln Ser Ala Leu Gly
 740 745 750
 Ser Ser Glu Ile Asp Ser Lys Thr Val Glu Asn Cys Val Cys Ile Leu
 755 760 765
 Arg Asn Leu Ser Tyr Arg Leu Ala Ala Glu Thr Ser Gln Gly Gln His
 770 775 780
 Met Gly Thr Asp Glu Leu Asp Gly Leu Leu Cys Gly Glu Ala Asn Gly
 785 790 795 800
 Lys Asp Ala Glu Ser Ser Gly Cys Trp Gly Lys Lys Lys Lys Lys Lys
 805 810 815
 Lys Ser Gln Asp Gln Trp Ser Val Tyr Ile Arg Ala Ala Val Arg Lys
 820 825 830
 Glu Lys Gly Leu Pro Ile Leu Val Glu Leu Leu Arg Ile Asp Asn Asp
 835 840 845
 Arg Val Val Cys Ala Val Ala Thr Ala Leu Arg Asn Met Ala Leu Asp
 850 855 860
 Val Arg Asn Lys Glu Leu Ile Gly Lys Tyr Ala Met Arg Asp Leu Val
 865 870 875 880
 His Arg Leu Pro Gly Gly Asn Asn Ser Asn Asn Thr Ala Ser Lys Ala
 885 890 895
 Met Ser Asp Asp Thr Val Thr Ala Val Cys Cys Thr Leu His Glu Val
 900 905 910
 Ile Thr Lys Asn Met Glu Asn Ala Lys Ala Leu Arg Asp Ala Gly Gly
 915 920 925
 Ile Glu Lys Leu Val Gly Ile Ser Lys Ser Lys Gly Asp Lys His Ser
 930 935 940
 Pro Lys Val Val Lys Ala Ala Ser Gln Val Leu Asn Ser Met Trp Gln
 945 950 955 960

ES 2 671 895 T3

Tyr Arg Asp Leu Arg Ser Leu Tyr Lys Lys Asp Gly Trp Ser Gln Tyr
 965 970 975
 His Phe Val Ala Ser Ser Ser Thr Ile Glu Arg Asp Arg Gln Arg Pro
 980 985 990
 Tyr Ser Ser Ser Arg Thr Pro Ser Ile Ser Pro Val Arg Val Ser Pro
 995 1000 1005
 Asn Asn Arg Ser Ala Ser Ala Pro Ala Ser Pro Arg Glu Met Ile
 1010 1015 1020
 Ser Leu Lys Glu Arg Lys Thr Asp Tyr Glu Cys Thr Gly Ser Asn
 1025 1030 1035
 Ala Thr Tyr His Gly Ala Lys Gly Glu His Thr Ser Arg Lys Asp
 1040 1045 1050
 Ala Met Thr Ala Gln Asn Thr Gly Ile Ser Thr Leu Tyr Arg Asn
 1055 1060 1065
 Ser Tyr Gly Ala Pro Ala Glu Asp Ile Lys His Asn Gln Val Ser
 1070 1075 1080
 Ala Gln Pro Val Pro Gln Glu Pro Ser Arg Lys Asp Tyr Glu Thr
 1085 1090 1095
 Tyr Gln Pro Phe Gln Asn Ser Thr Arg Asn Tyr Asp Glu Ser Phe
 1100 1105 1110
 Phe Glu Asp Gln Val His His Arg Pro Pro Ala Ser Glu Tyr Thr
 1115 1120 1125
 Met His Leu Gly Leu Lys Ser Thr Gly Asn Tyr Val Asp Phe Tyr
 1130 1135 1140
 Ser Ala Ala Arg Pro Tyr Ser Glu Leu Asn Tyr Glu Thr Ser His
 1145 1150 1155
 Tyr Pro Ala Ser Pro Asp Ser Trp Val
 1160 1165

<210> 76
 <211> 266
 <212> PRT
 <213> Humana
 <400> 76

Met Gln Gly Ser Thr Arg Arg Met Gly Val Met Thr Asp Val His Arg
 1 5 10 15

Arg Phe Leu Gln Leu Leu Met Thr His Gly Val Leu Glu Glu Trp Asp

ES 2 671 895 T3

20	25	30	
Val Lys Arg Leu Gln Thr His Cys Tyr Lys Val His Asp Arg Asn Ala	35	40	45
Thr Val Asp Lys Leu Glu Asp Phe Ile Asn Asn Ile Asn Ser Val Leu	50	55	60
Glu Ser Leu Tyr Ile Glu Ile Lys Arg Gly Val Thr Glu Asp Asp Gly	65	70	75
Arg Pro Ile Tyr Ala Leu Val Asn Leu Ala Thr Thr Ser Ile Ser Lys	85	90	95
Met Ala Thr Asp Phe Ala Glu Asn Glu Leu Asp Leu Phe Arg Lys Ala	100	105	110
Leu Glu Leu Ile Ile Asp Ser Glu Thr Gly Phe Ala Ser Ser Thr Asn	115	120	125
Ile Leu Asn Leu Val Asp Gln Leu Lys Gly Lys Lys Met Arg Lys Lys	130	135	140
Glu Ala Glu Gln Val Leu Gln Lys Phe Val Gln Asn Lys Trp Leu Ile	145	150	155
Glu Lys Glu Gly Glu Phe Thr Leu His Gly Arg Ala Ile Leu Glu Met	165	170	175
Glu Gln Tyr Ile Arg Glu Thr Tyr Pro Asp Ala Val Lys Ile Cys Asn	180	185	190
Ile Cys His Ser Leu Leu Ile Gln Gly Gln Ser Cys Glu Thr Cys Gly	195	200	205
Ile Arg Met His Leu Pro Cys Val Ala Lys Tyr Phe Gln Ser Asn Ala	210	215	220
Glu Pro Arg Cys Pro His Cys Asn Asp Tyr Trp Pro His Glu Ile Pro	225	230	235
Lys Val Phe Asp Pro Glu Lys Glu Arg Glu Ser Gly Val Leu Lys Ser	245	250	255
Asn Lys Lys Ser Leu Arg Ser Arg Gln His	260	265	

<210> 77
 <211> 145
 <212> PRT
 <213> Humana
 <400> 77

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Pro Tyr Pro Leu Ala Arg Trp Asp Ala Leu Gly Leu Pro Val Arg Ser
1 5 10 15
His Met Gln Gly Ser Thr Arg Arg Met Gly Val Met Thr Asp Val His
20 25 30
Arg Arg Phe Leu Gln Leu Leu Met Thr His Gly Val Leu Glu Glu Trp
35 40 45
Asp Val Lys Arg Leu Gln Thr His Cys Tyr Lys Val His Asp Arg Asn
50 55 60
Ala Thr Val Asp Lys Leu Glu Asp Phe Ile Asn Asn Ile Asn Ser Val
65 70 75 80
Leu Glu Ser Leu Tyr Ile Glu Ile Lys Arg Gly Val Thr Glu Asp Asp
85 90 95
Gly Arg Pro Ile Tyr Ala Leu Val Asn Leu Ala Thr Thr Ser Ile Ser
100 105 110
Lys Met Ala Thr Asp Phe Ala Glu Asn Glu Leu Asp Leu Phe Arg Lys
115 120 125
Ala Leu Glu Leu Ile Ile Asp Ser Glu Thr Leu Arg Leu Pro Gln Thr
130 135 140
Tyr
145

<210> 78
<211> 179
<212> PRT
<213> Humana

<400> 78

Val His Leu Ala Thr Val Ser Ala Ser Ala Ala Trp Asp Ala Leu Gly
1 5 10 15
Leu Pro Val Arg Ser His Met Gln Gly Ser Thr Arg Arg Met Gly Val
20 25 30
Met Thr Asp Val His Arg Arg Phe Leu Gln Leu Leu Met Thr His Gly
35 40 45
Val Leu Glu Glu Trp Asp Val Lys Arg Leu Gln Thr His Cys Tyr Lys
50 55 60
Val His Asp Arg Asn Ala Thr Val Asp Lys Leu Glu Asp Phe Ile Asn
65 70 75 80

Asn Ile Asn Ser Val Leu Glu Ser Leu Tyr Ile Glu Ile Lys Arg Gly
85 90 95

Val Thr Glu Asp Asp Gly Arg Pro Ile Tyr Ala Leu Val Asn Leu Ala
100 105 110

Thr Thr Ser Ile Ser Lys Met Ala Thr Asp Phe Ala Glu Asn Glu Leu
115 120 125

Asp Leu Phe Arg Lys Ala Leu Glu Leu Ile Ile Asp Ser Glu Thr Gly
130 135 140

Phe Ala Ser Ser Thr Asn Ile Leu Asn Leu Val Asp Gln Leu Lys Gly
145 150 155 160

Lys Lys Met Arg Lys Lys Glu Ala Arg Cys Cys Arg Ser Leu Phe Lys
165 170 175

Thr Ser Gly

<210> 79
<211> B92
<212> PRT
<213> Humana

<400> 79

Met Glu Trp Trp Ala Ser Ser Pro Leu Arg Leu Trp Leu Leu Phe
1 5 10 15

Leu Leu Pro Ser Ala Gln Gly Arg Gln Lys Glu Ser Gly Ser Lys Trp
20 25 30

Lys Val Phe Ile Asp Gln Ile Asn Arg Ser Leu Glu Asn Tyr Glu Pro
35 40 45

Cys Ser Ser Gln Asn Cys Ser Cys Tyr His Gly Val Ile Glu Glu Asp
50 55 60

Leu Thr Pro Phe Arg Gly Gly Ile Ser Arg Lys Met Met Ala Glu Val
65 70 75 80

Val Arg Arg Lys Leu Gly Thr His Tyr Gln Ile Thr Lys Asn Arg Leu
85 90 95

Tyr Arg Glu Asn Asp Cys Met Phe Pro Ser Arg Cys Ser Gly Val Glu
100 105 110

His Phe Ile Leu Glu Val Ile Gly Arg Leu Pro Asp Met Glu Met Val
115 120 125

ES 2 671 895 T3

Ile Asn Val Arg Asp Tyr Pro Gln Val Pro Lys Trp Met Glu Pro Ala
 130 135 140
 Ile Pro Val Phe Ser Phe Ser Lys Thr Ser Glu Tyr His Asp Ile Met
 145 150 155 160
 Tyr Pro Ala Trp Thr Phe Trp Glu Gly Gly Pro Ala Val Trp Pro Ile
 165 170 175
 Tyr Pro Thr Gly Leu Gly Arg Trp Asp Leu Phe Arg Glu Asp Leu Val
 180 185 190
 Arg Ser Ala Ala Gln Trp Pro Trp Lys Lys Lys Asn Ser Thr Ala Tyr
 195 200 205
 Phe Arg Gly Ser Arg Thr Ser Pro Glu Arg Asp Pro Leu Ile Leu Leu
 210 215 220
 Ser Arg Lys Asn Pro Lys Leu Val Asp Ala Glu Tyr Thr Lys Asn Gln
 225 230 235 240
 Ala Trp Lys Ser Met Lys Asp Thr Leu Gly Lys Pro Ala Ala Lys Asp
 245 250 255
 Val His Leu Val Asp His Cys Lys Tyr Lys Tyr Leu Phe Asn Phe Arg
 260 265 270
 Gly Val Ala Ala Ser Phe Arg Phe Lys His Leu Phe Leu Cys Gly Ser
 275 280 285
 Leu Val Phe His Val Gly Asp Glu Trp Leu Glu Phe Phe Tyr Pro Gln
 290 295 300
 Leu Lys Pro Trp Val His Tyr Ile Pro Val Lys Thr Asp Leu Ser Asn
 305 310 315 320
 Val Gln Glu Leu Leu Gln Phe Val Lys Ala Asn Asp Asp Val Ala Gln
 325 330 335
 Glu Ile Ala Glu Arg Gly Ser Gln Phe Ile Arg Asn His Leu Gln Met
 340 345 350
 Asp Asp Ile Thr Cys Tyr Trp Glu Asn Leu Leu Ser Glu Tyr Ser Lys
 355 360 365
 Phe Leu Ser Tyr Asn Val Thr Arg Arg Lys Gly Tyr Asp Gln Ile Ile
 370 375 380
 Pro Lys Met Leu Lys Thr Glu Leu
 385 390

<210> 80

ES 2 671 895 T3

<211> 411
<212> PRT
<213> Humana

5 <400> 80

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Met Arg Arg Arg Arg Ala Gly Gly Arg Thr Met Val Glu Arg Ala Ser
 1      5      10
Lys Phe Val Leu Val Val Ala Gly Ser Val Cys Phe Met Leu Ile Leu
      20      25      30
Tyr Gln Tyr Ala Gly Pro Gly Leu Ser Leu Gly Ala Pro Gly Gly Arg
      35      40      45
Ala Pro Pro Asp Asp Leu Asp Leu Phe Pro Thr Pro Asp Pro His Tyr
      50      55      60
Glu Lys Lys Tyr Tyr Phe Pro Val Arg Glu Leu Glu Arg Ser Leu Arg
65      70      75
Phe Asp Met Lys Gly Asp Asp Val Ile Val Phe Leu His Ile Gln Lys
      85      90      95
Thr Gly Gly Thr Thr Phe Gly Arg His Leu Val Gln Asn Val Arg Leu
      100      105      110
Glu Val Pro Cys Asp Cys Arg Pro Gly Gln Lys Lys Cys Thr Cys Tyr
      115      120      125
Arg Pro Asn Arg Arg Glu Thr Trp Leu Phe Ser Arg Phe Ser Thr Gly
      130      135      140
Trp Ser Cys Gly Leu His Ala Asp Trp Thr Glu Leu Thr Asn Cys Val
145      150      155      160
Pro Gly Val Leu Asp Arg Arg Asp Ser Ala Ala Leu Arg Thr Pro Arg
      165      170      175
Lys Phe Tyr Tyr Ile Thr Leu Leu Arg Asp Pro Val Ser Arg Tyr Leu
      180      185      190
Ser Glu Trp Arg His Val Gln Arg Gly Ala Thr Trp Lys Thr Ser Leu
      195      200      205
His Met Cys Asp Gly Arg Thr Pro Thr Pro Glu Glu Leu Pro Pro Cys
      210      215      220
Tyr Glu Gly Thr Asp Trp Ser Gly Cys Thr Leu Gln Glu Phe Met Asp
225      230      235      240
Cys Pro Tyr Asn Leu Ala Asn Asn Arg Gln Val Arg Met Leu Ala Asp

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245 250 255
 Leu Ser Leu Val Gly Cys Tyr Asn Leu Ser Phe Ile Pro Glu Gly Lys
 260 265 270
 Arg Ala Gln Leu Leu Leu Glu Ser Ala Lys Lys Asn Leu Arg Gly Met
 275 280 285
 Ala Phe Phe Gly Leu Thr Glu Phe Gln Arg Lys Thr Gln Tyr Leu Phe
 290 295 300
 Glu Arg Thr Phe Asn Leu Lys Phe Ile Arg Pro Phe Met Gln Tyr Asn
 305 310 315 320
 Ser Thr Arg Ala Gly Gly Val Glu Val Asp Glu Asp Thr Ile Arg Arg
 325 330 335
 Ile Glu Glu Leu Asn Asp Leu Asp Met Gln Leu Tyr Asp Tyr Ala Lys
 340 345 350
 Asp Leu Phe Gln Gln Arg Tyr Gln Tyr Lys Arg Gln Leu Glu Arg Arg
 355 360 365
 Glu Gln Arg Leu Arg Ser Arg Glu Glu Arg Leu Leu His Arg Ala Lys
 370 375 380
 Glu Ala Leu Pro Arg Glu Asp Ala Asp Glu Pro Gly Arg Val Pro Thr
 385 390 395 400
 Glu Asp Tyr Met Ser His Ile Ile Glu Lys Trp
 405 410

<210> 81
 <211> 464
 <212> PRT
 <213> Humana

<400> 81

Met Thr Ser Cys Arg Cys Ser Val Thr Ser Arg Ser Leu Trp Pro Ala
 1 5 10 15
 Leu Ala Pro Arg Arg Cys Gln His Thr Ser Pro Ala Ser Ala Gln Cys
 20 25 30
 Lys Gln Asp Lys Ala Cys Arg Phe Leu Ala Ala Gln Lys Gly Ala Tyr
 35 40 45
 Pro Ile Ile Phe Thr Ala Trp Lys Leu Ala Thr Ala Gly Asp Gln Gly
 50 55 60
 Leu Leu Leu Gln Ser Leu Asn Ala Leu Ser Val Leu Thr Asp Gly Gln
 65 70 75 80

ES 2 671 895 T3

Pro Asp Leu Leu Asp Ala Gln Gly Leu Gln Leu Leu Val Ala Thr Leu
 85 90 95
 Thr Gln Asn Ala Asp Glu Ala Asp Leu Thr Cys Ser Gly Ile Arg Cys
 100 105 110
 Val Arg His Ala Cys Leu Lys His Glu Gln Asn Arg Gln Asp Leu Val
 115 120 125
 Lys Ala Gly Val Leu Pro Leu Leu Thr Gly Ala Ile Thr His His Gly
 130 135 140
 His His Thr Asp Val Val Arg Glu Ala Cys Trp Ala Leu Arg Val Met
 145 150 155 160
 Thr Phe Asp Asp Asp Ile Arg Val Pro Phe Gly His Ala His Asn His
 165 170 175
 Ala Lys Met Ile Val Gln Glu Asn Lys Gly Leu Lys Val Leu Ile Glu
 180 185 190
 Ala Thr Lys Ala Phe Leu Asp Asn Pro Gly Ile Leu Ser Glu Leu Cys
 195 200 205
 Gly Thr Leu Ser Arg Leu Ala Ile Arg Asn Glu Phe Cys Gln Glu Val
 210 215 220
 Val Asp Leu Gly Gly Leu Ser Ile Leu Val Ser Leu Leu Ala Asp Cys
 225 230 235 240
 Asn Asp His Gln Met Arg Asp Gln Ser Gly Val Gln Glu Leu Val Lys
 245 250 255
 Gln Val Leu Ser Thr Leu Arg Ala Ile Ala Gly Asn Asp Asp Val Lys
 260 265 270
 Asp Ala Ile Val Arg Ala Gly Gly Thr Glu Ser Ile Val Ala Ala Met
 275 280 285
 Thr Gln His Leu Thr Ser Pro Gln Val Cys Glu Gln Ser Cys Ala Ala
 290 295 300
 Leu Cys Phe Leu Ala Leu Arg Lys Pro Asp Asn Ser Arg Ile Ile Val
 305 310 315 320
 Glu Gly Gly Gly Ala Val Ala Ala Leu Gln Ala Met Lys Ala His Pro
 325 330 335
 Gln Lys Ala Gly Val Gln Lys Gln Ala Cys Met Leu Ile Arg Asn Leu
 340 345 350

ES 2 671 895 T3

Val Ala His Arg Pro Ser Arg Ser Pro Ser Trp Thr Trp Gly Leu Arg
 355 360 365
 His Ser Ser Cys Arg Pro Asp Leu Pro Thr Val Thr Val Arg Thr Trp
 370 375 380
 Pro Arg Pro Pro Cys Gly Thr Trp Val Val Met Ser Ser Ser Glu Ser
 385 390 395 400
 Cys Gly Gln Ala Arg Gly Ala Thr Trp Arg His Asp Pro Arg Pro Ser
 405 410 415
 Leu Val Thr Leu Gly Glu Ser Cys Asp Ser Gly Met Gly Val Asp Pro
 420 425 430
 Cys Pro Pro Leu Ser Pro Ile Ser Ser Val Pro Phe Thr Met Arg Ser
 435 440 445
 Val Phe Trp Gln Ala Leu Gly Lys Gly Ser Gly Glu Gly Gly Ala Leu
 450 455 460

<210> 82
 <211> 501
 <212> PRT
 <213> Humana

<400> 82

Met Ser Glu Arg Cys Cys Ser Arg Tyr Ser Ser Gly Ala Ser Ile Gly
 1 5 10 15
 Cys Thr Pro Thr Ser Thr Gln Ala Lys Met Val Ser Lys Arg Ile Ala
 20 25 30
 Gln Glu Thr Phe Asp Ala Ala Val Arg Glu Asn Ile Glu Glu Phe Ala
 35 40 45
 Met Gly Pro Glu Glu Ala Val Lys Glu Ala Val Glu Gln Phe Glu Ser
 50 55 60
 Gln Gly Val Asp Leu Ser Asn Ile Val Lys Thr Ala Pro Lys Val Ser
 65 70 75 80
 Ala Asp Gly Ser Gln Glu Pro Thr His Asp Ile Leu Gln Met Leu Ser
 85 90 95
 Asp Leu Gln Glu Ser Val Ala Ser Ser Arg Pro Gln Glu Val Ser Ala
 100 105 110
 Tyr Leu Thr Arg Phe Cys Asp Gln Cys Lys Gln Asp Lys Ala Cys Arg
 115 120 125

ES 2 671 895 T3

Phe Leu Ala Ala Gln Lys Gly Ala Tyr Pro Ile Ile Phe Thr Ala Trp
 130 135 140
 Lys Leu Ala Thr Ala Gly Asp Gln Gly Leu Leu Leu Gln Ser Leu Asn
 145 150 155 160
 Ala Leu Ser Val Leu Thr Asp Gly Gln Pro Asp Leu Leu Asp Ala Gln
 165 170 175
 Gly Leu Gln Leu Leu Val Ala Thr Leu Thr Gln Asn Ala Asp Glu Ala
 180 185 190
 Asp Leu Thr Cys Ser Gly Ile Arg Cys Val Arg His Ala Cys Leu Lys
 195 200 205
 His Glu Gln Asn Arg Gln Asp Leu Val Lys Ala Gly Val Leu Pro Leu
 210 215 220
 Leu Thr Gly Ala Ile Thr His His Gly His His Thr Asp Val Val Arg
 225 230 235 240
 Glu Ala Cys Trp Ala Leu Arg Val Met Thr Phe Asp Asp Asp Ile Arg
 245 250 255
 Val Pro Phe Gly His Ala His Asn His Ala Lys Met Ile Val Gln Glu
 260 265 270
 Asn Lys Gly Leu Lys Val Leu Ile Glu Ala Thr Lys Ala Phe Leu Asp
 275 280 285
 Asn Pro Gly Ile Leu Ser Glu Leu Cys Gly Thr Leu Ser Arg Leu Ala
 290 295 300
 Ile Arg Asn Glu Phe Cys Gln Glu Val Val Asp Leu Gly Gly Leu Ser
 305 310 315 320
 Ile Leu Val Ser Leu Leu Ala Asp Cys Asn Asp His Gln Met Arg Asp
 325 330 335
 Gln Ser Gly Val Gln Glu Leu Val Lys Gln Val Leu Ser Thr Leu Arg
 340 345 350
 Ala Ile Ala Gly Asn Asp Asp Val Lys Asp Ala Ile Val Arg Ala Gly
 355 360 365
 Gly Thr Glu Ser Ile Val Ala Ala Met Thr Gln His Leu Thr Ser Pro
 370 375 380
 Gln Val Cys Glu Gln Ser Cys Ala Ala Leu Cys Phe Leu Ala Leu Arg
 385 390 395 400

ES 2 671 895 T3

Lys Pro Asp Asn Ser Arg Ile Ile Val Glu Gly Gly Gly Ala Val Ala
405 410 415
Ala Leu Gln Ala Met Lys Ala His Pro Gln Lys Ala Gly Val Gln Lys
420 425 430
Gln Ala Cys Met Leu Ile Arg Asn Leu Val Ala His Gly Gln Ala Phe
435 440 445
Ser Lys Pro Ile Leu Asp Leu Gly Ala Glu Ala Leu Ile Met Gln Ala
450 455 460
Arg Ser Ala His Arg Asp Cys Glu Asp Val Ala Lys Ala Ala Leu Arg
465 470 475 480
Asp Leu Gly Cys His Val Glu Leu Arg Glu Leu Trp Thr Gly Gln Arg
485 490 495
Gly Asn Leu Ala Pro
500

<210> 83
<211> 476
<212> PRT
<213> Humana

<400> 83

Met Val Ser Lys Arg Ile Ala Gln Glu Thr Phe Asp Ala Ala Val Arg
1 5 10 15
Glu Asn Ile Glu Glu Phe Ala Met Gly Pro Glu Glu Ala Val Lys Glu
20 25 30
Ala Val Glu Gln Phe Glu Ser Gln Gly Val Asp Leu Ser Asn Ile Val
35 40 45
Lys Thr Ala Pro Lys Val Ser Ala Asp Gly Ser Gln Glu Pro Thr His
50 55 60
Asp Ile Leu Gln Met Leu Ser Asp Leu Gln Glu Ser Val Ala Ser Ser
65 70 75 80
Arg Pro Gln Glu Val Ser Ala Tyr Leu Thr Arg Phe Cys Asp Gln Cys
85 90 95
Lys Gln Asp Lys Ala Cys Arg Phe Leu Ala Ala Gln Lys Gly Ala Tyr
100 105 110
Pro Ile Ile Phe Thr Ala Trp Lys Leu Ala Thr Ala Gly Asp Gln Gly
115 120 125

ES 2 671 895 T3

Leu Leu Leu Gln Ser Leu Asn Ala Leu Ser Val Leu Thr Asp Gly Gln
 130 135 140
 Pro Asp Leu Leu Asp Ala Gln Gly Leu Gln Leu Leu Val Ala Thr Leu
 145 150 155 160
 Thr Gln Asn Ala Asp Glu Ala Asp Leu Thr Cys Ser Gly Ile Arg Cys
 165 170 175
 Val Arg His Ala Cys Leu Lys His Glu Gln Asn Arg Gln Asp Leu Val
 180 185 190
 Lys Ala Gly Val Leu Pro Leu Leu Thr Gly Ala Ile Thr His His Gly
 195 200 205
 His His Thr Asp Val Val Arg Glu Ala Cys Trp Ala Leu Arg Val Met
 210 215 220
 Thr Phe Asp Asp Asp Ile Arg Val Pro Phe Gly His Ala His Asn His
 225 230 235 240
 Ala Lys Met Ile Val Gln Glu Asn Lys Gly Leu Lys Val Leu Ile Glu
 245 250 255
 Ala Thr Lys Ala Phe Leu Asp Asn Pro Gly Ile Leu Ser Glu Leu Cys
 260 265 270
 Gly Thr Leu Ser Arg Leu Ala Ile Arg Asn Glu Phe Cys Gln Glu Val
 275 280 285
 Val Asp Leu Gly Gly Leu Ser Ile Leu Val Ser Leu Leu Ala Asp Cys
 290 295 300
 Asn Asp His Gln Met Arg Asp Gln Ser Gly Val Gln Glu Leu Val Lys
 305 310 315 320
 Gln Val Leu Ser Thr Leu Arg Ala Ile Ala Gly Asn Asp Asp Val Lys
 325 330 335
 Asp Ala Ile Val Arg Ala Gly Gly Thr Glu Ser Ile Val Ala Ala Met
 340 345 350
 Thr Gln His Leu Thr Ser Pro Gln Val Cys Glu Gln Ser Cys Ala Ala
 355 360 365
 Leu Cys Phe Leu Ala Leu Arg Lys Pro Asp Asn Ser Arg Ile Ile Val
 370 375 380
 Glu Gly Gly Gly Ala Val Ala Ala Leu Gln Ala Met Lys Ala His Pro
 385 390 395 400

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Gln Lys Ala Gly Val Gln Lys Gln Ala Cys Met Leu Ile Arg Asn Leu
 405 410 415
 Val Ala His Gly Gln Ala Phe Ser Lys Pro Ile Leu Asp Leu Gly Ala
 420 425 430
 Glu Ala Leu Ile Met Gln Ala Arg Ser Ala His Arg Asp Cys Glu Asp
 435 440 445
 Val Ala Lys Ala Ala Leu Arg Asp Leu Gly Cys His Val Glu Leu Arg
 450 455 460
 Glu Leu Trp Thr Gly Gln Arg Gly Asn Leu Ala Pro
 465 470 475

<210> 84
 <211> 476
 <212> PRT
 <213> Humana

5

<400> 84

Met Val Ser Lys Arg Ile Ala Gln Glu Thr Phe Asp Ala Ala Val Arg
 1 5 10 15
 Glu Asn Ile Glu Glu Phe Ala Met Gly Pro Glu Glu Ala Val Lys Glu
 20 25 30
 Ala Val Glu Gln Phe Glu Ser Gln Gly Val Asp Leu Ser Asn Ile Val
 35 40 45
 Lys Thr Ala Pro Lys Val Ser Ala Asp Gly Ser Gln Glu Pro Thr His
 50 55 60
 Asp Ile Leu Gln Met Leu Ser Asp Leu Gln Glu Ser Val Ala Ser Ser
 65 70 75 80
 Arg Pro Gln Glu Val Ser Ala Tyr Leu Thr Arg Phe Cys Asp Gln Cys
 85 90 95
 Lys Gln Asp Lys Ala Cys Arg Phe Leu Ala Ala Gln Lys Gly Ala Tyr
 100 105 110
 Pro Ile Ile Phe Thr Ala Trp Lys Leu Ala Thr Ala Gly Asp Gln Gly
 115 120 125
 Leu Leu Leu Gln Ser Leu Asn Ala Leu Ser Val Leu Thr Asp Gly Gln
 130 135 140
 Pro Asp Leu Leu Asp Ala Gln Gly Leu Gln Leu Leu Val Ala Thr Leu
 145 150 155 160
 Thr Gln Asn Ala Asp Glu Ala Asp Leu Thr Cys Ser Gly Ile Arg Cys

10

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165																170																175															
Val	Arg	His	Ala 180	Cys	Leu	Lys	His	Glu 185	Gln	Asn	Arg	Gln	Asp 190	Leu	Val																																
Lys	Ala	Gly 195	Val	Leu	Pro	Leu	Leu 200	Thr	Gly	Ala	Ile	Thr 205	His	His	Gly																																
His	His 210	Thr	Asp	Val	Val	Arg 215	Glu	Ala	Cys	Trp	Ala 220	Leu	Arg	Val	Met																																
Thr 225	Phe	Asp	Asp	Asp	Ile 230	Arg	Val	Pro	Phe	Gly 235	His	Ala	His	Asn	His 240																																
Ala	Lys	Met	Ile	Val 245	Gln	Glu	Asn	Lys	Gly 250	Leu	Lys	Val	Leu	Ile 255	Glu																																
Ala	Thr	Lys	Ala 260	Phe	Leu	Asp	Asn	Pro 265	Gly	Ile	Leu	Ser	Glu 270	Leu	Cys																																
Gly	Thr	Leu 275	Ser	Arg	Leu	Ala	Ile 280	Arg	Asn	Glu	Phe	Cys 285	Gln	Glu	Val																																
Val	Asp 290	Leu	Gly	Gly	Leu	Ser 295	Ile	Leu	Val	Ser	Leu 300	Leu	Ala	Asp	Cys																																
Asn 305	Asp	His	Gln	Met	Arg 310	Asp	Gln	Ser	Gly	Val 315	Gln	Glu	Leu	Val	Lys 320																																
Gln	Val	Leu	Ser	Thr 325	Leu	Arg	Ala	Ile	Ala 330	Gly	Asn	Asp	Asp	Val 335	Lys																																
Asp	Ala	Ile	Val 340	Arg	Ala	Gly	Gly	Thr 345	Glu	Ser	Ile	Val	Ala 350	Ala	Met																																
Thr	Gln	His 355	Leu	Thr	Ser	Pro	Gln 360	Val	Cys	Glu	Gln	Ser 365	Cys	Ala	Ala																																
Leu	Cys 370	Phe	Leu	Ala	Leu	Arg 375	Lys	Pro	Asp	Asn	Ser 380	Arg	Ile	Ile	Val																																
Glu 385	Gly	Gly	Gly	Ala	Val 390	Ala	Ala	Leu	Gln	Ala 395	Met	Lys	Ala	His	Pro 400																																
Gln	Lys	Ala	Gly	Val 405	Gln	Lys	Gln	Ala	Cys 410	Met	Leu	Ile	Arg	Asn 415	Leu																																
Val	Ala	His	Gly 420	Gln	Ala	Phe	Ser	Lys 425	Pro	Ile	Leu	Asp	Leu 430	Gly	Ala																																
Glu	Ala	Leu	Ile	Met	Gln	Ala	Arg	Ser	Ala	His	Arg	Asp	Cys	Glu	Asp																																

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435

440

445

Val Ala Lys Ala Ala Leu Arg Asp Leu Gly Cys His Val Glu Leu Arg
450 455 460

Glu Leu Trp Thr Gly Gln Arg Gly Asn Leu Ala Pro
465 470 475

<210> 85
<211> 590
<212> PRT
<213> Humana

5

<400> 85

Met Ala Gly Ala Val Pro Gly Ala Ile Met Asp Glu Asp Tyr Tyr Gly
1 5 10 15

Ser Ala Ala Glu Trp Gly Asp Glu Ala Asp Gly Gly Gln Gln Glu Asp
20 25 30

Asp Ser Gly Glu Gly Glu Asp Asp Ala Glu Val Gln Gln Glu Cys Leu
35 40 45

His Lys Phe Ser Thr Arg Asp Tyr Ile Met Glu Pro Ser Ile Phe Asn
50 55 60

Thr Leu Lys Arg Tyr Phe Gln Ala Gly Gly Ser Pro Glu Asn Val Ile
65 70 75 80

Gln Leu Leu Ser Glu Asn Tyr Thr Ala Val Ala Gln Thr Val Asn Leu
85 90 95

Leu Ala Glu Trp Leu Ile Gln Thr Gly Val Glu Pro Val Gln Val Gln
100 105 110

Glu Thr Val Glu Asn His Leu Lys Ser Leu Leu Ile Lys His Phe Asp
115 120 125

Pro Arg Lys Ala Asp Ser Ile Phe Thr Glu Glu Gly Glu Thr Pro Ala
130 135 140

Trp Leu Glu Gln Met Ile Ala His Thr Thr Trp Arg Asp Leu Phe Tyr
145 150 155 160

Lys Leu Ala Glu Ala His Pro Asp Cys Leu Met Leu Asn Phe Thr Val
165 170 175

Lys Leu Ile Ser Asp Ala Gly Tyr Gln Gly Glu Ile Thr Ser Val Ser
180 185 190

Thr Ala Cys Gln Gln Leu Glu Val Phe Ser Arg Val Leu Arg Thr Ser
195 200 205

10

ES 2 671 895 T3

Leu Ala Thr Ile Leu Asp Gly Gly Glu Glu Asn Leu Glu Lys Asn Leu
 210 215 220
 Pro Glu Phe Ala Lys Met Val Cys His Gly Glu His Thr Tyr Leu Phe
 225 230 235 240
 Ala Gln Ala Met Met Ser Val Leu Ala Gln Glu Glu Gln Gly Gly Ser
 245 250 255
 Ala Val Arg Arg Ile Ala Gln Glu Val Gln Arg Phe Ala Gln Glu Lys
 260 265 270
 Gly His Asp Ala Ser Gln Ile Thr Leu Ala Leu Gly Thr Ala Ala Ser
 275 280 285
 Tyr Pro Arg Ala Cys Gln Ala Leu Gly Ala Met Leu Ser Lys Gly Ala
 290 295 300
 Leu Asn Pro Ala Asp Ile Thr Val Leu Phe Lys Met Phe Thr Ser Met
 305 310 315 320
 Asp Pro Pro Pro Val Glu Leu Ile Arg Val Pro Ala Phe Leu Asp Leu
 325 330 335
 Phe Met Gln Ser Leu Phe Lys Pro Gly Ala Arg Ile Asn Gln Asp His
 340 345 350
 Lys His Lys Tyr Ile His Ile Leu Ala Tyr Ala Ala Ser Val Val Glu
 355 360 365
 Thr Trp Lys Lys Asn Lys Arg Val Ser Ile Asn Lys Asp Glu Leu Lys
 370 375 380
 Ser Thr Ser Lys Ala Val Glu Thr Val His Asn Leu Cys Cys Asn Glu
 385 390 395 400
 Asn Lys Gly Ala Ser Glu Leu Val Ala Glu Leu Ser Thr Leu Tyr Gln
 405 410 415
 Cys Ile Arg Phe Pro Val Val Ala Met Gly Val Leu Lys Trp Val Asp
 420 425 430
 Trp Thr Val Ser Glu Pro Arg Tyr Phe Gln Leu Gln Thr Asp His Thr
 435 440 445
 Pro Val His Leu Ala Leu Leu Asp Glu Ile Ser Thr Cys His Gln Leu
 450 455 460
 Leu His Pro Gln Val Leu Gln Leu Leu Val Lys Leu Phe Glu Thr Glu
 465 470 475 480

ES 2 671 895 T3

His Ser Gln Leu Asp Val Met Glu Gln Leu Glu Leu Lys Lys Thr Leu
485 490 495

Leu Asp Arg Met Val His Leu Leu Ser Arg Gly Tyr Val Leu Pro Val
500 505 510

Val Ser Tyr Ile Arg Lys Cys Leu Glu Lys Leu Asp Thr Asp Ile Ser
515 520 525

Leu Ile Arg Tyr Phe Val Thr Glu Val Leu Asp Val Ile Ala Pro Pro
530 535 540

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

Ser Ile Ala Gly Thr Ile Lys Thr Glu Gly Glu His Asp Pro Val Thr
565 570 575

Glu Phe Ile Ala His Cys Lys Ser Asn Phe Ile Met Val Asn
580 585 590

<210> 86
<211> 250
<212> PRT
<213> Humana

<400> 86

Met Ala Met Leu Arg Val Gln Pro Glu Ala Gln Ala Lys Val Asp Val
1 5 10 15

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

Phe Pro Lys Lys Ile Ser Glu Leu Asp Ala Phe Leu Lys Glu Pro Ala
35 40 45

Leu Asn Glu Ala Asn Leu Ser Asn Leu Lys Ala Pro Leu Asp Ile Pro
50 55 60

Val Pro Asp Pro Val Lys Glu Lys Glu Lys Glu Glu Arg Lys Lys Gln
65 70 75 80

Gln Glu Lys Glu Asp Lys Asp Glu Lys Lys Lys Gly Glu Asp Glu Asp
85 90 95

Lys Gly Pro Pro Cys Gly Pro Val Asn Cys Asn Glu Lys Ile Val Val
100 105 110

Leu Leu Gln Arg Leu Lys Pro Glu Ile Lys Asp Val Ile Glu Gln Leu
115 120 125

ES 2 671 895 T3

Asn Leu Val Thr Thr Trp Leu Gln Leu Gln Ile Pro Arg Ile Glu Asp
 130 135 140
 Gly Asn Asn Phe Gly Val Ala Val Gln Glu Lys Val Phe Glu Leu Met
 145 150 155 160
 Thr Ser Leu His Thr Lys Leu Glu Gly Phe His Thr Gln Ile Ser Lys
 165 170 175
 Tyr Phe Ser Glu Arg Gly Asp Ala Val Thr Lys Ala Ala Lys Gln Pro
 180 185 190
 His Val Gly Asp Tyr Arg Gln Leu Val His Glu Leu Asp Glu Ala Glu
 195 200 205
 Tyr Arg Asp Ile Arg Leu Met Val Met Glu Ile Arg Asn Ala Tyr Val
 210 215 220
 Arg Arg Gln Gly Gln Gly Arg Gly Gly Gln Arg Gln Leu Ser Gln Ala
 225 230 235 240
 Thr His Ser Leu Thr Leu Gln Ala Arg Gly
 245 250

<210> 87
 <211> 249
 <212> PRT
 <213> Humana

<400> 87

Met Ala Met Leu Arg Val Gln Pro Glu Ala Gln Ala Lys Val Asp Val
 1 5 10 15
 Phe Arg Glu Asp Leu Cys Thr Lys Thr Glu Asn Leu Leu Gly Ser Tyr
 20 25 30
 Phe Pro Lys Lys Ile Ser Glu Leu Asp Ala Phe Leu Lys Glu Pro Ala
 35 40 45
 Leu Asn Glu Ala Asn Leu Ser Asn Leu Lys Ala Pro Leu Asp Ile Pro
 50 55 60
 Val Pro Asp Pro Val Lys Glu Lys Glu Lys Glu Glu Arg Lys Lys Gln
 65 70 75 80
 Gln Glu Lys Glu Asp Lys Asp Glu Lys Lys Lys Gly Glu Asp Glu Asp
 85 90 95
 Lys Gly Pro Pro Cys Gly Pro Val Asn Cys Asn Glu Lys Ile Val Val
 100 105 110

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Leu Leu Gln Arg Leu Lys Pro Glu Ile Lys Asp Val Ile Glu Gln Leu
 115 120 125
 Asn Leu Val Thr Thr Trp Leu Gln Leu Gln Ile Pro Arg Ile Glu Asp
 130 135 140
 Gly Asn Asn Phe Gly Val Ala Val Gln Glu Lys Val Phe Glu Leu Met
 145 150 155 160
 Thr Ser Leu His Thr Lys Leu Glu Gly Phe His Thr Gln Ile Ser Lys
 165 170 175
 Tyr Phe Ser Glu Arg Gly Asp Ala Val Thr Lys Ala Ala Lys Gln Pro
 180 185 190
 His Val Gly Asp Tyr Arg Gln Leu Val His Glu Leu Asp Glu Ala Glu
 195 200 205
 Tyr Arg Asp Ile Arg Leu Met Val Met Glu Ile Arg Asn Ala Tyr Ala
 210 215 220
 Val Leu Tyr Asp Ile Ile Leu Lys Asn Phe Glu Lys Leu Lys Lys Pro
 225 230 235 240
 Arg Gly Glu Thr Lys Gly Met Ile Tyr
 245

<210> 88
 <211> 558
 <212> PRT
 <213> Humana

<400> 88

Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
 1 5 10 15
 Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
 20 25 30
 Gly Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
 35 40 45
 Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
 50 55 60
 Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn Arg
 65 70 75 80
 Ser His Ala Glu Leu Glu Thr Ala Leu Arg Asp Ser Ser Arg Val Leu
 85 90 95
 Gln Ala Met Leu Ala Thr Gln Leu Arg Ser Phe Asp Asp His Phe Gln

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100					105					110					
His	Leu	Leu	Asn	Asp	Ser	Glu	Arg	Thr	Leu	Gln	Ala	Thr	Phe	Pro	Gly
		115					120					125			
Ala	Phe	Gly	Glu	Leu	Tyr	Thr	Gln	Asn	Ala	Arg	Ala	Phe	Arg	Asp	Leu
	130					135					140				
Tyr	Ser	Glu	Leu	Arg	Leu	Tyr	Tyr	Arg	Gly	Ala	Asn	Leu	His	Leu	Glu
145					150					155					160
Glu	Thr	Leu	Ala	Glu	Phe	Trp	Ala	Arg	Leu	Leu	Glu	Arg	Leu	Phe	Lys
				165					170					175	
Gln	Leu	His	Pro	Gln	Leu	Leu	Leu	Pro	Asp	Asp	Tyr	Leu	Asp	Cys	Leu
			180					185					190		
Gly	Lys	Gln	Ala	Glu	Ala	Leu	Arg	Pro	Phe	Gly	Glu	Ala	Pro	Arg	Glu
		195					200					205			
Leu	Arg	Leu	Arg	Ala	Thr	Arg	Ala	Phe	Val	Ala	Ala	Arg	Ser	Phe	Val
	210					215					220				
Gln	Gly	Leu	Gly	Val	Ala	Ser	Asp	Val	Val	Arg	Lys	Val	Ala	Gln	Val
225					230					235					240
Pro	Leu	Gly	Pro	Glu	Cys	Ser	Arg	Ala	Val	Met	Lys	Leu	Val	Tyr	Cys
				245					250					255	
Ala	His	Cys	Leu	Gly	Val	Pro	Gly	Ala	Arg	Pro	Cys	Pro	Asp	Tyr	Cys
			260					265					270		
Arg	Asn	Val	Leu	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	Ala
		275					280					285			
Glu	Trp	Arg	Asn	Leu	Leu	Asp	Ser	Met	Val	Leu	Ile	Thr	Asp	Lys	Phe
	290					295					300				
Trp	Gly	Thr	Ser	Gly	Val	Glu	Ser	Val	Ile	Gly	Ser	Val	His	Thr	Trp
305					310					315					320
Leu	Ala	Glu	Ala	Ile	Asn	Ala	Leu	Gln	Asp	Asn	Arg	Asp	Thr	Leu	Thr
				325					330					335	
Ala	Lys	Val	Ile	Gln	Gly	Cys	Gly	Asn	Pro	Lys	Val	Asn	Pro	Gln	Gly
			340					345					350		
Pro	Gly	Pro	Glu	Glu	Lys	Arg	Arg	Arg	Gly	Lys	Leu	Ala	Pro	Arg	Glu
		355					360					365			
Arg	Pro	Pro	Ser	Gly	Thr	Leu	Glu	Lys	Leu	Val	Ser	Glu	Ala	Lys	Ala

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370 375 380
 Gln Leu Arg Asp Val Gln Asp Phe Trp Ile Ser Leu Pro Gly Thr Leu
 385 390 395 400
 Cys Ser Glu Lys Met Ala Leu Ser Thr Ala Ser Asp Asp Arg Cys Trp
 405 410 415
 Asn Gly Met Ala Arg Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly
 420 425 430
 Leu Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys
 435 440 445
 Pro Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr
 450 455 460
 Asn Arg Leu Arg Ser Ala Tyr Asn Gly Asn Asp Val Asp Phe Gln Asp
 465 470 475 480
 Ala Ser Asp Asp Gly Ser Gly Ser Gly Ser Gly Asp Gly Cys Leu Asp
 485 490 495
 Asp Leu Cys Ser Arg Lys Val Ser Arg Lys Ser Ser Ser Ser Arg Thr
 500 505 510
 Pro Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys
 515 520 525
 Thr Ser Ala Ala Ser Cys Pro Gln Pro Pro Thr Phe Leu Leu Pro Leu
 530 535 540
 Leu Leu Phe Leu Ala Leu Thr Val Ala Arg Pro Arg Trp Arg
 545 550 555

<210> 89
 <211> 1214
 <212> PRT
 <213> Humana

<400> 89

Met Ala Ser Cys Ala Ser Ile Asp Ile Glu Asp Ala Thr Gln His Leu
 1 5 10 15
 Arg Asp Ile Leu Lys Leu Asp Arg Pro Ala Gly Gly Pro Ser Ala Glu
 20 25 30
 Ser Pro Arg Pro Ser Ser Ala Tyr Asn Gly Asp Leu Asn Gly Leu Leu
 35 40 45
 Val Pro Asp Pro Leu Cys Ser Gly Asp Ser Thr Ser Ala Asn Lys Thr
 50 55 60

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Gly Leu Arg Thr Met Pro Pro Ile Asn Leu Gln Glu Lys Gln Val Ile
 65 70 75 80
 Cys Leu Ser Gly Asp Asp Ser Ser Thr Cys Ile Gly Ile Leu Ala Lys
 85 90 95
 Glu Val Glu Ile Val Ala Ser Ser Asp Ser Ser Ile Ser Ser Lys Ala
 100 105 110
 Arg Gly Ser Asn Lys Val Lys Ile Gln Pro Val Ala Lys Tyr Asp Trp
 115 120 125
 Glu Gln Lys Tyr Tyr Tyr Gly Asn Leu Ile Ala Val Ser Asn Ser Phe
 130 135 140
 Leu Ala Tyr Ala Ile Arg Ala Ala Asn Asn Gly Ser Ala Met Val Arg
 145 150 155 160
 Val Ile Ser Val Ser Thr Ser Glu Arg Thr Leu Leu Lys Gly Phe Thr
 165 170 175
 Gly Ser Val Ala Asp Leu Ala Phe Ala His Leu Asn Ser Pro Gln Leu
 180 185 190
 Ala Cys Leu Asp Glu Ala Gly Asn Leu Phe Val Trp Arg Leu Ala Leu
 195 200 205
 Val Asn Gly Lys Ile Gln Glu Glu Ile Leu Val His Ile Arg Gln Pro
 210 215 220
 Glu Gly Thr Pro Leu Asn His Phe Arg Arg Ile Ile Trp Cys Pro Phe
 225 230 235 240
 Ile Pro Glu Glu Ser Glu Asp Cys Cys Glu Glu Ser Ser Pro Thr Val
 245 250 255
 Ala Leu Leu His Glu Asp Arg Ala Glu Val Trp Asp Leu Asp Met Leu
 260 265 270
 Arg Ser Ser His Ser Thr Trp Pro Val Asp Val Ser Gln Ile Lys Gln
 275 280 285
 Gly Phe Ile Val Val Lys Gly His Ser Thr Cys Leu Ser Glu Gly Ala
 290 295 300
 Leu Ser Pro Asp Gly Thr Val Leu Ala Thr Ala Ser His Asp Gly Tyr
 305 310 315 320
 Val Lys Phe Trp Gln Ile Tyr Ile Glu Gly Gln Asp Glu Pro Arg Cys
 325 330 335

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Leu His Glu Trp Lys Pro His Asp Gly Arg Pro Leu Ser Cys Leu Leu
 340 345 350
 Phe Cys Asp Asn His Lys Lys Gln Asp Pro Asp Val Pro Phe Trp Arg
 355 360 365
 Phe Leu Ile Thr Gly Ala Asp Gln Asn Arg Glu Leu Lys Met Trp Cys
 370 375 380
 Thr Val Ser Trp Thr Cys Leu Gln Thr Ile Arg Phe Ser Pro Asp Ile
 385 390 395 400
 Phe Ser Ser Val Ser Val Pro Pro Ser Leu Lys Val Cys Leu Asp Leu
 405 410 415
 Ser Ala Glu Tyr Leu Ile Leu Ser Asp Val Gln Arg Lys Val Leu Tyr
 420 425 430
 Val Met Glu Leu Leu Gln Asn Gln Glu Glu Gly His Ala Cys Phe Ser
 435 440 445
 Ser Ile Ser Glu Phe Leu Leu Thr His Pro Val Leu Ser Phe Gly Ile
 450 455 460
 Gln Val Val Ser Arg Cys Arg Leu Arg His Thr Glu Val Leu Pro Ala
 465 470 475 480
 Glu Glu Glu Asn Asp Ser Leu Gly Ala Asp Gly Thr His Gly Ala Gly
 485 490 495
 Ala Met Glu Ser Ala Ala Gly Val Leu Ile Lys Leu Phe Cys Val His
 500 505 510
 Thr Lys Ala Leu Gln Asp Val Gln Ile Arg Phe Gln Pro Gln Leu Asn
 515 520 525
 Pro Asp Val Val Ala Pro Leu Pro Thr His Thr Ala His Glu Asp Phe
 530 535 540
 Thr Phe Gly Glu Ser Arg Pro Glu Leu Gly Ser Glu Gly Leu Gly Ser
 545 550 555 560
 Ala Ala His Gly Ser Gln Pro Asp Leu Arg Arg Ile Val Glu Leu Pro
 565 570 575
 Ala Pro Ala Asp Phe Leu Ser Leu Ser Ser Glu Thr Lys Pro Lys Leu
 580 585 590
 Met Thr Pro Asp Ala Phe Met Thr Pro Ser Ala Ser Leu Gln Gln Ile
 595 600 605

ES 2 671 895 T3

Thr Ala Ser Pro Ser Ser Ser Ser Ser Gly Ser Ser Ser Ser Ser
 610 615 620
 Ser Ser Ser Ser Ser Leu Thr Ala Val Ser Ala Met Ser Ser Thr Ser
 625 630 635 640
 Ala Val Asp Pro Ser Leu Thr Arg Pro Pro Glu Glu Leu Thr Leu Ser
 645 650 655
 Pro Lys Leu Gln Leu Asp Gly Ser Leu Thr Met Ser Ser Ser Gly Ser
 660 665 670
 Leu Gln Ala Ser Pro Arg Gly Leu Leu Pro Gly Leu Leu Pro Ala Pro
 675 680 685
 Ala Asp Lys Leu Thr Pro Lys Gly Pro Gly Gln Val Pro Thr Ala Thr
 690 695 700
 Ser Ala Leu Ser Leu Glu Leu Gln Glu Val Glu Pro Leu Gly Leu Pro
 705 710 715 720
 Gln Ala Ser Pro Ser Arg Thr Arg Ser Pro Asp Val Ile Ser Ser Ala
 725 730 735
 Ser Thr Ala Leu Ser Gln Asp Ile Pro Glu Ile Ala Ser Glu Ala Leu
 740 745 750
 Ser Arg Gly Phe Gly Ser Ser Ala Pro Glu Gly Leu Glu Pro Asp Ser
 755 760 765
 Met Ala Ser Ala Ala Ser Ala Leu His Leu Leu Ser Pro Arg Pro Arg
 770 775 780
 Pro Gly Pro Glu Leu Gly Pro Gln Leu Gly Leu Asp Gly Gly Pro Gly
 785 790 795 800
 Asp Gly Asp Arg His Asn Thr Pro Ser Leu Leu Glu Ala Ala Leu Thr
 805 810 815
 Gln Glu Ala Ser Thr Pro Asp Ser Gln Val Trp Pro Thr Ala Pro Asp
 820 825 830
 Ile Thr Arg Glu Thr Cys Ser Thr Leu Ala Glu Ser Pro Arg Asn Gly
 835 840 845
 Leu Gln Glu Lys His Lys Ser Leu Ala Phe His Arg Pro Pro Tyr His
 850 855 860
 Leu Leu Gln Gln Arg Asp Ser Gln Asp Ala Ser Ala Glu Gln Ser Asp
 865 870 875 880

ES 2 671 895 T3

His Asp Asp Glu Val Ala Ser Leu Ala Ser Ala Ser Gly Gly Phe Gly
 885 890 895
 Thr Lys Val Pro Ala Pro Arg Leu Pro Ala Lys Asp Trp Lys Thr Lys
 900 905 910
 Gly Ser Pro Arg Thr Ser Pro Lys Leu Lys Arg Lys Ser Lys Lys Asp
 915 920 925
 Asp Gly Asp Ala Ala Met Gly Ser Arg Leu Thr Glu His Gln Val Ala
 930 935 940
 Glu Pro Pro Glu Asp Trp Pro Ala Leu Ile Trp Gln Gln Gln Arg Glu
 945 950 955 960
 Leu Ala Glu Leu Arg His Ser Gln Glu Glu Leu Leu Gln Arg Leu Cys
 965 970 975
 Thr Gln Leu Glu Gly Leu Gln Ser Thr Val Thr Gly His Val Glu Arg
 980 985 990
 Ala Leu Glu Thr Arg His Glu Gln Glu Gln Arg Arg Leu Glu Arg Ala
 995 1000 1005
 Leu Ala Glu Gly Gln Gln Arg Gly Gly Gln Leu Gln Glu Gln Leu
 1010 1015 1020
 Thr Gln Gln Leu Ser Gln Ala Leu Ser Ser Ala Val Ala Gly Arg
 1025 1030 1035
 Leu Glu Arg Ser Ile Arg Asp Glu Ile Lys Lys Thr Val Pro Pro
 1040 1045 1050
 Cys Val Ser Arg Ser Leu Glu Pro Met Ala Gly Gln Leu Ser Asn
 1055 1060 1065
 Ser Val Ala Thr Lys Leu Thr Ala Val Glu Gly Ser Met Lys Glu
 1070 1075 1080
 Asn Ile Ser Lys Leu Leu Lys Ser Lys Asn Leu Thr Asp Ala Ile
 1085 1090 1095
 Ala Arg Ala Ala Ala Asp Thr Leu Gln Gly Pro Met Gln Ala Ala
 1100 1105 1110
 Tyr Arg Glu Ala Phe Gln Ser Val Val Leu Pro Ala Phe Glu Lys
 1115 1120 1125
 Ser Cys Gln Ala Met Phe Gln Gln Ile Asn Asp Ser Phe Arg Leu
 1130 1135 1140

ES 2 671 895 T3

Gly Thr Gln Glu Tyr Leu Gln Gln Leu Glu Ser His Met Lys Ser
 1145 1150 1155
 Arg Lys Ala Arg Glu Gln Glu Ala Arg Glu Pro Val Leu Ala Gln
 1160 1165 1170
 Leu Arg Gly Leu Val Ser Thr Leu Gln Ser Ala Thr Glu Gln Met
 1175 1180 1185
 Pro Pro Trp Pro Ala Val Phe Val Leu Arg Cys Ser Thr Ser Cys
 1190 1195 1200
 Met Trp Leu Trp Ala Ala Cys Arg Ser Pro Phe
 1205 1210

<210> 90
 <211> 1401
 <212> PRT
 <213> Humana
 <400> 90

Met Ala Ser Cys Ala Ser Ile Asp Ile Glu Asp Ala Thr Gln His Leu
 1 5 10 15
 Arg Asp Ile Leu Lys Leu Asp Arg Pro Ala Gly Gly Pro Ser Ala Glu
 20 25 30
 Ser Pro Arg Pro Ser Ser Ala Tyr Asn Gly Asp Leu Asn Gly Leu Leu
 35 40 45
 Val Pro Asp Pro Leu Cys Ser Gly Asp Ser Thr Ser Ala Asn Lys Thr
 50 55 60
 Gly Leu Arg Thr Met Pro Pro Ile Asn Leu Gln Glu Lys Gln Val Ile
 65 70 75 80
 Cys Leu Ser Gly Asp Asp Ser Ser Thr Cys Ile Gly Ile Leu Ala Lys
 85 90 95
 Glu Val Glu Ile Val Ala Ser Ser Asp Ser Ser Ile Ser Ser Lys Ala
 100 105 110
 Arg Gly Ser Asn Lys Val Lys Ile Gln Pro Val Ala Lys Tyr Asp Trp
 115 120 125
 Glu Gln Lys Tyr Tyr Tyr Gly Asn Leu Ile Ala Val Ser Asn Ser Phe
 130 135 140
 Leu Ala Tyr Ala Ile Arg Ala Ala Asn Asn Gly Ser Ala Met Val Arg
 145 150 155 160

ES 2 671 895 T3

Val Ile Ser Val Ser Thr Ser Glu Arg Thr Leu Leu Lys Gly Phe Thr
 165 170 175
 Gly Ser Val Ala Asp Leu Ala Phe Ala His Leu Asn Ser Pro Gln Leu
 180 185 190
 Ala Cys Leu Asp Glu Ala Gly Asn Leu Phe Val Trp Arg Leu Ala Leu
 195 200 205
 Val Asn Gly Lys Ile Gln Glu Glu Ile Leu Val His Ile Arg Gln Pro
 210 215 220
 Glu Gly Thr Pro Leu Asn His Phe Arg Arg Ile Ile Trp Cys Pro Phe
 225 230 235 240
 Ile Pro Glu Glu Ser Glu Asp Cys Cys Glu Glu Ser Ser Pro Thr Val
 245 250 255
 Ala Leu Leu His Glu Asp Arg Ala Glu Val Trp Asp Leu Asp Met Leu
 260 265 270
 Arg Ser Ser His Ser Thr Trp Pro Val Asp Val Ser Gln Ile Lys Gln
 275 280 285
 Gly Phe Ile Val Val Lys Gly His Ser Thr Cys Leu Ser Glu Gly Ala
 290 295 300
 Leu Ser Pro Asp Gly Thr Val Leu Ala Thr Ala Ser His Asp Gly Tyr
 305 310 315 320
 Val Lys Phe Trp Gln Ile Tyr Ile Glu Gly Gln Asp Glu Pro Arg Cys
 325 330 335
 Leu His Glu Trp Lys Pro His Asp Gly Arg Pro Leu Ser Cys Leu Leu
 340 345 350
 Phe Cys Asp Asn His Lys Lys Gln Asp Pro Asp Val Pro Phe Trp Arg
 355 360 365
 Phe Leu Ile Thr Gly Ala Asp Gln Asn Arg Glu Leu Lys Met Trp Cys
 370 375 380
 Thr Val Ser Trp Thr Cys Leu Gln Thr Ile Arg Phe Ser Pro Asp Ile
 385 390 395 400
 Phe Ser Ser Val Ser Val Pro Pro Ser Leu Lys Val Cys Leu Asp Leu
 405 410 415
 Ser Ala Glu Tyr Leu Ile Leu Ser Asp Val Gln Arg Lys Val Leu Tyr
 420 425 430

ES 2 671 895 T3

Val Met Glu Leu Leu Gln Asn Gln Glu Glu Gly His Ala Cys Phe Ser
 435 440 445
 Ser Ile Ser Glu Phe Leu Leu Thr His Pro Val Leu Ser Phe Gly Ile
 450 455 460
 Gln Val Val Ser Arg Cys Arg Leu Arg His Thr Glu Val Leu Pro Ala
 465 470 475 480
 Glu Glu Glu Asn Asp Ser Leu Gly Ala Asp Gly Thr His Gly Ala Gly
 485 490 495
 Ala Met Glu Ser Ala Ala Gly Val Leu Ile Lys Leu Phe Cys Val His
 500 505 510
 Thr Lys Ala Leu Gln Asp Val Gln Ile Arg Phe Gln Pro Gln Leu Asn
 515 520 525
 Pro Asp Val Val Ala Pro Leu Pro Thr His Thr Ala His Glu Asp Phe
 530 535 540
 Thr Phe Gly Glu Ser Arg Pro Glu Leu Gly Ser Glu Gly Leu Gly Ser
 545 550 555 560
 Ala Ala His Gly Ser Gln Pro Asp Leu Arg Arg Ile Val Glu Leu Pro
 565 570 575
 Ala Pro Ala Asp Phe Leu Ser Leu Ser Ser Glu Thr Lys Pro Lys Leu
 580 585 590
 Met Thr Pro Asp Ala Phe Met Thr Pro Ser Ala Ser Leu Gln Gln Ile
 595 600 605
 Thr Ala Ser Pro Ser Ser Ser Ser Ser Gly Ser Ser Ser Ser Ser Ser
 610 615 620
 Ser Ser Ser Ser Ser Leu Thr Ala Val Ser Ala Met Ser Ser Thr Ser
 625 630 635 640
 Ala Val Asp Pro Ser Leu Thr Arg Pro Pro Glu Glu Leu Thr Leu Ser
 645 650 655
 Pro Lys Leu Gln Leu Asp Gly Ser Leu Thr Met Ser Ser Ser Gly Ser
 660 665 670
 Leu Gln Ala Ser Pro Arg Gly Leu Leu Pro Gly Leu Leu Pro Ala Pro
 675 680 685
 Ala Asp Lys Leu Thr Pro Lys Gly Pro Gly Gln Val Pro Thr Ala Thr
 690 695 700

ES 2 671 895 T3

Ser Ala Leu Ser Leu Glu Leu Gln Glu Val Glu Pro Leu Gly Leu Pro
 705 710 715 720
 Gln Ala Ser Pro Ser Arg Thr Arg Ser Pro Asp Val Ile Ser Ser Ala
 725 730 735
 Ser Thr Ala Leu Ser Gln Asp Ile Pro Glu Ile Ala Ser Glu Ala Leu
 740 745 750
 Ser Arg Gly Phe Gly Ser Ser Ala Pro Glu Gly Leu Glu Pro Asp Ser
 755 760 765
 Met Ala Ser Ala Ala Ser Ala Leu His Leu Leu Ser Pro Arg Pro Arg
 770 775 780
 Pro Gly Pro Glu Leu Gly Pro Gln Leu Gly Leu Asp Gly Gly Pro Gly
 785 790 795 800
 Asp Gly Asp Arg His Asn Thr Pro Ser Leu Leu Glu Ala Ala Leu Thr
 805 810 815
 Gln Glu Ala Ser Thr Pro Asp Ser Gln Val Trp Pro Thr Ala Pro Asp
 820 825 830
 Ile Thr Arg Glu Thr Cys Ser Thr Leu Ala Glu Ser Pro Arg Asn Gly
 835 840 845
 Leu Gln Glu Lys His Lys Ser Leu Ala Phe His Arg Pro Pro Tyr His
 850 855 860
 Leu Leu Gln Gln Arg Asp Ser Gln Asp Ala Ser Ala Glu Gln Ser Asp
 865 870 875 880
 His Asp Asp Glu Val Ala Ser Leu Ala Ser Ala Ser Gly Gly Phe Gly
 885 890 895
 Thr Lys Val Pro Ala Pro Arg Leu Pro Ala Lys Asp Trp Lys Thr Lys
 900 905 910
 Gly Ser Pro Arg Thr Ser Pro Lys Leu Lys Arg Lys Ser Lys Lys Asp
 915 920 925
 Asp Gly Asp Ala Ala Met Gly Ser Arg Leu Thr Glu His Gln Val Ala
 930 935 940
 Glu Pro Pro Glu Asp Trp Pro Ala Leu Ile Trp Gln Gln Gln Arg Glu
 945 950 955 960
 Leu Ala Glu Leu Arg His Ser Gln Glu Glu Leu Leu Gln Arg Leu Cys
 965 970 975

Thr Gln Leu Glu Gly Leu Gln Ser Thr Val Thr Gly His Val Glu Arg
980 985 990

Ala Leu Glu Thr Arg His Glu Gln Glu Gln Arg Arg Leu Glu Arg Ala
995 1000 1005

Leu Ala Glu Gly Gln Gln Arg Gly Gly Gln Leu Gln Glu Gln Leu
1010 1015 1020

Thr Gln Gln Leu Ser Gln Ala Leu Ser Ser Ala Val Ala Gly Arg
1025 1030 1035

Leu Glu Arg Ser Ile Arg Asp Glu Ile Lys Lys Thr Val Pro Pro
1040 1045 1050

Cys Val Ser Arg Ser Leu Glu Pro Met Ala Gly Gln Leu Ser Asn
1055 1060 1065

Ser Val Ala Thr Lys Leu Thr Ala Val Glu Gly Ser Met Lys Glu
1070 1075 1080

Asn Ile Ser Lys Leu Leu Lys Ser Lys Asn Leu Thr Asp Ala Ile
1085 1090 1095

Ala Arg Ala Ala Ala Asp Thr Leu Gln Gly Pro Met Gln Ala Ala
1100 1105 1110

Tyr Arg Glu Ala Phe Gln Ser Val Val Leu Pro Ala Phe Glu Lys
1115 1120 1125

Ser Cys Gln Ala Met Phe Gln Gln Ile Asn Asp Ser Phe Arg Leu
1130 1135 1140

Gly Thr Gln Glu Tyr Leu Gln Gln Leu Glu Ser His Met Lys Ser
1145 1150 1155

Arg Lys Ala Arg Glu Gln Glu Ala Arg Glu Pro Val Leu Ala Gln
1160 1165 1170

Leu Arg Gly Leu Val Ser Thr Leu Gln Ser Ala Thr Glu Gln Met
1175 1180 1185

Ala Ala Thr Val Ala Gly Ser Val Arg Ala Glu Val Gln His Gln
1190 1195 1200

Leu His Val Ala Val Gly Ser Leu Gln Glu Ser Ile Leu Ala Gln
1205 1210 1215

Val Gln Arg Ile Val Lys Gly Glu Val Ser Val Ala Leu Lys Glu
1220 1225 1230

Gln Gln Ala Ala Val Thr Ser Ser Ile Met Gln Ala Met Arg Ser
1235 1240 1245
Ala Ala Gly Thr Pro Val Pro Ser Ala His Leu Asp Cys Gln Ala
1250 1255 1260
Gln Gln Ala His Ile Leu Gln Leu Leu Gln Gln Gly His Leu Asn
1265 1270 1275
Gln Ala Phe Gln Gln Ala Leu Thr Ala Ala Asp Leu Asn Leu Val
1280 1285 1290
Leu Tyr Val Cys Glu Thr Val Asp Pro Ala Gln Val Phe Gly Gln
1295 1300 1305
Pro Pro Cys Pro Leu Ser Gln Pro Val Leu Leu Ser Leu Ile Gln
1310 1315 1320
Gln Leu Ala Ser Asp Leu Gly Thr Arg Thr Asp Leu Lys Leu Ser
1325 1330 1335
Tyr Leu Glu Glu Ala Val Met His Leu Asp His Ser Asp Pro Ile
1340 1345 1350
Thr Arg Asp His Met Gly Ser Val Met Ala Gln Val Arg Gln Lys
1355 1360 1365
Leu Phe Gln Phe Leu Gln Ala Glu Pro His Asn Ser Leu Gly Lys
1370 1375 1380
Ala Ala Arg Arg Leu Ser Leu Met Leu His Gly Leu Val Thr Pro
1385 1390 1395
Ser Leu Pro
1400

<210> 91
<211> 620
5 <212> PRT
<213> Humana
<400> 91

Met Arg Arg Ser Glu Val Leu Ala Glu Glu Ser Ile Val Cys Leu Gln
1 5 10 15
Lys Ala Leu Asn His Leu Arg Glu Ile Trp Glu Leu Ile Gly Ile Pro
20 25 30
Glu Asp Gln Arg Leu Gln Arg Thr Glu Val Val Lys Lys His Ile Lys
35 40 45

10

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Glu Leu Leu Asp Met Met Ile Ala Glu Glu Glu Ser Leu Lys Glu Arg
 50 55 60
 Leu Ile Lys Ser Ile Ser Val Cys Gln Lys Glu Leu Asn Thr Leu Cys
 65 70 75 80
 Ser Glu Leu His Val Glu Pro Phe Gln Glu Glu Gly Glu Thr Thr Ile
 85 90 95
 Leu Gln Leu Glu Lys Asp Leu Arg Thr Gln Val Glu Leu Met Arg Lys
 100 105 110
 Gln Lys Lys Glu Arg Lys Gln Glu Leu Lys Leu Leu Gln Glu Gln Asp
 115 120 125
 Gln Glu Leu Cys Glu Ile Leu Cys Met Pro His Tyr Asp Ile Asp Ser
 130 135 140
 Ala Ser Val Pro Ser Leu Glu Glu Leu Asn Gln Phe Arg Gln His Val
 145 150 155 160
 Thr Thr Leu Arg Glu Thr Lys Ala Ser Arg Arg Glu Glu Phe Val Ser
 165 170 175
 Ile Lys Arg Gln Ile Ile Leu Cys Met Glu Ala Leu Asp His Thr Pro
 180 185 190
 Asp Thr Ser Phe Glu Arg Asp Val Val Cys Glu Asp Glu Asp Ala Phe
 195 200 205
 Cys Leu Ser Leu Glu Asn Ile Ala Thr Leu Gln Lys Leu Leu Arg Gln
 210 215 220
 Leu Glu Met Gln Lys Ser Gln Asn Glu Ala Val Cys Glu Gly Leu Arg
 225 230 235 240
 Thr Gln Ile Arg Glu Leu Trp Asp Arg Leu Gln Ile Pro Glu Glu Glu
 245 250 255
 Arg Glu Ala Val Ala Thr Ile Met Ser Gly Ser Lys Ala Lys Val Arg
 260 265 270
 Lys Ala Leu Gln Leu Glu Val Asp Arg Leu Glu Glu Leu Lys Met Gln
 275 280 285
 Asn Met Lys Lys Val Ile Glu Ala Ile Arg Val Glu Leu Val Gln Tyr
 290 295 300
 Trp Asp Gln Cys Phe Tyr Ser Gln Glu Gln Arg Gln Ala Phe Ala Pro
 305 310 315 320

ES 2 671 895 T3

Phe Cys Ala Glu Asp Tyr Thr Glu Ser Leu Leu Gln Leu His Asp Ala
 325 330 335
 Glu Ile Val Arg Leu Lys Asn Tyr Tyr Glu Val His Lys Glu Leu Phe
 340 345 350
 Glu Gly Val Gln Lys Trp Glu Glu Thr Trp Arg Leu Phe Leu Glu Phe
 355 360 365
 Glu Arg Lys Ala Ser Asp Pro Asn Arg Phe Thr Asn Arg Gly Gly Asn
 370 375 380
 Leu Leu Lys Glu Glu Lys Gln Arg Ala Lys Leu Gln Lys Met Leu Pro
 385 390 395 400
 Lys Leu Glu Glu Glu Leu Lys Ala Arg Ile Glu Leu Trp Glu Gln Glu
 405 410 415
 His Ser Lys Ala Phe Met Val Asn Gly Gln Lys Phe Met Glu Tyr Val
 420 425 430
 Ala Glu Gln Trp Glu Met His Arg Leu Glu Lys Glu Arg Ala Lys Gln
 435 440 445
 Glu Arg Gln Leu Lys Asn Lys Lys Gln Thr Glu Thr Glu Met Leu Tyr
 450 455 460
 Gly Ser Ala Pro Arg Thr Pro Ser Lys Arg Arg Gly Leu Ala Pro Asn
 465 470 475 480
 Thr Pro Gly Lys Ala Arg Lys Leu Asn Thr Thr Thr Met Ser Asn Ala
 485 490 495
 Thr Ala Asn Ser Ser Ile Arg Pro Ile Phe Gly Gly Thr Val Tyr His
 500 505 510
 Ser Pro Val Ser Arg Leu Pro Pro Ser Gly Ser Lys Pro Val Ala Ala
 515 520 525
 Ser Thr Cys Ser Gly Lys Lys Thr Pro Arg Thr Gly Arg His Gly Ala
 530 535 540
 Asn Lys Glu Asn Leu Glu Leu Asn Gly Ser Ile Leu Ser Gly Gly Tyr
 545 550 555 560
 Pro Gly Ser Ala Pro Leu Gln Arg Asn Phe Ser Ile Asn Ser Val Ala
 565 570 575
 Ser Thr Tyr Ser Glu Phe Ala Lys Asp Pro Ser Leu Ser Asp Ser Ser
 580 585 590

ES 2 671 895 T3

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

Thr Ser Gly Ile Leu Asn Ser Thr Asn Ile Gln Ser
610 615 620

<210> 92
<211> 674
<212> PRT
<213> Humana

<400> 92

Thr Arg Leu Arg Pro Val Ala Arg Phe Glu Ile Leu Arg Gly Ser Thr
1 5 10 15

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

Leu Leu Leu Ser Gly Pro Cys Gly Val Gly Leu Asp Leu Asp Ser Arg
35 40 45

Leu Leu Gly Ala Ser Ala Met Arg Arg Ser Glu Val Leu Ala Glu Glu
50 55 60

Ser Ile Val Cys Leu Gln Lys Ala Leu Asn His Leu Arg Glu Ile Trp
65 70 75 80

Glu Leu Ile Gly Ile Pro Glu Asp Gln Arg Leu Gln Arg Thr Glu Val
85 90 95

Val Lys Lys His Ile Lys Glu Leu Leu Asp Met Met Ile Ala Glu Glu
100 105 110

Glu Ser Leu Lys Glu Arg Leu Ile Lys Ser Ile Ser Val Cys Gln Lys
115 120 125

Glu Leu Asn Thr Leu Cys Ser Glu Leu His Val Glu Pro Phe Gln Glu
130 135 140

Glu Gly Glu Thr Thr Ile Leu Gln Leu Glu Lys Asp Leu Arg Thr Gln
145 150 155 160

Val Glu Leu Met Arg Lys Gln Lys Lys Glu Arg Lys Gln Glu Leu Lys
165 170 175

Leu Leu Gln Glu Gln Asp Gln Glu Leu Cys Glu Ile Leu Cys Met Pro
180 185 190

His Tyr Asp Ile Asp Ser Ala Ser Val Pro Ser Leu Glu Glu Leu Asn
195 200 205

Gln Phe Arg Gln His Val Thr Thr Leu Arg Glu Thr Lys Ala Ser Arg

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210	215	220
Arg Glu Glu Phe Val 225	Ser Ile Lys Arg Gln 230	Ile Ile Leu Cys Met Glu 235 240
Ala Leu Asp His Thr 245	Pro Asp Thr Ser Phe 250	Glu Arg Asp Val Val Cys 255
Glu Asp Glu Asp Ala Phe Cys 260	Leu Ser Leu Glu Asn Ile 265 270	Ala Thr Leu
Gln Lys Leu Leu Arg Gln Leu 275	Glu Met Gln Lys Ser 280	Gln Asn Glu Ala 285
Val Cys Glu Gly Leu Arg Thr 290	Gln Ile Arg Glu 295	Leu Trp Asp Arg Leu 300
Gln Ile Pro Glu Glu Glu Arg 305 310	Glu Ala Val Ala Thr Ile Met Ser 315	Gly 320
Ser Lys Ala Lys Val Arg Lys Ala Leu 325	Gln Leu Glu Val Asp Arg 330 335	Leu
Glu Glu Leu Lys Met Gln Asn Met 340	Lys Lys Val Ile Glu Ala Ile Arg 345 350	
Val Glu Leu Val Gln Tyr Trp 355	Asp Gln Cys Phe Tyr Ser Gln Glu Gln 360 365	
Arg Gln Ala Phe Ala Pro Phe 370 375	Cys Ala Glu Asp Tyr Thr Glu Ser Leu 380	
Leu Gln Leu His Asp Ala Glu Ile Val Arg 385 390	Leu Lys Asn Tyr Tyr Glu 395 400	
Val His Lys Glu Leu Phe Glu Gly Val 405	Gln Lys Trp Glu Glu Thr Trp 410 415	
Arg Leu Phe Leu Glu Phe Glu Arg 420	Lys Ala Ser Asp Pro Asn Arg Phe 425 430	
Thr Asn Arg Gly Gly Asn Leu 435	Leu Lys Glu Glu Lys Gln Arg Ala Lys 440 445	
Leu Gln Lys Met Leu Pro Lys 450	Leu Glu Glu Glu Leu Lys Ala Arg Ile 455 460	
Glu Leu Trp Glu Gln Glu His Ser Lys Ala 465 470	Phe Met Val Asn Gly Gln 475 480	
Lys Phe Met Glu Tyr Val Ala Glu Gln Trp Glu Met His Arg Leu Glu		

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485 490 495
 Lys Glu Arg Ala Lys Gln Glu Arg Gln Leu Lys Asn Lys Lys Gln Thr
 500 505 510
 Glu Thr Glu Met Leu Tyr Gly Ser Ala Pro Arg Thr Pro Ser Lys Arg
 515 520 525
 Arg Gly Leu Ala Pro Asn Thr Pro Gly Lys Ala Arg Lys Leu Asn Thr
 530 535 540
 Thr Thr Met Ser Asn Ala Thr Ala Asn Ser Ser Ile Arg Pro Ile Phe
 545 550 555 560
 Gly Gly Thr Val Tyr His Ser Pro Val Ser Arg Leu Pro Pro Ser Gly
 565 570 575
 Ser Lys Pro Val Ala Ala Ser Thr Cys Ser Gly Lys Lys Thr Pro Arg
 580 585 590
 Thr Gly Arg His Gly Ala Asn Lys Glu Asn Leu Glu Leu Asn Gly Ser
 595 600 605
 Ile Leu Ser Gly Gly Tyr Pro Gly Ser Ala Pro Leu Gln Arg Asn Phe
 610 615 620
 Ser Ile Asn Ser Val Ala Ser Thr Tyr Ser Glu Phe Ala Lys Asp Pro
 625 630 635 640
 Ser Leu Ser Asp Ser Ser Thr Val Gly Leu Gln Arg Glu Leu Ser Lys
 645 650 655
 Ala Ser Lys Ser Asp Ala Thr Ser Gly Ile Leu Asn Ser Thr Asn Ile
 660 665 670
 Gln Ser

<210> 93
 <211> 660
 <212> PRT
 <213> Humana

<400> 93

Thr Arg Leu Arg Pro Val Ala Arg Phe Glu Ile Leu Arg Gly Ser Thr
 1 5 10 15
 Ala Arg Gly Ala Ala Thr Arg Ser Asp Ile Ala Gly Val Cys Gly Trp
 20 25 30
 Leu Leu Leu Ser Gly Pro Cys Gly Val Gly Leu Asp Leu Asp Ser Arg
 35 40 45

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Leu 50 Leu Gly Ala Ser Ala Met 55 Arg Arg Ser Glu 60 Val Leu Ala Glu Glu
 Ser 65 Ile Val Cys Leu 70 Gln Lys Ala Leu Asn 75 His Leu Arg Glu Ile 80 Trp
 Glu Leu Ile Gly 85 Ile Pro Glu Asp Gln 90 Arg Leu Gln Arg Thr Glu 95 Val
 Val Lys Lys 100 His Ile Lys Glu Leu 105 Leu Asp Met Met Ile 110 Ala Glu Glu
 Glu Ser 115 Leu Lys Glu Arg Leu 120 Ile Lys Ser Ile Ser Val 125 Cys Gln Lys
 Glu 130 Leu Asn Thr Leu Cys 135 Ser Glu Leu His Val 140 Glu Pro Phe Gln Glu
 Glu 145 Gly Glu Thr Thr 150 Ile Leu Gln Leu Glu 155 Lys Asp Leu Arg Thr Gln 160
 Val Glu Leu Met 165 Arg Lys Gln Lys Lys 170 Glu Arg Lys Gln Glu 175 Leu Lys
 Leu Leu Gln 180 Glu Gln Asp Gln Glu 185 Leu Cys Glu Ile Leu 190 Cys Met Pro
 His Tyr 195 Asp Ile Asp Ser Ala 200 Ser Val Pro Ser Leu 205 Glu Glu Leu Asn
 Gln 210 Phe Arg Gln His Val 215 Thr Thr Leu Arg Glu 220 Thr Lys Ala Ser Arg
 Arg 225 Glu Glu Phe Val 230 Ser Ile Lys Arg Gln 235 Ile Ile Leu Cys Met Glu 240
 Ala Leu Asp 245 His Thr Pro Asp Thr Ser 250 Phe Glu Arg Asp Val 255 Val Cys
 Glu Asp Glu 260 Asp Ala Phe Cys Leu 265 Ser Leu Glu Asn Ile 270 Ala Thr Leu
 Gln Lys 275 Leu Leu Arg Gln Leu 280 Glu Met Gln Lys Ser 285 Gln Asn Glu Ala
 Val 290 Cys Glu Gly Leu Arg Thr 295 Gln Ile Arg Glu 300 Leu Trp Asp Arg Leu
 Gln 305 Ile Pro Glu Glu 310 Glu Arg Glu Ala Val 315 Ala Thr Ile Met Ser Gly 320

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Ser Lys Ala Lys Val Arg Lys Ala Leu Gln Leu Glu Val Asp Arg Leu
 325 330 335
 Glu Glu Leu Lys Met Gln Asn Met Lys Lys Val Ile Glu Ala Ile Arg
 340 345 350
 Val Glu Leu Val Gln Tyr Trp Asp Gln Cys Phe Tyr Ser Gln Glu Gln
 355 360 365
 Arg Gln Ala Phe Ala Pro Phe Cys Ala Glu Asp Tyr Thr Glu Ser Leu
 370 375 380
 Leu Gln Leu His Asp Ala Glu Ile Val Arg Leu Lys Asn Tyr Tyr Glu
 385 390 395 400
 Val His Lys Glu Leu Phe Glu Gly Val Gln Lys Trp Glu Glu Thr Trp
 405 410 415
 Arg Leu Phe Leu Glu Phe Glu Arg Lys Ala Ser Asp Pro Asn Arg Phe
 420 425 430
 Thr Asn Arg Gly Gly Asn Leu Leu Lys Glu Glu Lys Gln Arg Ala Lys
 435 440 445
 Leu Gln Lys Met Leu Pro Lys Leu Glu Glu Glu Leu Lys Ala Arg Ile
 450 455 460
 Glu Leu Trp Glu Gln Glu His Ser Lys Ala Phe Met Val Asn Gly Gln
 465 470 475 480
 Lys Phe Met Glu Tyr Val Ala Glu Gln Trp Glu Met His Arg Leu Glu
 485 490 495
 Lys Glu Arg Ala Lys Gln Glu Arg Gln Leu Lys Asn Lys Lys Gln Thr
 500 505 510
 Glu Thr Glu Met Leu Tyr Gly Ser Ala Pro Arg Thr Pro Ser Lys Arg
 515 520 525
 Arg Gly Leu Ala Pro Asn Thr Pro Gly Lys Ala Arg Lys Leu Asn Thr
 530 535 540
 Thr Thr Met Ser Asn Ala Thr Ala Asn Ser Ser Ile Arg Pro Ile Phe
 545 550 555 560
 Gly Gly Thr Val Tyr His Ser Pro Val Ser Arg Leu Pro Pro Ser Gly
 565 570 575
 Ser Lys Pro Val Ala Ala Ser Thr Cys Ser Gly Lys Lys Thr Pro Arg
 580 585 590

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Thr Gly Arg His Gly Ala Asn Lys Glu Asn Leu Glu Leu Asn Gly Ser
595 600 605

Ile Leu Ser Gly Gly Tyr Pro Gly Ser Ala Pro Leu Gln Arg Asn Phe
610 615 620

Ser Ile Asn Ser Val Ala Ser Thr Tyr Ser Glu Phe Ala Arg Glu Leu
625 630 635 640

Ser Lys Ala Ser Lys Ser Asp Ala Thr Ser Gly Ile Leu Asn Ser Thr
645 650 655

Asn Ile Gln Ser
660

<210> 94
<211> 417
<212> PRT
<213> Humana

<400> 94

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

Leu Gly Cys Gly Gln Pro Leu Pro Gln Val Pro Glu Arg Pro Phe Ser
20 25 30

Val Leu Trp Asn Val Pro Ser Ala His Cys Glu Ala Arg Phe Gly Val
35 40 45

His Leu Pro Leu Asn Ala Leu Gly Ile Ile Ala Asn Arg Gly Gln His
50 55 60

Phe His Gly Gln Asn Met Thr Ile Phe Tyr Lys Asn Gln Leu Gly Leu
65 70 75 80

Tyr Pro Tyr Phe Gly Pro Arg Gly Thr Ala His Asn Gly Gly Ile Pro
85 90 95

Gln Ala Leu Pro Leu Asp Arg His Leu Ala Leu Ala Ala Tyr Gln Ile
100 105 110

His His Ser Leu Arg Pro Gly Phe Ala Gly Pro Ala Val Leu Asp Trp
115 120 125

Glu Glu Trp Cys Pro Leu Trp Ala Gly Asn Trp Gly Arg Arg Arg Ala
130 135 140

Tyr Gln Ala Ala Ser Trp Ala Trp Ala Gln Gln Val Phe Pro Asp Leu
145 150 155 160

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Asp Pro Gln Glu Gln Leu Tyr Lys Ala Tyr Thr Gly Phe Glu Gln Ala
 165 170 175
 Ala Arg Ala Leu Met Glu Asp Thr Leu Arg Val Ala Gln Ala Leu Arg
 180 185 190
 Pro His Gly Leu Trp Gly Phe Tyr His Tyr Pro Ala Cys Gly Asn Gly
 195 200 205
 Trp His Ser Met Ala Ser Asn Tyr Thr Gly Arg Cys His Ala Ala Thr
 210 215 220
 Leu Ala Arg Asn Thr Gln Leu His Trp Leu Trp Ala Ala Ser Ser Ala
 225 230 235 240
 Leu Phe Pro Ser Ile Tyr Leu Pro Pro Arg Leu Pro Pro Ala His His
 245 250 255
 Gln Ala Phe Val Arg His Arg Leu Glu Glu Ala Phe Arg Val Ala Leu
 260 265 270
 Val Gly His Arg His Pro Leu Pro Val Leu Ala Tyr Val Arg Leu Thr
 275 280 285
 His Arg Arg Ser Gly Arg Phe Leu Ser Gln Asp Asp Leu Val Gln Ser
 290 295 300
 Ile Gly Val Ser Ala Ala Leu Gly Ala Ala Gly Val Val Leu Trp Gly
 305 310 315 320
 Asp Leu Ser Leu Ser Ser Ser Glu Glu Glu Cys Trp His Leu His Asp
 325 330 335
 Tyr Leu Val Asp Thr Leu Gly Pro Tyr Val Ile Asn Val Thr Arg Ala
 340 345 350
 Ala Met Ala Cys Ser His Gln Arg Cys His Gly His Gly Arg Cys Ala
 355 360 365
 Arg Arg Asp Pro Gly Gln Met Glu Ala Phe Leu His Leu Trp Pro Asp
 370 375 380
 Gly Ser Leu Gly Asp Trp Lys Ser Phe Ser Cys His Cys Tyr Trp Gly
 385 390 395 400
 Trp Ala Gly Pro Thr Cys Gln Glu Pro Arg Pro Gly Pro Lys Glu Ala
 405 410 415
 Val

<210> 95
 <211> 462

<212> PRT
 <213> Humana

<400> 95

5

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

Leu Gly Cys Gly Gln Pro Leu Pro Gln Val Pro Glu Arg Pro Phe Ser
 20      25      30

Val Leu Trp Asn Val Pro Ser Ala His Cys Glu Ala Arg Phe Gly Val
 35      40      45

His Leu Pro Leu Asn Ala Leu Gly Ile Ile Ala Asn Arg Gly Gln His
 50      55      60

Phe His Gly Gln Asn Met Thr Ile Phe Tyr Lys Asn Gln Leu Gly Leu
 65      70      75      80

Tyr Pro Tyr Phe Gly Pro Arg Gly Thr Ala His Asn Gly Gly Ile Pro
 85      90      95

Gln Ala Leu Pro Leu Asp Arg His Leu Ala Leu Ala Ala Tyr Gln Ile
 100     105     110

His His Ser Leu Arg Pro Gly Phe Ala Gly Pro Ala Val Leu Asp Trp
 115     120     125

Glu Glu Trp Cys Pro Leu Trp Ala Gly Asn Trp Gly Arg Arg Arg Ala
 130     135     140

Tyr Gln Ala Ala Ser Trp Ala Trp Ala Gln Gln Val Phe Pro Asp Leu
 145     150     155     160

Asp Pro Gln Glu Gln Leu Tyr Lys Ala Tyr Thr Gly Phe Glu Gln Ala
 165     170     175

Ala Arg Ala Leu Met Glu Asp Thr Leu Arg Val Ala Gln Ala Leu Arg
 180     185     190

Pro His Gly Leu Trp Gly Phe Tyr His Tyr Pro Ala Cys Gly Asn Gly
 195     200     205

Trp His Ser Met Ala Ser Asn Tyr Thr Gly Arg Cys His Ala Ala Thr
 210     215     220

Leu Ala Arg Asn Thr Gln Leu His Trp Leu Trp Ala Ala Ser Ser Ala
 225     230     235     240

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Leu Phe Pro Ser Ile Tyr Leu Pro Pro Arg Leu Pro Pro Ala His His
 245 250 255
 Gln Ala Phe Val Arg His Arg Leu Glu Glu Ala Phe Arg Val Ala Leu
 260 265 270
 Val Gly His Arg His Pro Leu Pro Val Leu Ala Tyr Val Arg Leu Thr
 275 280 285
 His Arg Arg Ser Gly Arg Phe Leu Ser Gln Asp Asp Leu Val Gln Ser
 290 295 300
 Ile Gly Val Ser Ala Ala Leu Gly Ala Ala Gly Val Val Leu Trp Gly
 305 310 315 320
 Asp Leu Ser Leu Ser Ser Ser Glu Glu Glu Cys Trp His Leu His Asp
 325 330 335
 Tyr Leu Val Asp Thr Leu Gly Pro Tyr Val Ile Asn Val Thr Arg Ala
 340 345 350
 Ala Met Ala Cys Ser His Gln Arg Cys His Gly His Gly Arg Cys Ala
 355 360 365
 Arg Arg Asp Pro Gly Gln Met Glu Ala Phe Leu His Leu Trp Pro Asp
 370 375 380
 Gly Ser Leu Gly Asp Trp Lys Ser Phe Ser Cys His Cys Tyr Trp Gly
 385 390 395 400
 Trp Ala Gly Pro Thr Cys Gln Glu Pro Leu Gly Leu Lys Lys Gln Tyr
 405 410 415
 Lys Ala Arg Ala Pro Ala Thr Ala Ser Ser Phe Pro Cys Cys His Phe
 420 425 430
 Ser Ser Pro Gly Thr Thr Leu Ser His Ser Cys Ser Ile Gln Phe Thr
 435 440 445
 Val Asn Pro Pro Lys His Thr Pro Arg Phe Pro Trp Asn Pro
 450 455 460

<210> 96
 <211> 387
 <212> PRT
 <213> Humana

<400> 96

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

Leu Gly Cys Gly Gln Pro Leu Pro Gln Val Pro Glu Arg Pro Phe Ser

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20					25					30					
Val	Leu	Trp	Asn	Val	Pro	Ser	Ala	His	Cys	Glu	Ala	Arg	Phe	Gly	Val
		35					40					45			
His	Leu	Pro	Leu	Asn	Ala	Leu	Gly	Ile	Ile	Ala	Asn	Arg	Gly	Gln	His
	50					55					60				
Phe	His	Gly	Gln	Asn	Met	Thr	Ile	Phe	Tyr	Lys	Asn	Gln	Leu	Gly	Leu
65					70					75					80
Tyr	Pro	Tyr	Phe	Gly	Pro	Arg	Gly	Thr	Ala	His	Asn	Gly	Gly	Ile	Pro
				85					90					95	
Gln	Ala	Leu	Pro	Leu	Asp	Arg	His	Leu	Ala	Leu	Ala	Ala	Tyr	Gln	Ile
			100					105					110		
His	His	Ser	Leu	Arg	Pro	Gly	Phe	Ala	Gly	Pro	Ala	Val	Leu	Asp	Trp
		115					120					125			
Glu	Glu	Trp	Cys	Pro	Leu	Trp	Ala	Gly	Asn	Trp	Gly	Arg	Arg	Arg	Ala
	130					135					140				
Tyr	Gln	Ala	Ala	Ser	Trp	Ala	Trp	Ala	Gln	Gln	Val	Phe	Pro	Asp	Leu
145					150					155					160
Asp	Pro	Gln	Glu	Gln	Leu	Tyr	Lys	Ala	Tyr	Thr	Gly	Phe	Glu	Gln	Ala
				165					170					175	
Ala	Arg	Ala	Leu	Met	Glu	Asp	Thr	Leu	Arg	Val	Ala	Gln	Ala	Leu	Arg
			180					185					190		
Pro	His	Gly	Leu	Trp	Gly	Phe	Tyr	His	Tyr	Pro	Ala	Cys	Gly	Asn	Gly
		195					200					205			
Trp	His	Ser	Met	Ala	Ser	Asn	Tyr	Thr	Gly	Arg	Cys	His	Ala	Ala	Thr
	210					215					220				
Leu	Ala	Arg	Asn	Thr	Gln	Leu	His	Trp	Leu	Trp	Ala	Ala	Ser	Ser	Ala
225					230					235					240
Leu	Phe	Pro	Ser	Ile	Tyr	Leu	Pro	Pro	Arg	Leu	Pro	Pro	Ala	His	His
				245					250					255	
Gln	Ala	Phe	Val	Arg	His	Arg	Leu	Glu	Glu	Ala	Phe	Arg	Val	Ala	Leu
			260					265					270		
Val	Gly	His	Arg	His	Pro	Leu	Pro	Val	Leu	Ala	Tyr	Val	Arg	Leu	Thr
		275					280					285			
His	Arg	Arg	Ser	Gly	Arg	Phe	Leu	Ser	Gln	Glu	Glu	Cys	Trp	His	Leu

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290

295

300

His Asp Tyr Leu Val Asp Thr Leu Gly Pro Tyr Val Ile Asn Val Thr
305 310 315 320

Arg Ala Ala Met Ala Cys Ser His Gln Arg Cys His Gly His Gly Arg
325 330 335

Cys Ala Arg Arg Asp Pro Gly Gln Met Glu Ala Phe Leu His Leu Trp
340 345 350

Pro Asp Gly Ser Leu Gly Asp Trp Lys Ser Phe Ser Cys His Cys Tyr
355 360 365

Trp Gly Trp Ala Gly Pro Thr Cys Gln Glu Pro Arg Pro Gly Pro Lys
370 375 380

Glu Ala Val
385

<210> 97

<211> 462

<212> PRT

<213> Humana

<400> 97

Met Gly Lys Glu Lys Thr His Ile Asn Ile Val Val Ile Gly His Val
1 5 10 15

Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Cys Gly
20 25 30

Gly Ile Asp Lys Arg Thr Ile Glu Lys Phe Glu Lys Glu Ala Ala Glu
35 40 45

Met Gly Lys Gly Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
50 55 60

Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ser Leu Trp Lys Phe
65 70 75 80

Glu Thr Ser Lys Tyr Tyr Val Thr Ile Ile Asp Ala Pro Gly His Arg
85 90 95

Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
100 105 110

Val Leu Ile Val Ala Ala Gly Val Gly Glu Phe Glu Ala Gly Ile Ser
115 120 125

Lys Asn Gly Gln Thr Arg Glu His Ala Leu Leu Ala Tyr Thr Leu Gly
130 135 140

5

10

ES 2 671 895 T3

Val Lys Gln Leu Ile Val Gly Val Asn Lys Met Asp Ser Thr Glu Pro
 145 150 155 160
 Pro Tyr Ser Gln Lys Arg Tyr Glu Glu Ile Val Lys Glu Val Ser Thr
 165 170 175
 Tyr Ile Lys Lys Ile Gly Tyr Asn Pro Asp Thr Val Ala Phe Val Pro
 180 185 190
 Ile Ser Gly Trp Asn Gly Asp Asn Met Leu Glu Pro Ser Ala Asn Met
 195 200 205
 Pro Trp Phe Lys Gly Trp Lys Val Thr Arg Lys Asp Gly Asn Ala Ser
 210 215 220
 Gly Thr Thr Leu Leu Glu Ala Leu Asp Cys Ile Leu Pro Pro Thr Arg
 225 230 235 240
 Pro Thr Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile
 245 250 255
 Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu
 260 265 270
 Lys Pro Gly Met Val Val Thr Phe Ala Pro Val Asn Val Thr Thr Glu
 275 280 285
 Val Lys Ser Val Glu Met His His Glu Ala Leu Ser Glu Ala Leu Pro
 290 295 300
 Gly Asp Asn Val Gly Phe Lys Val Lys Asn Val Ser Val Lys Asp Val
 305 310 315 320
 Arg Arg Gly Asn Val Ala Gly Asp Ser Lys Asn Asp Pro Pro Met Glu
 325 330 335
 Ala Ala Gly Phe Thr Ala Gln Val Ile Ile Leu Asn His Pro Gly Gln
 340 345 350
 Ile Ser Ala Gly Tyr Ala Pro Val Leu Asp Cys His Met Ala His Ile
 355 360 365
 Ala Cys Lys Phe Ala Glu Leu Lys Glu Lys Ile Asp Arg Arg Ser Gly
 370 375 380
 Lys Lys Leu Glu Asp Gly Pro Lys Phe Leu Lys Ser Gly Asp Ala Ala
 385 390 395 400
 Ile Val Asp Met Val Pro Gly Lys Pro Met Cys Val Glu Ser Phe Ser
 405 410 415

ES 2 671 895 T3

Asp Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr
420 425 430

Val Ala Val Gly Val Ile Lys Ala Val Asp Lys Lys Ala Ala Gly Ala
435 440 445

Gly Lys Val Thr Lys Ser Ala Gln Lys Ala Gln Lys Ala Lys
450 455 460

<210> 98

<211> 381

<212> PRT

<213> Humana

<400> 98

Met Ala Leu Lys Ala Glu Gly Ala Ala Leu Asp Cys Phe Glu Val Thr
1 5 10 15

Leu Lys Cys Glu Glu Gly Glu Asp Glu Glu Glu Ala Met Val Val Ala
20 25 30

Val Ile Pro Arg Pro Glu Pro Met Leu Arg Val Thr Gln Gln Glu Lys
35 40 45

Thr Pro Pro Pro Arg Pro Ser Pro Leu Glu Ala Gly Ser Asp Gly Cys
50 55 60

Glu Glu Pro Lys Gln Gln Val Ser Trp Glu Gln Glu Phe Leu Val Gly
65 70 75 80

Ser Ser Pro Gly Gly Ser Gly Arg Ala Leu Cys Met Val Cys Gly Ala
85 90 95

Glu Ile Arg Ala Pro Ser Ala Asp Thr Ala Arg Ser His Ile Leu Glu
100 105 110

Gln His Pro His Thr Leu Asp Leu Ser Pro Ser Glu Lys Ser Asn Ile
115 120 125

Leu Glu Ala Trp Ser Glu Gly Val Ala Leu Leu Gln Asp Val Arg Ala
130 135 140

Glu Gln Pro Ser Pro Pro Asn Ser Asp Ser Gly Gln Asp Ala His Pro
145 150 155 160

Asp Pro Asp Ala Asn Pro Asp Ala Ala Arg Met Pro Ala Glu Ile Val
165 170 175

Val Leu Leu Asp Ser Glu Asp Asn Pro Ser Leu Pro Lys Arg Ser Arg
180 185 190

5

10

ES 2 671 895 T3

Pro Arg Gly Leu Arg Pro Leu Glu Leu Pro Ala Val Pro Ala Thr Glu
195 200 205

Pro Gly Asn Lys Lys Pro Arg Gly Gln Arg Trp Lys Glu Pro Pro Gly
210 215 220

Glu Glu Pro Val Arg Lys Lys Arg Gly Arg Pro Met Thr Lys Asn Leu
225 230 235 240

Asp Pro Asp Pro Glu Pro Pro Ser Pro Asp Ser Pro Thr Glu Thr Phe
245 250 255

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

Gly Phe Val Leu Gln Leu Phe Ser His Thr Gln Leu Arg Gly Pro Asp
275 280 285

Ser Lys Asp Ser Pro Lys Asp Arg Glu Val Ala Glu Gly Gly Leu Pro
290 295 300

Arg Ala Glu Ser Pro Ser Pro Ala Pro Pro Pro Gly Leu Arg Gly Thr
305 310 315 320

Leu Asp Leu Gln Val Ile Arg Val Arg Met Glu Glu Pro Pro Ala Val
325 330 335

Ser Leu Leu Gln Asp Trp Ser Arg His Pro Gln Gly Thr Lys Arg Val
340 345 350

Gly Ala Gly Asp Thr Ser Asp Trp Pro Thr Val Leu Ser Glu Ser Ser
355 360 365

Thr Thr Val Ala Gly Lys Pro Glu Lys Gly Asn Gly Val
370 375 380

<210> 99
<211> 1909
5 <212> PRT
<213> Humana
<400> 99

Met Ser Thr His Arg Ser Arg Leu Leu Thr Ala Ala Pro Leu Ser Met
1 5 10 15

Glu Gln Arg Arg Pro Trp Pro Arg Ala Leu Glu Val Asp Ser Arg Ser
20 25 30

Val Val Leu Leu Ser Val Val Trp Val Leu Leu Ala Pro Pro Ala Ala
35 40 45

10

ES 2 671 895 T3

Gly Met Pro Gln Phe Ser Thr Phe His Ser Glu Asn Arg Asp Trp Thr
 50 55 60
 Phe Asn His Leu Thr Val His Gln Gly Thr Gly Ala Val Tyr Val Gly
 65 70 75 80
 Ala Ile Asn Arg Val Tyr Lys Leu Thr Gly Asn Leu Thr Ile Gln Val
 85 90 95
 Ala His Lys Thr Gly Pro Glu Glu Asp Asn Lys Ser Cys Tyr Pro Pro
 100 105 110
 Leu Ile Val Gln Pro Cys Ser Glu Val Leu Thr Leu Thr Asn Asn Val
 115 120 125
 Asn Lys Leu Leu Ile Ile Asp Tyr Ser Glu Asn Arg Leu Leu Ala Cys
 130 135 140
 Gly Ser Leu Tyr Gln Gly Val Cys Lys Leu Leu Arg Leu Asp Asp Leu
 145 150 155 160
 Phe Ile Leu Val Glu Pro Ser His Lys Lys Glu His Tyr Leu Ser Ser
 165 170 175
 Val Asn Lys Thr Gly Thr Met Tyr Gly Val Ile Val Arg Ser Glu Gly
 180 185 190
 Glu Asp Gly Lys Leu Phe Ile Gly Thr Ala Val Asp Gly Lys Gln Asp
 195 200 205
 Tyr Phe Pro Thr Leu Ser Ser Arg Lys Leu Pro Arg Asp Pro Glu Ser
 210 215 220
 Ser Ala Met Leu Asp Tyr Glu Leu His Ser Asp Phe Val Ser Ser Leu
 225 230 235 240
 Ile Lys Ile Pro Ser Asp Thr Leu Ala Leu Val Ser His Phe Asp Ile
 245 250 255
 Phe Tyr Ile Tyr Gly Phe Ala Ser Gly Gly Phe Val Tyr Phe Leu Thr
 260 265 270
 Val Gln Pro Glu Thr Pro Glu Gly Val Ala Ile Asn Ser Ala Gly Asp
 275 280 285
 Leu Phe Tyr Thr Ser Arg Ile Val Arg Leu Cys Lys Asp Asp Pro Lys
 290 295 300
 Phe His Ser Tyr Val Ser Leu Pro Phe Gly Cys Thr Arg Ala Gly Val
 305 310 315 320

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Glu Tyr Arg Leu Leu Gln Ala Ala Tyr Leu Ala Lys Pro Gly Asp Ser
 325 330 335
 Leu Ala Gln Ala Phe Asn Ile Thr Ser Gln Asp Asp Val Leu Phe Ala
 340 345 350
 Ile Phe Ser Lys Gly Gln Lys Gln Tyr His His Pro Pro Asp Asp Ser
 355 360 365
 Ala Leu Cys Ala Phe Pro Ile Arg Ala Ile Asn Leu Gln Ile Lys Glu
 370 375 380
 Arg Leu Gln Ser Cys Tyr Gln Gly Glu Gly Asn Leu Glu Leu Asn Trp
 385 390 395 400
 Leu Leu Gly Lys Asp Val Gln Cys Thr Lys Ala Pro Val Pro Ile Asp
 405 410 415
 Asp Asn Phe Cys Gly Leu Asp Ile Asn Gln Pro Leu Gly Gly Ser Thr
 420 425 430
 Pro Val Glu Gly Leu Thr Leu Tyr Thr Thr Ser Arg Asp Arg Met Thr
 435 440 445
 Ser Val Ala Ser Tyr Val Tyr Asn Gly Tyr Ser Val Val Phe Val Gly
 450 455 460
 Thr Lys Ser Gly Lys Leu Lys Lys Ile Arg Ala Asp Gly Pro Pro His
 465 470 475 480
 Gly Gly Val Gln Tyr Glu Met Val Ser Val Leu Lys Asp Gly Ser Pro
 485 490 495
 Ile Leu Arg Asp Met Ala Phe Ser Ile Asp Gln Arg Tyr Leu Tyr Val
 500 505 510
 Met Ser Glu Arg Gln Val Thr Arg Val Pro Val Glu Ser Cys Glu Gln
 515 520 525
 Tyr Thr Thr Cys Gly Glu Cys Leu Ser Ser Gly Asp Pro His Cys Gly
 530 535 540
 Trp Cys Ala Leu His Asn Met Cys Ser Arg Arg Asp Lys Cys Gln Gln
 545 550 555 560
 Ala Trp Glu Pro Asn Arg Phe Ala Ala Ser Ile Ser Gln Cys Val Ser
 565 570 575
 Leu Ala Val His Pro Ser Ser Ile Ser Val Ser Glu His Ser Arg Leu
 580 585 590

ES 2 671 895 T3

Leu Ser Leu Val Val Ser Asp Ala Pro Asp Leu Ser Ala Gly Ile Ala
 595 600 605
 Cys Ala Phe Gly Asn Leu Thr Glu Val Glu Gly Gln Val Ser Gly Ser
 610 615 620
 Gln Val Ile Cys Ile Ser Pro Gly Pro Lys Asp Val Pro Val Ile Pro
 625 630 635 640
 Leu Asp Gln Asp Trp Phe Gly Leu Glu Leu Gln Leu Arg Ser Lys Glu
 645 650 655
 Thr Gly Lys Ile Phe Val Ser Thr Glu Phe Lys Phe Tyr Asn Cys Ser
 660 665 670
 Ala His Gln Leu Cys Leu Ser Cys Val Asn Ser Ala Phe Arg Cys His
 675 680 685
 Trp Cys Lys Tyr Arg Asn Leu Cys Thr His Asp Pro Thr Thr Cys Ser
 690 695 700
 Phe Gln Glu Gly Arg Ile Asn Ile Ser Glu Asp Cys Pro Gln Leu Val
 705 710 715 720
 Pro Thr Glu Glu Ile Leu Ile Pro Val Gly Glu Val Lys Pro Ile Thr
 725 730 735
 Leu Lys Ala Arg Asn Leu Pro Gln Pro Gln Ser Gly Gln Arg Gly Tyr
 740 745 750
 Glu Cys Val Leu Asn Ile Gln Gly Ala Ile His Arg Val Pro Ala Leu
 755 760 765
 Arg Phe Asn Ser Ser Ser Val Gln Cys Gln Asn Ser Ser Tyr Gln Tyr
 770 775 780
 Asp Gly Met Asp Ile Ser Asn Leu Ala Val Asp Phe Ala Val Val Trp
 785 790 795 800
 Asn Gly Asn Phe Ile Ile Asp Asn Pro Gln Asp Leu Lys Val His Leu
 805 810 815
 Tyr Lys Cys Ala Ala Gln Arg Glu Ser Cys Gly Leu Cys Leu Lys Ala
 820 825 830
 Asp Arg Lys Phe Glu Cys Gly Trp Cys Ser Gly Glu Arg Arg Cys Thr
 835 840 845
 Leu His Gln His Cys Thr Ser Pro Ser Ser Pro Trp Leu Asp Trp Ser
 850 855 860

Ser His Asn Val Lys Cys Ser Asn Pro Gln Ile Thr Glu Ile Leu Thr
 865 870 875 880
 Val Ser Gly Pro Pro Glu Gly Gly Thr Arg Val Thr Ile His Gly Val
 885 890 895
 Asn Leu Gly Leu Asp Phe Ser Glu Ile Ala His His Val Gln Val Ala
 900 905 910
 Gly Val Pro Cys Thr Pro Leu Pro Gly Glu Tyr Ile Ile Ala Glu Gln
 915 920 925
 Ile Val Cys Glu Met Gly His Ala Leu Val Gly Thr Thr Ser Gly Pro
 930 935 940
 Val Arg Leu Cys Ile Gly Glu Cys Lys Pro Glu Phe Met Thr Lys Ser
 945 950 955 960
 His Gln Gln Tyr Thr Phe Val Asn Pro Ser Val Leu Ser Leu Asn Pro
 965 970 975
 Ile Arg Gly Pro Glu Ser Gly Gly Thr Met Val Thr Ile Thr Gly His
 980 985 990
 Tyr Leu Gly Ala Gly Ser Ser Val Ala Val Tyr Leu Gly Asn Gln Thr
 995 1000 1005
 Cys Glu Phe Tyr Gly Arg Ser Met Ser Glu Ile Val Cys Val Ser
 1010 1015 1020
 Pro Pro Ser Ser Asn Gly Leu Gly Pro Val Pro Val Ser Val Ser
 1025 1030 1035
 Val Asp Arg Ala His Val Asp Ser Asn Leu Gln Phe Glu Tyr Ile
 1040 1045 1050
 Asp Asp Pro Arg Val Gln Arg Ile Glu Pro Glu Trp Ser Ile Ala
 1055 1060 1065
 Ser Gly His Thr Pro Leu Thr Ile Thr Gly Phe Asn Leu Asp Val
 1070 1075 1080
 Ile Gln Glu Pro Arg Ile Arg Val Lys Phe Asn Gly Lys Glu Ser
 1085 1090 1095
 Val Asn Val Cys Lys Val Val Asn Thr Thr Thr Leu Thr Cys Leu
 1100 1105 1110
 Ala Pro Ser Leu Thr Thr Asp Tyr Arg Pro Gly Leu Asp Thr Val
 1115 1120 1125

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Glu	Arg	Pro	Asp	Glu	Phe	Gly	Phe	Val	Phe	Asn	Asn	Val	Gln	Ser
	1130					1135					1140			
Leu	Leu	Ile	Tyr	Asn	Asp	Thr	Lys	Phe	Ile	Tyr	Tyr	Pro	Asn	Pro
	1145					1150					1155			
Thr	Phe	Glu	Leu	Leu	Ser	Pro	Thr	Gly	Val	Leu	Asp	Gln	Lys	Pro
	1160					1165					1170			
Gly	Ser	Pro	Ile	Ile	Leu	Lys	Gly	Lys	Asn	Leu	Cys	Pro	Pro	Ala
	1175					1180					1185			
Ser	Gly	Gly	Ala	Lys	Leu	Asn	Tyr	Thr	Val	Leu	Ile	Gly	Glu	Thr
	1190					1195					1200			
Pro	Cys	Ala	Val	Thr	Val	Ser	Glu	Thr	Gln	Leu	Leu	Cys	Glu	Pro
	1205					1210					1215			
Pro	Asn	Leu	Thr	Gly	Gln	His	Lys	Val	Met	Val	His	Val	Gly	Gly
	1220					1225					1230			
Met	Val	Phe	Ser	Pro	Gly	Ser	Val	Ser	Val	Ile	Ser	Asp	Ser	Leu
	1235					1240					1245			
Leu	Thr	Leu	Pro	Ala	Ile	Val	Ser	Ile	Ala	Ala	Gly	Gly	Ser	Leu
	1250					1255					1260			
Leu	Leu	Ile	Ile	Val	Ile	Ile	Val	Leu	Ile	Ala	Tyr	Lys	Arg	Lys
	1265					1270					1275			
Ser	Arg	Glu	Asn	Asp	Leu	Thr	Leu	Lys	Arg	Leu	Gln	Met	Gln	Met
	1280					1285					1290			
Asp	Asn	Leu	Glu	Ser	Arg	Val	Ala	Leu	Glu	Cys	Lys	Glu	Ala	Phe
	1295					1300					1305			
Ala	Glu	Leu	Gln	Thr	Asp	Ile	Asn	Glu	Leu	Thr	Ser	Asp	Leu	Asp
	1310					1315					1320			
Arg	Ser	Gly	Ile	Pro	Tyr	Leu	Asp	Tyr	Arg	Thr	Tyr	Ala	Met	Arg
	1325					1330					1335			
Val	Leu	Phe	Pro	Gly	Ile	Glu	Asp	His	Pro	Val	Leu	Arg	Glu	Leu
	1340					1345					1350			
Glu	Val	Gln	Gly	Asn	Gly	Gln	Gln	His	Val	Glu	Lys	Ala	Leu	Lys
	1355					1360					1365			
Leu	Phe	Ala	Gln	Leu	Ile	Asn	Asn	Lys	Val	Phe	Leu	Leu	Thr	Phe
	1370					1375					1380			

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Ile	Arg	Thr	Leu	Glu	Leu	Gln	Arg	Ser	Phe	Ser	Met	Arg	Asp	Arg
	1385					1390					1395			
Gly	Asn	Val	Ala	Ser	Leu	Ile	Met	Thr	Gly	Leu	Gln	Gly	Arg	Leu
	1400					1405					1410			
Glu	Tyr	Ala	Thr	Asp	Val	Leu	Lys	Gln	Leu	Leu	Ser	Asp	Leu	Ile
	1415					1420					1425			
Asp	Lys	Asn	Leu	Glu	Asn	Lys	Asn	His	Pro	Lys	Leu	Leu	Leu	Arg
	1430					1435					1440			
Arg	Thr	Glu	Ser	Val	Ala	Glu	Lys	Met	Leu	Thr	Asn	Trp	Phe	Ala
	1445					1450					1455			
Phe	Leu	Leu	His	Lys	Phe	Leu	Lys	Glu	Cys	Ala	Gly	Glu	Pro	Leu
	1460					1465					1470			
Phe	Met	Leu	Tyr	Cys	Ala	Ile	Lys	Gln	Gln	Met	Glu	Lys	Gly	Pro
	1475					1480					1485			
Ile	Asp	Ala	Ile	Thr	Gly	Glu	Ala	Arg	Tyr	Ser	Leu	Ser	Glu	Asp
	1490					1495					1500			
Lys	Leu	Ile	Arg	Gln	Gln	Ile	Glu	Tyr	Lys	Thr	Leu	Ile	Leu	Asn
	1505					1510					1515			
Cys	Val	Asn	Pro	Asp	Asn	Glu	Asn	Ser	Pro	Glu	Ile	Pro	Val	Lys
	1520					1525					1530			
Val	Leu	Asn	Cys	Asp	Thr	Ile	Thr	Gln	Val	Lys	Glu	Lys	Ile	Leu
	1535					1540					1545			
Asp	Ala	Val	Tyr	Lys	Asn	Val	Pro	Tyr	Ser	Gln	Arg	Pro	Arg	Ala
	1550					1555					1560			
Val	Asp	Met	Asp	Leu	Glu	Trp	Arg	Gln	Gly	Arg	Ile	Ala	Arg	Val
	1565					1570					1575			
Val	Leu	Gln	Asp	Glu	Asp	Ile	Thr	Thr	Lys	Ile	Glu	Gly	Asp	Trp
	1580					1585					1590			
Lys	Arg	Leu	Asn	Thr	Leu	Met	His	Tyr	Gln	Val	Ser	Asp	Arg	Ser
	1595					1600					1605			
Val	Val	Ala	Leu	Val	Pro	Lys	Gln	Thr	Ser	Ser	Tyr	Asn	Ile	Pro
	1610					1615					1620			
Ala	Ser	Ala	Ser	Ile	Ser	Arg	Thr	Ser	Ile	Ser	Arg	Tyr	Asp	Ser
	1625					1630					1635			

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Ser	Phe	Arg	Tyr	Thr	Gly	Ser	Pro	Asp	Ser	Leu	Arg	Ser	Arg	Ala
	1640					1645					1650			
Pro	Met	Ile	Thr	Pro	Asp	Leu	Glu	Ser	Gly	Val	Lys	Val	Trp	His
	1655					1660					1665			
Leu	Val	Lys	Asn	His	Asp	His	Gly	Asp	Gln	Lys	Glu	Gly	Asp	Arg
	1670					1675					1680			
Gly	Ser	Lys	Met	Val	Ser	Glu	Ile	Tyr	Leu	Thr	Arg	Leu	Leu	Ala
	1685					1690					1695			
Thr	Lys	Gly	Thr	Leu	Gln	Lys	Phe	Val	Asp	Asp	Leu	Phe	Glu	Thr
	1700					1705					1710			
Leu	Phe	Ser	Thr	Val	His	Arg	Gly	Ser	Ala	Leu	Pro	Leu	Ala	Ile
	1715					1720					1725			
Lys	Tyr	Met	Phe	Asp	Phe	Leu	Asp	Glu	Gln	Ala	Asp	Arg	His	Ser
	1730					1735					1740			
Ile	His	Asp	Thr	Asp	Val	Arg	His	Thr	Trp	Lys	Ser	Asn	Cys	Leu
	1745					1750					1755			
Pro	Leu	Arg	Phe	Trp	Val	Asn	Val	Ile	Lys	Asn	Pro	Gln	Phe	Val
	1760					1765					1770			
Phe	Asp	Ile	His	Lys	Gly	Ser	Ile	Thr	Asp	Ala	Cys	Leu	Ser	Val
	1775					1780					1785			
Val	Ala	Gln	Thr	Phe	Met	Asp	Ser	Cys	Ser	Thr	Ser	Glu	His	Arg
	1790					1795					1800			
Leu	Gly	Lys	Asp	Ser	Pro	Ser	Asn	Lys	Leu	Leu	Tyr	Ala	Lys	Asp
	1805					1810					1815			
Ile	Pro	Ser	Tyr	Lys	Ser	Trp	Val	Glu	Arg	Tyr	Tyr	Ala	Asp	Ile
	1820					1825					1830			
Ala	Lys	Leu	Pro	Ala	Ile	Ser	Asp	Gln	Asp	Met	Asn	Ala	Tyr	Leu
	1835					1840					1845			
Ala	Glu	Gln	Ser	Arg	Leu	His	Ala	Val	Glu	Phe	Asn	Met	Leu	Ser
	1850					1855					1860			
Ala	Leu	Asn	Glu	Ile	Tyr	Ser	Tyr	Val	Ser	Lys	Tyr	Ser	Glu	Glu
	1865					1870					1875			
Leu	Ile	Gly	Ala	Leu	Glu	Gln	Asp	Glu	Gln	Ala	Arg	Arg	Gln	Arg
	1880					1885					1890			

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Leu Ala Tyr Lys Val Glu Gln Leu Ile Asn Ala Met Ser Ile Glu
1895 1900 1905

Ser

5

<210> 100
<211> 1894
<212> PRT
<213> Humana

<400> 100

Met Glu Gln Arg Arg Pro Trp Pro Arg Ala Leu Glu Val Asp Ser Arg
1 5 10 15

Ser Val Val Leu Leu Ser Val Val Trp Val Leu Leu Ala Pro Pro Ala
20 25 30

Ala Gly Met Pro Gln Phe Ser Thr Phe His Ser Glu Asn Arg Asp Trp
35 40 45

Thr Phe Asn His Leu Thr Val His Gln Gly Thr Gly Ala Val Tyr Val
50 55 60

Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr Gly Asn Leu Thr Ile Gln
65 70 75 80

Val Ala His Lys Thr Gly Pro Glu Glu Asp Asn Lys Ser Cys Tyr Pro
85 90 95

Pro Leu Ile Val Gln Pro Cys Ser Glu Val Leu Thr Leu Thr Asn Asn
100 105 110

Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser Glu Asn Arg Leu Leu Ala
115 120 125

Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys Leu Leu Arg Leu Asp Asp
130 135 140

Leu Phe Ile Leu Val Glu Pro Ser His Lys Lys Glu His Tyr Leu Ser
145 150 155 160

Ser Val Asn Lys Thr Gly Thr Met Tyr Gly Val Ile Val Arg Ser Glu
165 170 175

Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr Ala Val Asp Gly Lys Gln
180 185 190

Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys Leu Pro Arg Asp Pro Glu
195 200 205

10

Ser Ser Ala Met Leu Asp Tyr Glu Leu His Ser Asp Phe Val Ser Ser

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210	215	220
Leu 225	Ile Lys Ile Pro Ser 230	Asp Thr Leu Ala Leu 235
		Val Ser His Phe Asp 240
Ile Phe Tyr Ile	Tyr 245	Gly Phe Ala Ser Gly 250
		Gly Phe Val Tyr Phe Leu 255
Thr Val Gln	Pro 260	Glu Thr Pro Glu Gly 265
		Val Ala Ile Asn Ser Ala Gly 270
Asp Leu Phe 275	Tyr Thr Ser Arg Ile 280	Val Arg Leu Cys Lys 285
		Asp Asp Pro
Lys Phe His Ser Tyr Val	Ser 295	Leu Pro Phe Gly Cys 300
		Thr Arg Ala Gly
Val 305	Glu Tyr Arg Leu Leu 310	Gln Ala Ala Tyr Leu 315
		Ala Lys Pro Gly Asp 320
Ser Leu Ala Gln	Ala 325	Phe Asn Ile Thr Ser 330
		Gln Asp Asp Val Leu Phe 335
Ala Ile Phe	Ser 340	Lys Gly Gln Lys Gln 345
		Tyr His His Pro Pro 350
Ser Ala Leu 355	Cys Ala Phe Pro Ile 360	Arg Ala Ile Asn Leu 365
		Gln Ile Lys
Glu Arg 370	Leu Gln Ser Cys Tyr 375	Gln Gly Glu Gly Asn 380
		Leu Glu Leu Asn
Trp 385	Leu Leu Gly Lys Asp 390	Val Gln Cys Thr Lys 395
		Ala Pro Val Pro Ile 400
Asp Asp Asn Phe	Cys 405	Gly Leu Asp Ile Asn 410
		Gln Pro Leu Gly Gly Ser 415
Thr Pro Val	Glu 420	Gly Leu Thr Leu Tyr 425
		Thr Thr Ser Arg Asp Arg Met 430
Thr Ser Val 435	Ala Ser Tyr Val Tyr 440	Asn Gly Tyr Ser Val 445
		Val Phe Val
Gly Thr 450	Lys Ser Gly Lys Leu 455	Lys Lys Ile Arg Ala Asp Gly Pro Pro 460
His 465	Gly Gly Val Gln Tyr 470	Glu Met Val Ser Val 475
		Leu Lys Asp Gly Ser 480
Pro Ile Leu Arg Asp Met Ala Phe Ser Ile Asp Gln Arg Tyr Leu Tyr		

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485								490				495			
Val	Met	Ser	Glu 500	Arg	Gln	Val	Thr	Arg 505	Val	Pro	Val	Glu	Ser 510	Cys	Glu
Gln	Tyr	Thr 515	Thr	Cys	Gly	Glu	Cys 520	Leu	Ser	Ser	Gly	Asp 525	Pro	His	Cys
Gly	Trp 530	Cys	Ala	Leu	His	Asn 535	Met	Cys	Ser	Arg	Arg 540	Asp	Lys	Cys	Gln
Gln	Ala	Trp	Glu	Pro	Asn 550	Arg	Phe	Ala	Ala	Ser 555	Ile	Ser	Gln	Cys	Val 560
Ser	Leu	Ala	Val	His 565	Pro	Ser	Ser	Ile	Ser 570	Val	Ser	Glu	His	Ser	Arg
Leu	Leu	Ser	Leu 580	Val	Val	Ser	Asp	Ala 585	Pro	Asp	Leu	Ser	Ala 590	Gly	Ile
Ala	Cys	Ala 595	Phe	Gly	Asn	Leu	Thr 600	Glu	Val	Glu	Gly	Gln 605	Val	Ser	Gly
Ser	Gln 610	Val	Ile	Cys	Ile	Ser 615	Pro	Gly	Pro	Lys	Asp 620	Val	Pro	Val	Ile
Pro	Leu	Asp	Gln	Asp	Trp 630	Phe	Gly	Leu	Glu	Leu 635	Gln	Leu	Arg	Ser	Lys 640
Glu	Thr	Gly	Lys	Ile 645	Phe	Val	Ser	Thr	Glu 650	Phe	Lys	Phe	Tyr	Asn 655	Cys
Ser	Ala	His	Gln 660	Leu	Cys	Leu	Ser	Cys 665	Val	Asn	Ser	Ala	Phe	Arg	Cys
His	Trp	Cys 675	Lys	Tyr	Arg	Asn	Leu 680	Cys	Thr	His	Asp 685	Pro	Thr	Thr	Cys
Ser	Phe 690	Gln	Glu	Gly	Arg	Ile 695	Asn	Ile	Ser	Glu	Asp 700	Cys	Pro	Gln	Leu
Val	Pro	Thr	Glu	Glu	Ile 710	Leu	Ile	Pro	Val	Gly 715	Glu	Val	Lys	Pro	Ile 720
Thr	Leu	Lys	Ala	Arg 725	Asn	Leu	Pro	Gln	Pro	Gln	Ser	Gly	Gln	Arg	Gly
Tyr	Glu	Cys	Val 740	Leu	Asn	Ile	Gln	Gly 745	Ala	Ile	His	Arg	Val 750	Pro	Ala
Leu	Arg	Phe	Asn	Ser	Ser	Ser	Val	Gln	Cys	Gln	Asn	Ser	Ser	Tyr	Gln

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755					760					765					
Tyr	Asp 770	Gly	Met	Asp	Ile	Ser 775	Asn	Leu	Ala	Val	Asp 780	Phe	Ala	Val	Val
Trp 785	Asn	Gly	Asn	Phe	Ile 790	Ile	Asp	Asn	Pro	Gln 795	Asp	Leu	Lys	Val	His 800
Leu	Tyr	Lys	Cys	Ala 805	Ala	Gln	Arg	Glu	Ser 810	Cys	Gly	Leu	Cys	Leu 815	Lys
Ala	Asp	Arg	Lys 820	Phe	Glu	Cys	Gly	Trp 825	Cys	Ser	Gly	Glu	Arg 830	Arg	Cys
Thr	Leu	His 835	Gln	His	Cys	Thr	Ser 840	Pro	Ser	Ser	Pro	Trp 845	Leu	Asp	Trp
Ser	Ser 850	His	Asn	Val	Lys	Cys 855	Ser	Asn	Pro	Gln	Ile 860	Thr	Glu	Ile	Leu
Thr 865	Val	Ser	Gly	Pro	Pro 870	Glu	Gly	Gly	Thr	Arg 875	Val	Thr	Ile	His	Gly 880
Val	Asn	Leu	Gly	Leu 885	Asp	Phe	Ser	Glu	Ile 890	Ala	His	His	Val	Gln 895	Val
Ala	Gly	Val	Pro 900	Cys	Thr	Pro	Leu	Pro 905	Gly	Glu	Tyr	Ile	Ile 910	Ala	Glu
Gln	Ile	Val 915	Cys	Glu	Met	Gly	His 920	Ala	Leu	Val	Gly	Thr 925	Thr	Ser	Gly
Pro	Val 930	Arg	Leu	Cys	Ile	Gly 935	Glu	Cys	Lys	Pro	Glu 940	Phe	Met	Thr	Lys
Ser 945	His	Gln	Gln	Tyr	Thr 950	Phe	Val	Asn	Pro	Ser 955	Val	Leu	Ser	Leu	Asn 960
Pro	Ile	Arg	Gly	Pro 965	Glu	Ser	Gly	Gly	Thr 970	Met	Val	Thr	Ile	Thr 975	Gly
His	Tyr	Leu	Gly 980	Ala	Gly	Ser	Ser	Val 985	Ala	Val	Tyr	Leu	Gly 990	Asn	Gln
Thr	Cys	Glu 995	Phe	Tyr	Gly	Arg	Ser 1000	Met	Ser	Glu	Ile	Val 1005	Cys	Val	Ser
Pro	Pro 1010	Ser	Ser	Asn	Gly	Leu 1015	Gly	Pro	Val	Pro	Val 1020	Ser	Val	Ser	
Val	Asp	Arg	Ala	His	Val	Asp	Ser	Asn	Leu	Gln	Phe	Glu	Tyr	Ile	

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1025	1030	1035
Asp Asp 1040	Pro Arg Val Gln Arg 1045	Ile Glu Pro Glu Trp 1050
Ser Gly 1055	His Thr Pro Leu Thr 1060	Ile Thr Gly Phe Asn 1065
Ile Gln 1070	Glu Pro Arg Ile Arg 1075	Val Lys Phe Asn Gly 1080
Val Asn 1085	Val Cys Lys Val Val 1090	Asn Thr Thr Thr Leu 1095
Ala Pro 1100	Ser Leu Thr Thr Asp 1105	Tyr Arg Pro Gly Leu 1110
Glu Arg 1115	Pro Asp Glu Phe Gly 1120	Phe Val Phe Asn Asn 1125
Leu Leu 1130	Ile Tyr Asn Asp Thr 1135	Lys Phe Ile Tyr Tyr 1140
Thr Phe 1145	Glu Leu Leu Ser Pro 1150	Thr Gly Val Leu Asp 1155
Gly Ser 1160	Pro Ile Ile Leu Lys 1165	Gly Lys Asn Leu Cys 1170
Ser Gly 1175	Gly Ala Lys Leu Asn 1180	Tyr Thr Val Leu Ile 1185
Pro Cys 1190	Ala Val Thr Val Ser 1195	Glu Thr Gln Leu Leu 1200
Pro Asn 1205	Leu Thr Gly Gln His 1210	Lys Val Met Val His 1215
Met Val 1220	Phe Ser Pro Gly Ser 1225	Val Ser Val Ile Ser 1230
Leu Thr 1235	Leu Pro Ala Ile Val 1240	Ser Ile Ala Ala Gly 1245
Leu Leu 1250	Ile Ile Val Ile Ile 1255	Val Leu Ile Ala Tyr 1260
Ser Arg 1265	Glu Asn Asp Leu Thr 1270	Leu Lys Arg Leu Gln 1275
Asp Asn	Leu Glu Ser Arg Val	Ala Leu Glu Cys Lys
		Glu Ala Phe

1280						1285						1290		
Ala	Glu	Leu	Gln	Thr	Asp	Ile	Asn	Glu	Leu	Thr	Ser	Asp	Leu	Asp
	1295					1300					1305			
Arg	Ser	Gly	Ile	Pro	Tyr	Leu	Asp	Tyr	Arg	Thr	Tyr	Ala	Met	Arg
	1310					1315					1320			
Val	Leu	Phe	Pro	Gly	Ile	Glu	Asp	His	Pro	Val	Leu	Arg	Glu	Leu
	1325					1330					1335			
Glu	Val	Gln	Gly	Asn	Gly	Gln	Gln	His	Val	Glu	Lys	Ala	Leu	Lys
	1340					1345					1350			
Leu	Phe	Ala	Gln	Leu	Ile	Asn	Asn	Lys	Val	Phe	Leu	Leu	Thr	Phe
	1355					1360					1365			
Ile	Arg	Thr	Leu	Glu	Leu	Gln	Arg	Ser	Phe	Ser	Met	Arg	Asp	Arg
	1370					1375					1380			
Gly	Asn	Val	Ala	Ser	Leu	Ile	Met	Thr	Gly	Leu	Gln	Gly	Arg	Leu
	1385					1390					1395			
Glu	Tyr	Ala	Thr	Asp	Val	Leu	Lys	Gln	Leu	Leu	Ser	Asp	Leu	Ile
	1400					1405					1410			
Asp	Lys	Asn	Leu	Glu	Asn	Lys	Asn	His	Pro	Lys	Leu	Leu	Leu	Arg
	1415					1420					1425			
Arg	Thr	Glu	Ser	Val	Ala	Glu	Lys	Met	Leu	Thr	Asn	Trp	Phe	Ala
	1430					1435					1440			
Phe	Leu	Leu	His	Lys	Phe	Leu	Lys	Glu	Cys	Ala	Gly	Glu	Pro	Leu
	1445					1450					1455			
Phe	Met	Leu	Tyr	Cys	Ala	Ile	Lys	Gln	Gln	Met	Glu	Lys	Gly	Pro
	1460					1465					1470			
Ile	Asp	Ala	Ile	Thr	Gly	Glu	Ala	Arg	Tyr	Ser	Leu	Ser	Glu	Asp
	1475					1480					1485			
Lys	Leu	Ile	Arg	Gln	Gln	Ile	Glu	Tyr	Lys	Thr	Leu	Ile	Leu	Asn
	1490					1495					1500			
Cys	Val	Asn	Pro	Asp	Asn	Glu	Asn	Ser	Pro	Glu	Ile	Pro	Val	Lys
	1505					1510					1515			
Val	Leu	Asn	Cys	Asp	Thr	Ile	Thr	Gln	Val	Lys	Glu	Lys	Ile	Leu
	1520					1525					1530			
Asp	Ala	Val	Tyr	Lys	Asn	Val	Pro	Tyr	Ser	Gln	Arg	Pro	Arg	Ala

1535		1540		1545
Val Asp 1550	Met Asp Leu Glu	Trp 1555	Arg Gln Gly Arg	Ile 1560 Ala Arg Val
Val Leu 1565	Gln Asp Glu Asp	Ile 1570	Thr Thr Lys Ile	Glu 1575 Gly Asp Trp
Lys Arg 1580	Leu Asn Thr Leu	Met 1585	His Tyr Gln Val	Ser 1590 Asp Arg Ser
Val Val 1595	Ala Leu Val Pro	Lys 1600	Gln Thr Ser Ser	Tyr 1605 Asn Ile Pro
Ala Ser 1610	Ala Ser Ile Ser	Arg 1615	Thr Ser Ile Ser	Arg 1620 Tyr Asp Ser
Ser Phe 1625	Arg Tyr Thr Gly	Ser 1630	Pro Asp Ser Leu	Arg 1635 Ser Arg Ala
Pro Met 1640	Ile Thr Pro Asp	Leu 1645	Glu Ser Gly Val	Lys 1650 Val Trp His
Leu Val 1655	Lys Asn His Asp	His 1660	Gly Asp Gln Lys	Glu 1665 Gly Asp Arg
Gly Ser 1670	Lys Met Val Ser	Glu 1675	Ile Tyr Leu Thr	Arg 1680 Leu Leu Ala
Thr Lys 1685	Gly Thr Leu Gln	Lys 1690	Phe Val Asp Asp	Leu 1695 Phe Glu Thr
Leu Phe 1700	Ser Thr Val His	Arg 1705	Gly Ser Ala Leu	Pro 1710 Leu Ala Ile
Lys Tyr 1715	Met Phe Asp Phe	Leu 1720	Asp Glu Gln Ala	Asp 1725 Arg His Ser
Ile His 1730	Asp Thr Asp Val	Arg 1735	His Thr Trp Lys	Ser 1740 Asn Cys Leu
Pro Leu 1745	Arg Phe Trp Val	Asn 1750	Val Ile Lys Asn	Pro 1755 Gln Phe Val
Phe Asp 1760	Ile His Lys Gly	Ser 1765	Ile Thr Asp Ala	Cys 1770 Leu Ser Val
Val Ala 1775	Gln Thr Phe Met	Asp 1780	Ser Cys Ser Thr	Ser 1785 Glu His Arg
Leu Gly	Lys Asp Ser Pro Ser	Asn Lys Leu Leu Tyr	Ala Lys Asp	

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1790 1795 1800

Ile Pro Ser Tyr Lys Ser Trp Val Glu Arg Tyr Tyr Ala Asp Ile
1805 1810 1815

Ala Lys Leu Pro Ala Ile Ser Asp Gln Asp Met Asn Ala Tyr Leu
1820 1825 1830

Ala Glu Gln Ser Arg Leu His Ala Val Glu Phe Asn Met Leu Ser
1835 1840 1845

Ala Leu Asn Glu Ile Tyr Ser Tyr Val Ser Lys Tyr Ser Glu Glu
1850 1855 1860

Leu Ile Gly Ala Leu Glu Gln Asp Glu Gln Ala Arg Arg Gln Arg
1865 1870 1875

Leu Ala Tyr Lys Val Glu Gln Leu Ile Asn Ala Met Ser Ile Glu
1880 1885 1890

Ser

<210> 101
<211> 720
<212> PRT
<213> Humana

<400> 101

Met Pro Pro Pro Ser Asp Ile Val Lys Val Ala Ile Glu Trp Pro Gly
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Ala Asn Ala Gln Leu Leu Glu Ile Asp Gln Lys Arg Pro Leu Ala Ser
20 25 30

Ile Ile Lys Glu Val Cys Asp Gly Trp Ser Leu Pro Asn Pro Glu Tyr
35 40 45

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

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

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

Met Glu Thr Arg Leu Asp Ala Met Lys Glu Leu Ala Lys Leu Ser Ala
100 105 110

Asp Val Thr Phe Ala Thr Glu Phe Ile Asn Met Asp Gly Ile Ile Val
115 120 125

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Leu Thr Arg Leu Val Glu Ser Gly Thr Lys Leu Leu Ser His Tyr Ser
 130 135 140
 Glu Met Leu Ala Phe Thr Leu Thr Ala Phe Leu Glu Leu Met Asp His
 145 150 155 160
 Gly Ile Val Ser Trp Asp Met Val Ser Ile Thr Phe Ile Lys Gln Ile
 165 170 175
 Ala Gly Tyr Val Ser Gln Pro Met Val Asp Val Ser Ile Leu Gln Arg
 180 185 190
 Ser Leu Ala Ile Leu Glu Ser Met Val Leu Asn Ser Gln Ser Leu Tyr
 195 200 205
 Gln Lys Ile Ala Glu Glu Ile Thr Val Gly Gln Leu Ile Ser His Leu
 210 215 220
 Gln Val Ser Asn Gln Glu Ile Gln Thr Tyr Ala Ile Ala Leu Ile Asn
 225 230 235 240
 Ala Leu Phe Leu Lys Ala Pro Glu Asp Lys Arg Gln Asp Met Ala Asn
 245 250 255
 Ala Phe Ala Gln Lys His Leu Arg Ser Ile Ile Leu Asn His Val Ile
 260 265 270
 Arg Gly Asn Arg Pro Ile Lys Thr Glu Met Ala His Gln Leu Tyr Val
 275 280 285
 Leu Gln Val Leu Thr Phe Asn Leu Leu Glu Glu Arg Met Met Thr Lys
 290 295 300
 Met Asp Pro Asn Asp Gln Ala Gln Arg Asp Ile Ile Phe Glu Leu Arg
 305 310 315 320
 Arg Ile Ala Phe Asp Ala Glu Ser Asp Pro Ser Asn Ala Pro Gly Ser
 325 330 335
 Gly Thr Glu Lys Arg Lys Ala Met Tyr Thr Lys Asp Tyr Lys Met Leu
 340 345 350
 Gly Phe Thr Asn His Ile Asn Pro Ala Met Asp Phe Thr Gln Thr Pro
 355 360 365
 Pro Gly Met Leu Ala Leu Asp Asn Met Leu Tyr Leu Ala Lys Val His
 370 375 380
 Gln Asp Thr Tyr Ile Arg Ile Val Leu Glu Asn Ser Ser Arg Glu Asp
 385 390 395 400

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Lys His Glu Cys Pro Phe Gly Arg Ser Ala Ile Glu Leu Thr Lys Met
 405 410 415
 Leu Cys Glu Ile Leu Gln Val Gly Glu Leu Pro Asn Glu Gly Arg Asn
 420 425 430
 Asp Tyr His Pro Met Phe Phe Thr His Asp Arg Ala Phe Glu Glu Leu
 435 440 445
 Phe Gly Ile Cys Ile Gln Leu Leu Asn Lys Thr Trp Lys Glu Met Arg
 450 455 460
 Ala Thr Ala Glu Asp Phe Asn Lys Val Met Gln Val Val Arg Glu Gln
 465 470 475 480
 Ile Thr Arg Ala Leu Pro Ser Lys Pro Asn Ser Leu Asp Gln Phe Lys
 485 490 495
 Ser Lys Leu Arg Ser Leu Ser Tyr Ser Glu Ile Leu Arg Leu Arg Gln
 500 505 510
 Ser Glu Arg Met Ser Gln Asp Asp Phe Gln Ser Pro Pro Ile Val Glu
 515 520 525
 Leu Arg Glu Lys Ile Gln Pro Glu Ile Leu Glu Leu Ile Lys Gln Gln
 530 535 540
 Arg Leu Asn Arg Leu Cys Glu Gly Ser Ser Phe Arg Lys Ile Gly Asn
 545 550 555 560
 Arg Arg Arg Gln Glu Arg Phe Trp Tyr Cys Arg Leu Ala Leu Asn His
 565 570 575
 Lys Val Leu His Tyr Gly Asp Leu Asp Asp Asn Pro Gln Gly Glu Val
 580 585 590
 Thr Phe Glu Ser Leu Gln Glu Lys Ile Pro Val Ala Asp Ile Lys Ala
 595 600 605
 Ile Val Thr Gly Lys Asp Cys Pro His Met Lys Glu Lys Ser Ala Leu
 610 615 620
 Lys Gln Asn Lys Glu Val Leu Glu Leu Ala Phe Ser Ile Leu Tyr Asp
 625 630 635 640
 Pro Asp Glu Thr Leu Asn Phe Ile Ala Pro Asn Lys Tyr Glu Tyr Cys
 645 650 655
 Ile Trp Ile Asp Gly Leu Ser Ala Leu Leu Gly Lys Asp Met Ser Ser
 660 665 670

Glu Leu Thr Lys Ser Asp Leu Asp Thr Leu Leu Ser Met Glu Met Lys
675 680 685

Leu Arg Leu Leu Asp Leu Glu Asn Ile Gln Ile Pro Glu Ala Pro Pro
690 695 700

Pro Ile Pro Lys Glu Pro Ser Ser Tyr Asp Phe Val Tyr His Tyr Gly
705 710 715 720

<210> 102

<211> 720

<212> PRT

<213> Humana

<400> 102

Met Pro Pro Pro Ser Asp Ile Val Lys Val Ala Ile Glu Trp Pro Gly
1 5 10 15

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

Ile Ile Lys Glu Val Cys Asp Gly Trp Ser Leu Pro Asn Pro Glu Tyr
35 40 45

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

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

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

Met Glu Thr Arg Leu Asp Ala Met Lys Glu Leu Ala Lys Leu Ser Ala
100 105 110

Asp Val Thr Phe Ala Thr Glu Phe Ile Asn Met Asp Gly Ile Ile Val
115 120 125

Leu Thr Arg Leu Val Glu Ser Gly Thr Lys Leu Leu Ser His Tyr Ser
130 135 140

Glu Met Leu Ala Phe Thr Leu Thr Ala Phe Leu Glu Leu Met Asp His
145 150 155 160

Gly Ile Val Ser Trp Asp Met Val Ser Ile Thr Phe Ile Lys Gln Ile
165 170 175

Ala Gly Tyr Val Ser Gln Pro Met Val Asp Val Ser Ile Leu Gln Arg
180 185 190

5

10

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Ser Leu Ala Ile Leu Glu Ser Met Val Leu Asn Ser Gln Ser Leu Tyr
 195 200 205
 Gln Lys Ile Ala Glu Glu Ile Thr Val Gly Gln Leu Ile Ser His Leu
 210 215 220
 Gln Val Ser Asn Gln Glu Ile Gln Thr Tyr Ala Ile Ala Leu Ile Asn
 225 230 235 240
 Ala Leu Phe Leu Lys Ala Pro Glu Asp Lys Arg Gln Asp Met Ala Asn
 245 250 255
 Ala Phe Ala Gln Lys His Leu Arg Ser Ile Ile Leu Asn His Val Ile
 260 265 270
 Arg Gly Asn Arg Pro Ile Lys Thr Glu Met Ala His Gln Leu Tyr Val
 275 280 285
 Leu Gln Val Leu Thr Phe Asn Leu Leu Glu Glu Arg Met Met Thr Lys
 290 295 300
 Met Asp Pro Asn Asp Gln Ala Gln Arg Asp Ile Ile Phe Glu Leu Arg
 305 310 315 320
 Arg Ile Ala Phe Asp Ala Glu Ser Asp Pro Ser Asn Ala Pro Gly Ser
 325 330 335
 Gly Thr Glu Lys Arg Lys Ala Met Tyr Thr Lys Asp Tyr Lys Met Leu
 340 345 350
 Gly Phe Thr Asn His Ile Asn Pro Ala Met Asp Phe Thr Gln Thr Pro
 355 360 365
 Pro Gly Met Leu Ala Leu Asp Asn Met Leu Tyr Leu Ala Lys Val His
 370 375 380
 Gln Asp Thr Tyr Ile Arg Ile Val Leu Glu Asn Ser Ser Arg Glu Asp
 385 390 395 400
 Lys His Glu Cys Pro Phe Gly Arg Ser Ala Ile Glu Leu Thr Lys Met
 405 410 415
 Leu Cys Glu Ile Leu Gln Val Gly Glu Leu Pro Asn Glu Gly Arg Asn
 420 425 430
 Asp Tyr His Pro Met Phe Phe Thr His Asp Arg Ala Phe Glu Glu Leu
 435 440 445
 Phe Gly Ile Cys Ile Gln Leu Leu Asn Lys Thr Trp Lys Glu Met Arg
 450 455 460

ES 2 671 895 T3

Ala Thr Ala Glu Asp Phe Asn Lys Val Met Gln Val Val Arg Glu Gln
465 470 475 480

Ile Thr Arg Ala Leu Pro Ser Lys Pro Asn Ser Leu Asp Gln Phe Lys
485 490 495

Ser Lys Leu Arg Ser Leu Ser Tyr Ser Glu Ile Leu Arg Leu Arg Gln
500 505 510

Ser Glu Arg Met Ser Gln Asp Asp Phe Gln Ser Pro Pro Ile Val Glu
515 520 525

Leu Arg Glu Lys Ile Gln Pro Glu Ile Leu Glu Leu Ile Lys Gln Gln
530 535 540

Arg Leu Asn Arg Leu Cys Glu Gly Ser Ser Phe Arg Lys Ile Gly Asn
545 550 555 560

Arg Arg Arg Gln Glu Arg Phe Trp Tyr Cys Arg Leu Ala Leu Asn His
565 570 575

Lys Val Leu His Tyr Gly Asp Leu Asp Asp Asn Pro Gln Gly Glu Val
580 585 590

Thr Phe Glu Ser Leu Gln Glu Lys Ile Pro Val Ala Asp Ile Lys Ala
595 600 605

Ile Val Thr Gly Lys Asp Cys Pro His Met Lys Glu Lys Ser Ala Leu
610 615 620

Lys Gln Asn Lys Glu Val Leu Glu Leu Ala Phe Ser Ile Leu Tyr Asp
625 630 635 640

Pro Asp Glu Thr Leu Asn Phe Ile Ala Pro Asn Lys Tyr Glu Tyr Cys
645 650 655

Ile Trp Ile Asp Gly Leu Ser Ala Leu Leu Gly Lys Asp Met Ser Ser
660 665 670

Glu Leu Thr Lys Ser Asp Leu Asp Thr Leu Leu Ser Met Glu Met Lys
675 680 685

Leu Arg Leu Leu Asp Leu Glu Asn Ile Gln Ile Pro Glu Ala Pro Pro
690 695 700

Pro Ile Pro Lys Glu Pro Ser Ser Tyr Asp Phe Val Tyr His Tyr Gly
705 710 715 720

<210> 103
<211> 718
<212> PRT
<213> Humana

ES 2 671 895 T3

<400> 103

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Met Pro Pro Pro Ser Asp Ile Val Lys Val Ala Ile Glu Trp Pro Gly
1      5      10      15
Ala Asn Ala Gln Leu Leu Glu Ile Asp Gln Lys Arg Pro Leu Ala Ser
20      25      30
Ile Ile Lys Glu Val Cys Asp Gly Trp Ser Leu Pro Asn Pro Glu Tyr
35      40      45
Tyr Thr Leu Arg Tyr Ala Asp Gly Pro Gln Leu Tyr Ile Thr Glu Gln
50      55      60
Thr Arg Ser Asp Ile Lys Asn Gly Thr Ile Leu Gln Leu Ala Ile Ser
65      70      75      80
Pro Ser Arg Ala Ala Arg Gln Leu Met Glu Arg Thr Gln Ser Ser Asn
85      90      95
Met Glu Thr Arg Leu Asp Ala Met Lys Glu Leu Ala Lys Leu Ser Ala
100     105     110
Asp Val Thr Phe Ala Thr Glu Phe Ile Asn Met Asp Gly Ile Ile Val
115     120     125
Leu Thr Arg Leu Val Glu Ser Gly Thr Lys Leu Leu Ser His Glu Met
130     135     140
Leu Ala Phe Thr Leu Thr Ala Phe Leu Glu Leu Met Asp His Gly Ile
145     150     155     160
Val Ser Trp Asp Met Val Ser Ile Thr Phe Ile Lys Gln Ile Ala Gly
165     170     175
Tyr Val Ser Gln Pro Met Val Asp Val Ser Ile Leu Gln Arg Ser Leu
180     185     190
Ala Ile Leu Glu Ser Met Val Leu Asn Ser Gln Ser Leu Tyr Gln Lys
195     200     205
Ile Ala Glu Glu Ile Thr Val Gly Gln Leu Ile Ser His Leu Gln Val
210     215     220
Ser Asn Gln Glu Ile Gln Thr Tyr Ala Ile Ala Leu Ile Asn Ala Leu
225     230     235     240
Phe Leu Lys Ala Pro Glu Asp Lys Arg Gln Asp Met Ala Asn Ala Phe
245     250     255

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Ala Gln Lys His Leu Arg Ser Ile Ile Leu Asn His Val Ile Arg Gly
 260 265 270
 Asn Arg Pro Ile Lys Thr Glu Met Ala His Gln Leu Tyr Val Leu Gln
 275 280 285
 Val Leu Thr Phe Asn Leu Leu Glu Glu Arg Met Met Thr Lys Met Asp
 290 295 300
 Pro Asn Asp Gln Ala Gln Arg Asp Ile Ile Phe Glu Leu Arg Arg Ile
 305 310 315 320
 Ala Phe Asp Ala Glu Ser Asp Pro Ser Asn Ala Pro Gly Ser Gly Thr
 325 330 335
 Glu Lys Arg Lys Ala Met Tyr Thr Lys Asp Tyr Lys Met Leu Gly Phe
 340 345 350
 Thr Asn His Ile Asn Pro Ala Met Asp Phe Thr Gln Thr Pro Pro Gly
 355 360 365
 Met Leu Ala Leu Asp Asn Met Leu Tyr Leu Ala Lys Val His Gln Asp
 370 375 380
 Thr Tyr Ile Arg Ile Val Leu Glu Asn Ser Ser Arg Glu Asp Lys His
 385 390 395 400
 Glu Cys Pro Phe Gly Arg Ser Ala Ile Glu Leu Thr Lys Met Leu Cys
 405 410 415
 Glu Ile Leu Gln Val Gly Glu Leu Pro Asn Glu Gly Arg Asn Asp Tyr
 420 425 430
 His Pro Met Phe Phe Thr His Asp Arg Ala Phe Glu Glu Leu Phe Gly
 435 440 445
 Ile Cys Ile Gln Leu Leu Asn Lys Thr Trp Lys Glu Met Arg Ala Thr
 450 455 460
 Ala Glu Asp Phe Asn Lys Val Met Gln Val Val Arg Glu Gln Ile Thr
 465 470 475 480
 Arg Ala Leu Pro Ser Lys Pro Asn Ser Leu Asp Gln Phe Lys Ser Lys
 485 490 495
 Leu Arg Ser Leu Ser Tyr Ser Glu Ile Leu Arg Leu Arg Gln Ser Glu
 500 505 510
 Arg Met Ser Gln Asp Asp Phe Gln Ser Pro Pro Ile Val Glu Leu Arg
 515 520 525

ES 2 671 895 T3

Glu Lys Ile Gln Pro Glu Ile Leu Glu Leu Ile Lys Gln Gln Arg Leu
 530 535 540
 Asn Arg Leu Cys Glu Gly Ser Ser Phe Arg Lys Ile Gly Asn Arg Arg
 545 550 555 560
 Arg Gln Glu Arg Phe Trp Tyr Cys Arg Leu Ala Leu Asn His Lys Val
 565 570 575
 Leu His Tyr Gly Asp Leu Asp Asp Asn Pro Gln Gly Glu Val Thr Phe
 580 585 590
 Glu Ser Leu Gln Glu Lys Ile Pro Val Ala Asp Ile Lys Ala Ile Val
 595 600 605
 Thr Gly Lys Asp Cys Pro His Met Lys Glu Lys Ser Ala Leu Lys Gln
 610 615 620
 Asn Lys Glu Val Leu Glu Leu Ala Phe Ser Ile Leu Tyr Asp Pro Asp
 625 630 635 640
 Glu Thr Leu Asn Phe Ile Ala Pro Asn Lys Tyr Glu Tyr Cys Ile Trp
 645 650 655
 Ile Asp Gly Leu Ser Ala Leu Leu Gly Lys Asp Met Ser Ser Glu Leu
 660 665 670
 Thr Lys Ser Asp Leu Asp Thr Leu Leu Ser Met Glu Met Lys Leu Arg
 675 680 685
 Leu Leu Asp Leu Glu Asn Ile Gln Ile Pro Glu Ala Pro Pro Pro Ile
 690 695 700
 Pro Lys Glu Pro Ser Ser Tyr Asp Phe Val Tyr His Tyr Gly
 705 710 715

<210> 104
 <211> 632
 <212> PRT
 <213> Humana
 <400> 104

Met Glu Arg Thr Gln Ser Ser Asn Met Glu Thr Arg Leu Asp Ala Met
 1 5 10 15
 Lys Glu Leu Ala Lys Leu Ser Ala Asp Val Thr Phe Ala Thr Glu Phe
 20 25 30
 Ile Asn Met Asp Gly Ile Ile Val Leu Thr Arg Leu Val Glu Ser Gly
 35 40 45
 Thr Lys Leu Leu Ser His Tyr Ser Glu Met Leu Ala Phe Thr Leu Thr

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50		55		60											
Ala 65	Phe	Leu	Glu	Leu	Met 70	Asp	His	Gly	Ile	Val 75	Ser	Trp	Asp	Met	Val 80
Ser	Ile	Thr	Phe	Ile 85	Lys	Gln	Ile	Ala	Gly 90	Tyr	Val	Ser	Gln	Pro	Met 95
Val	Asp	Val	Ser 100	Ile	Leu	Gln	Arg	Ser 105	Leu	Ala	Ile	Leu	Glu 110	Ser	Met
Val	Leu	Asn 115	Ser	Gln	Ser	Leu	Tyr 120	Gln	Lys	Ile	Ala	Glu 125	Glu	Ile	Thr
Val	Gly 130	Gln	Leu	Ile	Ser	His 135	Leu	Gln	Val	Ser	Asn 140	Gln	Glu	Ile	Gln
Thr 145	Tyr	Ala	Ile	Ala	Leu 150	Ile	Asn	Ala	Leu	Phe 155	Leu	Lys	Ala	Pro	Glu 160
Asp	Lys	Arg	Gln	Asp 165	Met	Ala	Asn	Ala	Phe 170	Ala	Gln	Lys	His	Leu 175	Arg
Ser	Ile	Ile	Leu 180	Asn	His	Val	Ile	Arg 185	Gly	Asn	Arg	Pro	Ile 190	Lys	Thr
Glu	Met	Ala 195	His	Gln	Leu	Tyr	Val 200	Leu	Gln	Val	Leu	Thr 205	Phe	Asn	Leu
Leu	Glu 210	Glu	Arg	Met	Met	Thr 215	Lys	Met	Asp	Pro	Asn 220	Asp	Gln	Ala	Gln
Arg 225	Asp	Ile	Ile	Phe	Glu 230	Leu	Arg	Arg	Ile	Ala 235	Phe	Asp	Ala	Glu	Ser 240
Asp	Pro	Ser	Asn	Ala 245	Pro	Gly	Ser	Gly	Thr 250	Glu	Lys	Arg	Lys	Ala 255	Met
Tyr	Thr	Lys	Asp 260	Tyr	Lys	Met	Leu	Gly 265	Phe	Thr	Asn	His	Ile 270	Asn	Pro
Ala	Met	Asp 275	Phe	Thr	Gln	Thr	Pro 280	Pro	Gly	Met	Leu	Ala 285	Leu	Asp	Asn
Met	Leu 290	Tyr	Leu	Ala	Lys	Val 295	His	Gln	Asp	Thr	Tyr 300	Ile	Arg	Ile	Val
Leu 305	Glu	Asn	Ser	Ser	Arg 310	Glu	Asp	Lys	His	Glu 315	Cys	Pro	Phe	Gly	Arg 320
Ser	Ala	Ile	Glu	Leu	Thr	Lys	Met	Leu	Cys	Glu	Ile	Leu	Gln	Val	Gly

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325																330																335															
Glu	Leu	Pro	Asn	Glu	Gly	Arg	Asn	Asp	Tyr	His	Pro	Met	Phe	Phe	Thr																																
			340																																												
His	Asp	Arg	Ala	Phe	Glu	Glu	Leu	Phe	Gly	Ile	Cys	Ile	Gln	Leu	Leu																																
		355																																													
Asn	Lys	Thr	Trp	Lys	Glu	Met	Arg	Ala	Thr	Ala	Glu	Asp	Phe	Asn	Lys																																
		370																																													
Val	Met	Gln	Val	Val	Arg	Glu	Gln	Ile	Thr	Arg	Ala	Leu	Pro	Ser	Lys																																
			385																																												
Pro	Asn	Ser	Leu	Asp	Gln	Phe	Lys	Ser	Lys	Leu	Arg	Ser	Leu	Ser	Tyr																																
				405																																											
Ser	Glu	Ile	Leu	Arg	Leu	Arg	Gln	Ser	Glu	Arg	Met	Ser	Gln	Asp	Asp																																
			420																																												
Phe	Gln	Ser	Pro	Pro	Ile	Val	Glu	Leu	Arg	Glu	Lys	Ile	Gln	Pro	Glu																																
		435																																													
Ile	Leu	Glu	Leu	Ile	Lys	Gln	Gln	Arg	Leu	Asn	Arg	Leu	Cys	Glu	Gly																																
		450																																													
Ser	Ser	Phe	Arg	Lys	Ile	Gly	Asn	Arg	Arg	Arg	Gln	Glu	Arg	Phe	Trp																																
			465																																												
Tyr	Cys	Arg	Leu	Ala	Leu	Asn	His	Lys	Val	Leu	His	Tyr	Gly	Asp	Leu																																
				485																																											
Asp	Asp	Asn	Pro	Gln	Gly	Glu	Val	Thr	Phe	Glu	Ser	Leu	Gln	Glu	Lys																																
			500																																												
Ile	Pro	Val	Ala	Asp	Ile	Lys	Ala	Ile	Val	Thr	Gly	Lys	Asp	Cys	Pro																																
		515																																													
His	Met	Lys	Glu	Lys	Ser	Ala	Leu	Lys	Gln	Asn	Lys	Glu	Val	Leu	Glu																																
			530																																												
Leu	Ala	Phe	Ser	Ile	Leu	Tyr	Asp	Pro	Asp	Glu	Thr	Leu	Asn	Phe	Ile																																
		545																																													
Ala	Pro	Asn	Lys	Tyr	Glu	Tyr	Cys	Ile	Trp	Ile	Asp	Gly	Leu	Ser	Ala																																
			565																																												
Leu	Leu	Gly	Lys	Asp	Met	Ser	Ser	Glu	Leu	Thr	Lys	Ser	Asp	Leu	Asp																																
		580																																													
Thr	Leu	Leu	Ser	Met	Glu	Met	Lys	Leu	Arg	Leu	Leu	Asp	Leu	Glu	Asn																																

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595

600

605

Ile Gln Ile Pro Glu Ala Pro Pro Pro Ile Pro Lys Glu Pro Ser Ser
610 615 620

Tyr Asp Phe Val Tyr His Tyr Gly
625 630

<210> 105

<211> 463

<212> PRT

<213> Humana

<400> 105

Met Ala Ala Leu Arg Ala Leu Cys Gly Phe Arg Gly Val Ala Ala Gln
1 5 10 15

Val Leu Arg Pro Gly Ala Gly Val Arg Leu Pro Ile Gln Pro Ser Arg
20 25 30

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

Gly Ala Val Met Tyr Pro Ser Lys Glu Thr Ala His Trp Lys Pro Pro
50 55 60

Pro Trp Asn Asp Val Asp Pro Pro Lys Asp Thr Ile Val Lys Asn Ile
65 70 75 80

Thr Leu Asn Phe Gly Pro Gln His Pro Ala Ala His Gly Val Leu Arg
85 90 95

Leu Val Met Glu Leu Ser Gly Glu Met Val Arg Lys Cys Asp Pro His
100 105 110

Ile Gly Leu Leu His Arg Gly Thr Glu Lys Leu Ile Glu Tyr Lys Thr
115 120 125

Tyr Leu Gln Ala Leu Pro Tyr Phe Asp Arg Leu Asp Tyr Val Ser Met
130 135 140

Met Cys Asn Glu Gln Ala Tyr Ser Leu Ala Val Glu Lys Leu Leu Asn
145 150 155 160

Ile Arg Pro Pro Pro Arg Ala Gln Trp Ile Arg Val Leu Phe Gly Glu
165 170 175

Ile Thr Arg Leu Leu Asn His Ile Met Ala Val Thr Thr His Ala Leu
180 185 190

Asp Leu Gly Ala Met Thr Pro Phe Phe Trp Leu Phe Glu Glu Arg Glu
195 200 205

5

10

ES 2 671 895 T3

Lys Met Phe Glu Phe Tyr Glu Arg Val Ser Gly Ala Arg Met His Ala
 210 215 220
 Ala Tyr Ile Arg Pro Gly Gly Val His Gln Asp Leu Pro Leu Gly Leu
 225 230 235 240
 Met Asp Asp Ile Tyr Gln Phe Ser Lys Asn Phe Ser Leu Arg Leu Asp
 245 250 255
 Glu Leu Glu Glu Leu Leu Thr Asn Asn Arg Ile Trp Arg Asn Arg Thr
 260 265 270
 Ile Asp Ile Gly Val Val Thr Ala Glu Glu Ala Leu Asn Tyr Gly Phe
 275 280 285
 Ser Gly Val Met Leu Arg Gly Ser Gly Ile Gln Trp Asp Leu Arg Lys
 290 295 300
 Thr Gln Pro Tyr Asp Val Tyr Asp Gln Val Glu Phe Asp Val Pro Val
 305 310 315 320
 Gly Ser Arg Gly Asp Cys Tyr Asp Arg Tyr Leu Cys Arg Val Glu Glu
 325 330 335
 Met Arg Gln Ser Leu Arg Ile Ile Ala Gln Cys Leu Asn Lys Met Pro
 340 345 350
 Pro Gly Glu Ile Lys Val Asp Asp Ala Lys Val Ser Pro Pro Lys Arg
 355 360 365
 Ala Glu Met Lys Thr Ser Met Glu Ser Leu Ile His His Phe Lys Leu
 370 375 380
 Tyr Thr Glu Gly Tyr Gln Val Pro Pro Gly Ala Thr Tyr Thr Ala Ile
 385 390 395 400
 Glu Ala Pro Lys Gly Glu Phe Gly Val Tyr Leu Val Ser Asp Gly Ser
 405 410 415
 Ser Arg Pro Tyr Arg Cys Lys Ile Lys Ala Pro Gly Phe Ala His Leu
 420 425 430
 Ala Gly Leu Asp Lys Met Ser Lys Gly His Met Leu Ala Asp Val Val
 435 440 445
 Ala Ile Ile Gly Thr Gln Asp Ile Val Phe Gly Glu Val Asp Arg
 450 455 460

<210> 106
 <211> 463
 <212> PRT
 <213> Humana

<400> 106

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Met Ala Ala Leu Arg Ala Leu Cys Gly Phe Arg Gly Val Ala Ala Gln
 1          5          10          15

Val Leu Arg Pro Gly Ala Gly Val Arg Leu Pro Ile Gln Pro Ser Arg
 20          25          30

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

Gly Ala Val Met Tyr Pro Ser Lys Glu Thr Ala His Trp Lys Pro Pro
 50          55          60

Pro Trp Asn Asp Val Asp Pro Pro Lys Asp Thr Ile Val Lys Asn Ile
 65          70          75          80

Thr Leu Asn Phe Gly Pro Gln His Pro Ala Ala His Gly Val Leu Arg
 85          90          95

Leu Val Met Glu Leu Ser Gly Glu Met Val Arg Lys Cys Asp Pro His
100          105          110

Ile Gly Leu Leu His Arg Gly Thr Glu Lys Leu Ile Glu Tyr Lys Thr
115          120          125

Tyr Leu Gln Ala Leu Pro Tyr Phe Asp Arg Leu Asp Tyr Val Ser Met
130          135          140

Met Cys Asn Glu Gln Ala Tyr Ser Leu Ala Val Glu Lys Leu Leu Asn
145          150          155          160

Ile Arg Pro Pro Pro Arg Ala Gln Trp Ile Arg Val Leu Phe Gly Glu
165          170          175

Ile Thr Arg Leu Leu Asn His Ile Met Ala Val Thr Thr His Ala Leu
180          185          190

Asp Leu Gly Ala Met Thr Pro Phe Phe Trp Leu Phe Glu Glu Arg Glu
195          200          205

Lys Met Phe Glu Phe Tyr Glu Arg Val Ser Gly Ala Arg Met His Ala
210          215          220

Ala Tyr Ile Arg Pro Gly Gly Val His Gln Asp Leu Pro Leu Gly Leu
225          230          235          240

Met Asp Asp Ile Tyr Gln Phe Ser Lys Asn Phe Ser Leu Arg Leu Asp
245          250          255

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ES 2 671 895 T3

Glu Leu Glu Glu Leu Leu Thr Asn Asn Arg Ile Trp Arg Asn Arg Thr
 260 265 270
 Ile Asp Ile Gly Val Val Thr Ala Glu Glu Ala Leu Asn Tyr Gly Phe
 275 280 285
 Ser Gly Val Met Leu Arg Gly Ser Gly Ile Gln Trp Asp Leu Arg Lys
 290 295 300
 Thr Gln Pro Tyr Asp Val Tyr Asp Gln Val Glu Phe Asp Val Pro Val
 305 310 315 320
 Gly Ser Arg Gly Asp Cys Tyr Asp Arg Tyr Leu Cys Arg Val Glu Glu
 325 330 335
 Met Arg Gln Ser Leu Arg Ile Ile Ala Gln Cys Leu Asn Lys Met Pro
 340 345 350
 Pro Gly Glu Ile Lys Val Asp Asp Ala Lys Val Ser Pro Pro Lys Arg
 355 360 365
 Ala Glu Met Lys Thr Ser Met Glu Ser Leu Ile His His Phe Lys Leu
 370 375 380
 Tyr Thr Glu Gly Tyr Gln Val Pro Pro Gly Ala Thr Tyr Thr Ala Ile
 385 390 395 400
 Glu Ala Pro Lys Gly Glu Phe Gly Val Tyr Leu Val Ser Asp Gly Ser
 405 410 415
 Ser Arg Pro Tyr Arg Cys Lys Ile Lys Ala Pro Gly Phe Ala His Leu
 420 425 430
 Ala Gly Leu Asp Lys Met Ser Lys Gly His Met Leu Ala Asp Val Val
 435 440 445
 Ala Ile Ile Gly Thr Gln Asp Ile Val Phe Gly Glu Val Asp Arg
 450 455 460

<210> 107
 <211> 693
 <212> PRT
 <213> Humana

<400> 107

Met Ala Gly Gly Pro Gly Pro Gly Glu Pro Ala Ala Pro Gly Ala Gln
 1 5 10 15

His Phe Leu Tyr Glu Val Pro Pro Trp Val Met Cys Arg Phe Tyr Lys
 20 25 30

ES 2 671 895 T3

Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys Gln Phe Gly Gly Trp
 35 40 45
 Arg Arg Ala Ala Gly Gly Arg Glu Ala Arg Gly Leu Leu Ala Pro Thr
 50 55 60
 Pro Asp Ala Pro Arg Pro Ala Ala Ala Leu Ile Val Arg Asp Gln Thr
 65 70 75 80
 Glu Leu Arg Leu Cys Glu Arg Ser Gly Gln Arg Thr Ala Ser Val Leu
 85 90 95
 Trp Pro Trp Ile Asn Arg Asn Ala Arg Val Ala Asp Leu Val His Ile
 100 105 110
 Leu Thr His Leu Gln Leu Leu Arg Ala Arg Asp Ile Ile Thr Ala Trp
 115 120 125
 His Pro Pro Ala Pro Leu Pro Ser Pro Gly Thr Thr Ala Pro Arg Pro
 130 135 140
 Ser Ser Ile Pro Ala Pro Ala Glu Ala Glu Ala Trp Ser Pro Arg Lys
 145 150 155 160
 Leu Pro Ser Ser Ala Ser Thr Phe Leu Ser Pro Ala Phe Pro Gly Ser
 165 170 175
 Gln Thr His Ser Gly Pro Glu Leu Gly Leu Val Pro Ser Pro Ala Ser
 180 185 190
 Leu Trp Pro Pro Pro Pro Ser Pro Ala Pro Ser Ser Thr Lys Pro Gly
 195 200 205
 Pro Glu Ser Ser Val Ser Leu Leu Gln Gly Ala Arg Pro Phe Pro Phe
 210 215 220
 Cys Trp Pro Leu Cys Glu Ile Ser Arg Gly Thr His Asn Phe Ser Glu
 225 230 235 240
 Glu Leu Lys Ile Gly Glu Gly Gly Phe Gly Cys Val Tyr Arg Ala Val
 245 250 255
 Met Arg Asn Thr Val Tyr Ala Val Lys Arg Leu Lys Glu Asn Ala Asp
 260 265 270
 Leu Glu Trp Thr Ala Val Lys Gln Ser Phe Leu Thr Glu Val Glu Gln
 275 280 285
 Leu Ser Arg Phe Arg His Pro Asn Ile Val Asp Phe Ala Gly Tyr Cys
 290 295 300

ES 2 671 895 T3

Ala Gln Asn Gly Phe Tyr Cys Leu Val Tyr Gly Phe Leu Pro Asn Gly
 305 310 315 320
 Ser Leu Glu Asp Arg Leu His Cys Gln Thr Gln Ala Cys Pro Pro Leu
 325 330 335
 Ser Trp Pro Gln Arg Leu Asp Ile Leu Leu Gly Thr Ala Arg Ala Ile
 340 345 350
 Gln Phe Leu His Gln Asp Ser Pro Ser Leu Ile His Gly Asp Ile Lys
 355 360 365
 Ser Ser Asn Val Leu Leu Asp Glu Arg Leu Thr Pro Lys Leu Gly Asp
 370 375 380
 Phe Gly Leu Ala Arg Phe Ser Arg Phe Ala Gly Ser Ser Pro Ser Gln
 385 390 395 400
 Ser Ser Met Val Ala Arg Thr Gln Thr Val Arg Gly Thr Leu Ala Tyr
 405 410 415
 Leu Pro Glu Glu Tyr Ile Lys Thr Gly Arg Leu Ala Val Asp Thr Asp
 420 425 430
 Thr Phe Ser Phe Gly Val Val Val Leu Glu Thr Leu Ala Gly Gln Arg
 435 440 445
 Ala Val Lys Thr His Gly Ala Arg Thr Lys Tyr Leu Lys Asp Leu Val
 450 455 460
 Glu Glu Glu Ala Glu Glu Ala Gly Val Ala Leu Arg Ser Thr Gln Ser
 465 470 475 480
 Thr Leu Gln Ala Gly Leu Ala Ala Asp Ala Trp Ala Ala Pro Ile Ala
 485 490 495
 Met Gln Ile Tyr Lys Lys His Leu Gly Gln Leu Ala Cys Cys Cys Leu
 500 505 510
 His Arg Arg Ala Lys Arg Arg Pro Pro Met Thr Gln Glu Asn Ser Tyr
 515 520 525
 Val Ser Ser Thr Gly Arg Ala His Ser Gly Ala Ala Pro Trp Gln Pro
 530 535 540
 Leu Ala Ala Pro Ser Gly Ala Ser Ala Gln Ala Ala Glu Gln Leu Gln
 545 550 555 560
 Arg Gly Pro Asn Gln Pro Val Glu Ser Asp Glu Ser Leu Gly Gly Leu
 565 570 575

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Ser Ala Ala Leu Arg Ser Trp His Leu Thr Pro Ser Cys Pro Leu Asp
580 585 590

Pro Ala Pro Leu Arg Glu Ala Gly Cys Pro Gln Gly Asp Thr Ala Gly
595 600 605

Glu Ser Ser Trp Gly Ser Gly Pro Gly Ser Arg Pro Thr Ala Val Glu
610 615 620

Gly Leu Ala Leu Gly Ser Ser Ala Ser Ser Ser Ser Glu Pro Pro Gln
625 630 635 640

Ile Ile Ile Asn Pro Ala Arg Gln Lys Met Val Gln Lys Leu Ala Leu
645 650 655

Tyr Glu Asp Gly Ala Leu Asp Ser Leu Gln Leu Leu Ser Ser Ser
660 665 670

Leu Pro Gly Leu Gly Leu Glu Gln Asp Arg Gln Gly Pro Glu Glu Ser
675 680 685

Asp Glu Phe Gln Ser
690

<210> 108
<211> 712
<212> PRT
<213> Humana

5

<400> 108

Met Ala Gly Gly Pro Gly Pro Gly Glu Pro Ala Ala Pro Gly Ala Gln
1 5 10 15

His Phe Leu Tyr Glu Val Pro Pro Trp Val Met Cys Arg Phe Tyr Lys
20 25 30

Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys Gln Phe Ala Ala Leu
35 40 45

Ile Val Arg Asp Gln Thr Glu Leu Arg Leu Cys Glu Arg Ser Gly Gln
50 55 60

Arg Thr Ala Ser Val Leu Trp Pro Trp Ile Asn Arg Asn Ala Arg Val
65 70 75 80

Ala Asp Leu Val His Ile Leu Thr His Leu Gln Leu Leu Arg Ala Arg
85 90 95

Asp Ile Ile Thr Ala Trp His Pro Pro Ala Pro Leu Pro Ser Pro Gly
100 105 110

Thr Thr Ala Pro Arg Pro Ser Ser Ile Pro Ala Pro Ala Glu Ala Glu

10

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115	120	125													
Ala Trp Ser Pro Arg Lys Leu Pro Ser Ser Ala Ser Thr Phe Leu Ser	130	135	140												
Pro Ala Phe Pro Gly Ser Gln Thr His Ser Gly Pro Glu Leu Gly Leu	145	150	155												
Val Pro Ser Pro Ala Ser Leu Trp Pro Pro Pro Pro Ser Pro Ala Pro	165	170	175												
Ser Ser Thr Lys Pro Gly Pro Glu Ser Ser Val Ser Leu Leu Gln Gly	180	185	190												
Ala Arg Pro Phe Pro Phe Cys Trp Pro Leu Cys Glu Ile Ser Arg Gly	195	200	205												
Thr His Asn Phe Ser Glu Glu Leu Lys Ile Gly Glu Gly Gly Phe Gly	210	215	220												
Cys Val Tyr Arg Ala Val Met Arg Asn Thr Val Tyr Ala Val Lys Arg	225	230	235												
Leu Lys Glu Asn Ala Asp Leu Glu Trp Thr Ala Val Lys Gln Ser Phe	245	250	255												
Leu Thr Glu Val Glu Gln Leu Ser Arg Phe Arg His Pro Asn Ile Val	260	265	270												
Asp Phe Ala Gly Tyr Cys Ala Gln Asn Gly Phe Tyr Cys Leu Val Tyr	275	280	285												
Gly Phe Leu Pro Asn Gly Ser Leu Glu Asp Arg Leu His Cys Gln Thr	290	295	300												
Gln Ala Cys Pro Pro Leu Ser Trp Pro Gln Arg Leu Asp Ile Leu Leu	305	310	315												
Gly Thr Ala Arg Ala Ile Gln Phe Leu His Gln Asp Ser Pro Ser Leu	325	330	335												
Ile His Gly Asp Ile Lys Ser Ser Asn Val Leu Leu Asp Glu Arg Leu	340	345	350												
Thr Pro Lys Leu Gly Asp Phe Gly Leu Ala Arg Phe Ser Arg Phe Ala	355	360	365												
Gly Ser Ser Pro Ser Gln Ser Ser Met Val Ala Arg Thr Gln Thr Val	370	375	380												
Arg Gly Thr Leu Ala Tyr Leu Pro Glu Glu Tyr Ile Lys Thr Gly Arg															

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385		390		395		400									
Leu	Ala	Val	Asp	Thr	Asp	Thr	Phe	Ser	Phe	Gly	Val	Val	Val	Leu	Glu
				405					410					415	
Thr	Leu	Ala	Gly	Gln	Arg	Ala	Val	Lys	Thr	His	Gly	Ala	Arg	Thr	Lys
			420					425					430		
Tyr	Leu	Lys	Asp	Leu	Val	Glu	Glu	Glu	Ala	Glu	Glu	Ala	Gly	Val	Ala
		435					440					445			
Leu	Arg	Ser	Thr	Gln	Ser	Thr	Leu	Gln	Ala	Gly	Leu	Ala	Ala	Asp	Ala
	450					455					460				
Trp	Ala	Ala	Pro	Ile	Ala	Met	Gln	Ile	Tyr	Lys	Lys	His	Leu	Asp	Pro
465					470					475					480
Arg	Pro	Gly	Pro	Cys	Pro	Pro	Glu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Leu
				485					490					495	
Ala	Cys	Cys	Cys	Leu	His	Arg	Arg	Ala	Lys	Arg	Arg	Pro	Pro	Met	Thr
			500					505					510		
Gln	Val	Tyr	Glu	Arg	Leu	Glu	Lys	Leu	Gln	Ala	Val	Val	Ala	Gly	Val
		515					520					525			
Pro	Gly	His	Ser	Glu	Ala	Ala	Ser	Cys	Ile	Pro	Pro	Ser	Pro	Gln	Glu
	530					535					540				
Asn	Ser	Tyr	Val	Ser	Ser	Thr	Gly	Arg	Ala	His	Ser	Gly	Ala	Ala	Pro
545					550					555					560
Trp	Gln	Pro	Leu	Ala	Ala	Pro	Ser	Gly	Ala	Ser	Ala	Gln	Ala	Ala	Glu
				565					570					575	
Gln	Leu	Gln	Arg	Gly	Pro	Asn	Gln	Pro	Val	Glu	Ser	Asp	Glu	Ser	Leu
			580					585					590		
Gly	Gly	Leu	Ser	Ala	Ala	Leu	Arg	Ser	Trp	His	Leu	Thr	Pro	Ser	Cys
		595					600					605			
Pro	Leu	Asp	Pro	Ala	Pro	Leu	Arg	Glu	Ala	Gly	Cys	Pro	Gln	Gly	Asp
	610					615					620				
Thr	Ala	Gly	Glu	Ser	Ser	Trp	Gly	Ser	Gly	Pro	Gly	Ser	Arg	Pro	Thr
625					630					635					640
Ala	Val	Glu	Gly	Leu	Ala	Leu	Gly	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Glu
				645					650					655	
Pro	Pro	Gln	Ile	Ile	Ile	Asn	Pro	Ala	Arg	Gln	Lys	Met	Val	Gln	Lys

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660

665

670

Leu Ala Leu Tyr Glu Asp Gly Ala Leu Asp Ser Leu Gln Leu Leu Ser
675 680 685

Ser Ser Ser Leu Pro Gly Leu Gly Leu Glu Gln Asp Arg Gln Gly Pro
690 695 700

Glu Glu Ser Asp Glu Phe Gln Ser
705 710

<210> 109

<211> 682

<212> PRT

<213> Humana

<400> 109

Met Ala Gly Gly Pro Gly Pro Gly Glu Pro Ala Ala Pro Gly Ala Gln
1 5 10 15

His Phe Leu Tyr Glu Val Pro Pro Trp Val Met Cys Arg Phe Tyr Lys
20 25 30

Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys Gln Phe Ala Ala Leu
35 40 45

Ile Val Arg Asp Gln Thr Glu Leu Arg Leu Cys Glu Arg Ser Gly Gln
50 55 60

Arg Thr Ala Ser Val Leu Trp Pro Trp Ile Asn Arg Asn Ala Arg Val
65 70 75 80

Ala Asp Leu Val His Ile Leu Thr His Leu Gln Leu Leu Arg Ala Arg
85 90 95

Asp Ile Ile Thr Ala Trp His Pro Pro Ala Pro Leu Pro Ser Pro Gly
100 105 110

Thr Thr Ala Pro Arg Pro Ser Ser Ile Pro Ala Pro Ala Glu Ala Glu
115 120 125

Ala Trp Ser Pro Arg Lys Leu Pro Ser Ser Ala Ser Thr Phe Leu Ser
130 135 140

Pro Ala Phe Pro Gly Ser Gln Thr His Ser Gly Pro Glu Leu Gly Leu
145 150 155 160

Val Pro Ser Pro Ala Ser Leu Trp Pro Pro Pro Pro Ser Pro Ala Pro
165 170 175

Ser Ser Thr Lys Pro Gly Pro Glu Ser Ser Val Ser Leu Leu Gln Gly
180 185 190

5

10

ES 2 671 895 T3

Ala Arg Pro Phe Pro Phe Cys Trp Pro Leu Cys Glu Ile Ser Arg Gly
 195 200 205
 Thr His Asn Phe Ser Glu Glu Leu Lys Ile Gly Glu Gly Gly Phe Gly
 210 215 220
 Cys Val Tyr Arg Ala Val Met Arg Asn Thr Val Tyr Ala Val Lys Arg
 225 230 235 240
 Leu Lys Glu Asn Ala Asp Leu Glu Trp Thr Ala Val Lys Gln Ser Phe
 245 250 255
 Leu Thr Glu Val Glu Gln Leu Ser Arg Phe Arg His Pro Asn Ile Val
 260 265 270
 Asp Phe Ala Gly Tyr Cys Ala Gln Asn Gly Phe Tyr Cys Leu Val Tyr
 275 280 285
 Gly Phe Leu Pro Asn Gly Ser Leu Glu Asp Arg Leu His Cys Gln Thr
 290 295 300
 Gln Ala Cys Pro Pro Leu Ser Trp Pro Gln Arg Leu Asp Ile Leu Leu
 305 310 315 320
 Gly Thr Ala Arg Ala Ile Gln Phe Leu His Gln Asp Ser Pro Ser Leu
 325 330 335
 Ile His Gly Asp Ile Lys Ser Ser Asn Val Leu Leu Asp Glu Arg Leu
 340 345 350
 Thr Pro Lys Leu Gly Asp Phe Gly Leu Ala Arg Phe Ser Arg Phe Ala
 355 360 365
 Gly Ser Ser Pro Ser Gln Ser Ser Met Val Ala Arg Thr Gln Thr Val
 370 375 380
 Arg Gly Thr Leu Ala Tyr Leu Pro Glu Glu Tyr Ile Lys Thr Gly Arg
 385 390 395 400
 Leu Ala Val Asp Thr Asp Thr Phe Ser Phe Gly Val Val Val Leu Glu
 405 410 415
 Thr Leu Ala Gly Gln Arg Ala Val Lys Thr His Gly Ala Arg Thr Lys
 420 425 430
 Tyr Leu Lys Asp Leu Val Glu Glu Glu Ala Glu Glu Ala Gly Val Ala
 435 440 445
 Leu Arg Ser Thr Gln Ser Thr Leu Gln Ala Gly Leu Ala Ala Asp Ala
 450 455 460

ES 2 671 895 T3

Trp Ala Ala Pro Ile Ala Met Gln Ile Tyr Lys Lys His Leu Asp Pro
 465 470 475 480
 Arg Pro Gly Pro Cys Pro Pro Glu Leu Gly Leu Gly Leu Gly Gln Leu
 485 490 495
 Ala Cys Cys Cys Leu His Arg Arg Ala Lys Arg Arg Pro Pro Met Thr
 500 505 510
 Gln Glu Asn Ser Tyr Val Ser Ser Thr Gly Arg Ala His Ser Gly Ala
 515 520 525
 Ala Pro Trp Gln Pro Leu Ala Ala Pro Ser Gly Ala Ser Ala Gln Ala
 530 535 540
 Ala Glu Gln Leu Gln Arg Gly Pro Asn Gln Pro Val Glu Ser Asp Glu
 545 550 555 560
 Ser Leu Gly Gly Leu Ser Ala Ala Leu Arg Ser Trp His Leu Thr Pro
 565 570 575
 Ser Cys Pro Leu Asp Pro Ala Pro Leu Arg Glu Ala Gly Cys Pro Gln
 580 585 590
 Gly Asp Thr Ala Gly Glu Ser Ser Trp Gly Ser Gly Pro Gly Ser Arg
 595 600 605
 Pro Thr Ala Val Glu Gly Leu Ala Leu Gly Ser Ser Ala Ser Ser Ser
 610 615 620
 Ser Glu Pro Pro Gln Ile Ile Ile Asn Pro Ala Arg Gln Lys Met Val
 625 630 635 640
 Gln Lys Leu Ala Leu Tyr Glu Asp Gly Ala Leu Asp Ser Leu Gln Leu
 645 650 655
 Leu Ser Ser Ser Ser Leu Pro Gly Leu Gly Leu Glu Gln Asp Arg Gln
 660 665 670
 Gly Pro Glu Glu Ser Asp Glu Phe Gln Ser
 675 680

<2io> no
 <211> 633
 <212> PRT
 <213> Humana

5

<400> 110

Met Ala Gly Gly Pro Gly Pro Gly Glu Pro Ala Ala Pro Gly Ala Gln
 1 5 10 15

ES 2 671 895 T3

His Phe Leu Tyr Glu Val Pro Pro Trp Val Met Cys Arg Phe Tyr Lys
 20 25 30
 Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys Gln Phe Ala Ala Leu
 35 40 45
 Ile Val Arg Asp Gln Thr Glu Leu Arg Leu Cys Glu Arg Ser Gly Gln
 50 55 60
 Arg Thr Ala Ser Val Leu Trp Pro Trp Ile Asn Arg Asn Ala Arg Val
 65 70 75 80
 Ala Asp Leu Val His Ile Leu Thr His Leu Gln Leu Leu Arg Ala Arg
 85 90 95
 Asp Ile Ile Thr Ala Trp His Pro Pro Ala Pro Leu Pro Ser Pro Gly
 100 105 110
 Thr Thr Ala Pro Arg Pro Ser Ser Ile Pro Ala Pro Ala Glu Ala Glu
 115 120 125
 Ala Trp Ser Pro Arg Lys Leu Pro Ser Ser Ala Ser Thr Phe Leu Ser
 130 135 140
 Pro Ala Phe Pro Gly Ser Gln Thr His Ser Gly Pro Glu Leu Gly Leu
 145 150 155 160
 Val Pro Ser Pro Ala Ser Leu Trp Pro Pro Pro Pro Ser Pro Ala Pro
 165 170 175
 Ser Ser Thr Lys Pro Gly Pro Glu Ser Ser Val Ser Leu Leu Gln Gly
 180 185 190
 Ala Arg Pro Phe Pro Phe Cys Trp Pro Leu Cys Glu Ile Ser Arg Gly
 195 200 205
 Thr His Asn Phe Ser Glu Glu Leu Lys Ile Gly Glu Gly Gly Phe Gly
 210 215 220
 Cys Val Tyr Arg Ala Val Met Arg Asn Thr Val Tyr Ala Val Lys Arg
 225 230 235 240
 Leu Lys Glu Asn Ala Asp Leu Glu Trp Thr Ala Val Lys Gln Ser Phe
 245 250 255
 Leu Thr Glu Val Glu Gln Leu Ser Arg Phe Arg His Pro Asn Ile Val
 260 265 270
 Asp Phe Ala Gly Tyr Cys Ala Gln Asn Gly Phe Tyr Cys Leu Val Tyr
 275 280 285

Gly Phe Leu Pro Asn Gly Ser Leu Glu Asp Arg Leu His Cys Gln Thr
290 295 300

Gln Ala Cys Pro Pro Leu Ser Trp Pro Gln Arg Leu Asp Ile Leu Leu
305 310 315 320

Gly Thr Ala Arg Ala Ile Gln Phe Leu His Gln Asp Ser Pro Ser Leu
325 330 335

Ile His Gly Asp Ile Lys Ser Ser Asn Val Leu Leu Asp Glu Arg Leu
340 345 350

Thr Pro Lys Leu Gly Asp Phe Gly Leu Ala Arg Phe Ser Arg Phe Ala
355 360 365

Gly Ser Ser Pro Ser Gln Ser Ser Met Val Ala Arg Thr Gln Thr Val
370 375 380

Arg Gly Thr Leu Ala Tyr Leu Pro Glu Glu Tyr Ile Lys Thr Gly Arg
385 390 395 400

Leu Ala Val Asp Thr Asp Thr Phe Ser Phe Gly Val Val Val Leu Glu
405 410 415

Thr Leu Ala Gly Gln Arg Ala Val Lys Thr His Gly Ala Arg Thr Lys
420 425 430

Tyr Leu Val Tyr Glu Arg Leu Glu Lys Leu Gln Ala Val Val Ala Gly
435 440 445

Val Pro Gly His Ser Glu Ala Ala Ser Cys Ile Pro Pro Ser Pro Gln
450 455 460

Glu Asn Ser Tyr Val Ser Ser Thr Gly Arg Ala His Ser Gly Ala Ala
465 470 475 480

Pro Trp Gln Pro Leu Ala Ala Pro Ser Gly Ala Ser Ala Gln Ala Ala
485 490 495

Glu Gln Leu Gln Arg Gly Pro Asn Gln Pro Val Glu Ser Asp Glu Ser
500 505 510

Leu Gly Gly Leu Ser Ala Ala Leu Arg Ser Trp His Leu Thr Pro Ser
515 520 525

Cys Pro Leu Asp Pro Ala Pro Leu Arg Glu Ala Gly Cys Pro Gln Gly
530 535 540

Asp Thr Ala Gly Glu Ser Ser Trp Gly Ser Gly Pro Gly Ser Arg Pro
545 550 555 560

ES 2 671 895 T3

Thr Ala Val Glu Gly Leu Ala Leu Gly Ser Ser Ala Ser Ser Ser Ser
565 570 575
Glu Pro Pro Gln Ile Ile Ile Asn Pro Ala Arg Gln Lys Met Val Gln
580 585 590
Lys Leu Ala Leu Tyr Glu Asp Gly Ala Leu Asp Ser Leu Gln Leu Leu
595 600 605
Ser Ser Ser Ser Leu Pro Gly Leu Gly Leu Glu Gln Asp Arg Gln Gly
610 615 620
Pro Glu Glu Ser Asp Glu Phe Gln Ser
625 630

<210> 111
<211> 708
5 <212> PRT
<213> Humana
<400> 111

Met Ala Gly Gly Pro Gly Pro Gly Glu Pro Ala Ala Pro Gly Ala Gln
1 5 10 15
His Phe Leu Tyr Glu Val Pro Pro Trp Val Met Cys Arg Phe Tyr Lys
20 25 30
Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys Gln Phe Gly Gly Trp
35 40 45
Arg Arg Ala Ala Gly Gly Arg Glu Ala Arg Gly Leu Leu Ala Pro Thr
50 55 60
Pro Asp Ala Pro Arg Pro Ala Ala Ala Leu Ile Val Arg Asp Gln Thr
65 70 75 80
Glu Leu Arg Leu Cys Glu Arg Ser Gly Gln Arg Thr Ala Ser Val Leu
85 90 95
Trp Pro Trp Ile Asn Arg Asn Ala Arg Val Ala Asp Leu Val His Ile
100 105 110
Leu Thr His Leu Gln Leu Leu Arg Ala Arg Asp Ile Ile Thr Ala Trp
115 120 125
His Pro Pro Ala Pro Leu Pro Ser Pro Gly Thr Thr Ala Pro Arg Pro
130 135 140
Ser Ser Ile Pro Ala Pro Ala Glu Ala Glu Ala Trp Ser Pro Arg Lys
145 150 155 160

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Leu Pro Ser Ser Ala Ser Thr Phe Leu Ser Pro Ala Phe Pro Gly Ser
 165 170 175
 Gln Thr His Ser Gly Pro Glu Leu Gly Leu Val Pro Ser Pro Ala Ser
 180 185 190
 Leu Trp Pro Pro Pro Pro Ser Pro Ala Pro Ser Ser Thr Lys Pro Gly
 195 200 205
 Pro Glu Ser Ser Val Ser Leu Leu Gln Gly Ala Arg Pro Phe Pro Phe
 210 215 220
 Cys Trp Pro Leu Cys Glu Ile Ser Arg Gly Thr His Asn Phe Ser Glu
 225 230 235 240
 Glu Leu Lys Ile Gly Glu Gly Gly Phe Gly Cys Val Tyr Arg Ala Val
 245 250 255
 Met Arg Asn Thr Val Tyr Ala Val Lys Arg Leu Lys Glu Asn Ala Asp
 260 265 270
 Leu Glu Trp Thr Ala Val Lys Gln Ser Phe Leu Thr Glu Val Glu Gln
 275 280 285
 Leu Ser Arg Phe Arg His Pro Asn Ile Val Asp Phe Ala Gly Tyr Cys
 290 295 300
 Ala Gln Asn Gly Phe Tyr Cys Leu Val Tyr Gly Phe Leu Pro Asn Gly
 305 310 315 320
 Ser Leu Glu Asp Arg Leu His Cys Gln Thr Gln Ala Cys Pro Pro Leu
 325 330 335
 Ser Trp Pro Gln Arg Leu Asp Ile Leu Leu Gly Thr Ala Arg Ala Ile
 340 345 350
 Gln Phe Leu His Gln Asp Ser Pro Ser Leu Ile His Gly Asp Ile Lys
 355 360 365
 Ser Ser Asn Val Leu Leu Asp Glu Arg Leu Thr Pro Lys Leu Gly Asp
 370 375 380
 Phe Gly Leu Ala Arg Phe Ser Arg Phe Ala Gly Ser Ser Pro Ser Gln
 385 390 395 400
 Ser Ser Met Val Ala Arg Thr Gln Thr Val Arg Gly Thr Leu Ala Tyr
 405 410 415
 Leu Pro Glu Glu Tyr Ile Lys Thr Gly Arg Leu Ala Val Asp Thr Asp
 420 425 430

ES 2 671 895 T3

Thr Phe Ser Phe Gly Val Val Val Leu Glu Thr Leu Ala Gly Gln Arg
 435 440 445
 Ala Val Lys Thr His Gly Ala Arg Thr Lys Tyr Leu Lys Asp Leu Val
 450 455 460
 Glu Glu Glu Ala Glu Glu Ala Gly Val Ala Leu Arg Ser Thr Gln Ser
 465 470 475 480
 Thr Leu Gln Ala Gly Leu Ala Ala Asp Ala Trp Ala Ala Pro Ile Ala
 485 490 495
 Met Gln Ile Tyr Lys Lys His Leu Asp Pro Arg Pro Gly Pro Cys Pro
 500 505 510
 Pro Glu Leu Gly Leu Gly Leu Gly Gln Leu Ala Cys Cys Cys Leu His
 515 520 525
 Arg Arg Ala Lys Arg Arg Pro Pro Met Thr Gln Glu Asn Ser Tyr Val
 530 535 540
 Ser Ser Thr Gly Arg Ala His Ser Gly Ala Ala Pro Trp Gln Pro Leu
 545 550 555 560
 Ala Ala Pro Ser Gly Ala Ser Ala Gln Ala Ala Glu Gln Leu Gln Arg
 565 570 575
 Gly Pro Asn Gln Pro Val Glu Ser Asp Glu Ser Leu Gly Gly Leu Ser
 580 585 590
 Ala Ala Leu Arg Ser Trp His Leu Thr Pro Ser Cys Pro Leu Asp Pro
 595 600 605
 Ala Pro Leu Arg Glu Ala Gly Cys Pro Gln Gly Asp Thr Ala Gly Glu
 610 615 620
 Ser Ser Trp Gly Ser Gly Pro Gly Ser Arg Pro Thr Ala Val Glu Gly
 625 630 635 640
 Leu Ala Leu Gly Ser Ser Ala Ser Ser Ser Ser Glu Pro Pro Gln Ile
 645 650 655
 Ile Ile Asn Pro Ala Arg Gln Lys Met Val Gln Lys Leu Ala Leu Tyr
 660 665 670
 Glu Asp Gly Ala Leu Asp Ser Leu Gln Leu Leu Ser Ser Ser Ser Leu
 675 680 685
 Pro Gly Leu Gly Leu Glu Gln Asp Arg Gln Gly Pro Glu Glu Ser Asp
 690 695 700
 Glu Phe Gln Ser
 705

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<210> 112
<211> 140
<212> PRT
<213> Humana

5

<400> 112

```

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

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

Thr Glu Cys Pro Gly Glu Ala Ile Pro His Pro Pro Gly Glu Cys Arg
          35          40          45

Ile Ala Pro Phe Ser Pro Arg Ser Ser Arg Ser Trp Gln His Gln Asp
          50          55          60

Pro Thr Ser Leu Leu Ser Gly Leu Pro Lys Ala Asp Pro Gly His Trp
65          70          75          80

Trp Ala Ser Phe Phe Phe Gly Lys Ser Thr Leu Pro Phe Met Ala Thr
          85          90          95

Val Leu Glu Ser Ala Glu His Ser Glu Pro Pro Gln Ala Ser Ser Ser
          100          105          110

Met Thr Ala Cys Gly Leu Ala Arg Asp Ala Pro Arg Lys Gln Pro Gly
          115          120          125

Gly Gln Ser Ser Thr Ala Ser Ala Gly Pro Pro Ser
          130          135          140

```

10

<210> 113
<211> 70
<212> PRT
<213> Humana

15

<400> 113

```

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

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

Thr Glu Cys Pro Gly Glu Ala Ile Pro His Pro Pro Gly Leu Pro Lys
          35          40          45

Ala Asp Pro Gly His Trp Trp Ala Ser Phe Phe Phe Gly Lys Ser Thr
          50          55          60

Leu Pro Pro Pro Thr Leu
65          70

```

<210> 114
 <211> 114
 <212> PRT
 <213> Humana

5

<400> 114

```

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

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

Thr Glu Cys Pro Gly Glu Ala Ile Pro His Pro Pro Gly Leu Pro Lys
          35          40          45

Ala Asp Pro Gly His Trp Trp Ala Ser Phe Phe Phe Gly Lys Ser Thr
          50          55          60

Leu Pro Phe Met Ala Thr Val Leu Glu Ser Ala Glu His Ser Glu Pro
65          70          75          80

Pro Gln Ala Ser Ser Ser Met Thr Ala Cys Gly Leu Ala Arg Asp Ala
          85          90          95

Pro Arg Lys Gln Pro Gly Gly Gln Ser Ser Thr Ala Ser Ala Gly Pro
          100          105          110

Pro Ser
    
```

10

<210> 115
 <211> 400
 <212> PRT
 <213> Humana

15

<400> 115

```

Met Glu Asp Gly Val Tyr Glu Pro Pro Asp Leu Thr Pro Glu Glu Arg
1          5          10          15

Met Glu Leu Glu Asn Ile Arg Arg Arg Lys Gln Glu Leu Leu Val Glu
          20          25          30

Ile Gln Arg Leu Arg Glu Glu Leu Ser Glu Ala Met Ser Glu Val Glu
          35          40          45

Gly Leu Glu Ala Asn Glu Gly Ser Lys Thr Leu Gln Arg Asn Arg Lys
          50          55          60
    
```

ES 2 671 895 T3

Met Ala Met Gly Arg Lys Lys Phe Asn Met Asp Pro Lys Lys Gly Ile
 65 70 75 80
 Gln Phe Leu Val Glu Asn Glu Leu Leu Gln Asn Thr Pro Glu Glu Ile
 85 90 95
 Ala Arg Phe Leu Tyr Lys Gly Glu Gly Leu Asn Lys Thr Ala Ile Gly
 100 105 110
 Asp Tyr Leu Gly Glu Arg Glu Glu Leu Asn Leu Ala Val Leu His Ala
 115 120 125
 Phe Val Asp Leu His Glu Phe Thr Asp Leu Asn Leu Val Gln Ala Leu
 130 135 140
 Arg Gln Phe Leu Trp Ser Phe Arg Leu Pro Gly Glu Ala Gln Lys Ile
 145 150 155 160
 Asp Arg Met Met Glu Ala Phe Ala Gln Arg Tyr Cys Leu Cys Asn Pro
 165 170 175
 Gly Val Phe Gln Ser Thr Asp Thr Cys Tyr Val Leu Ser Phe Ala Val
 180 185 190
 Ile Met Leu Asn Thr Ser Leu His Asn Pro Asn Val Arg Asp Lys Pro
 195 200 205
 Gly Leu Glu Arg Phe Val Ala Met Asn Arg Gly Ile Asn Glu Gly Gly
 210 215 220
 Asp Leu Pro Glu Glu Leu Leu Arg Asn Leu Tyr Asp Ser Ile Arg Asn
 225 230 235 240
 Glu Pro Phe Lys Ile Pro Glu Asp Asp Gly Asn Asp Leu Thr His Thr
 245 250 255
 Phe Phe Asn Pro Asp Arg Glu Gly Trp Leu Leu Lys Leu Gly Arg Gly
 260 265 270
 Arg Val Lys Thr Trp Lys Arg Arg Trp Phe Ile Leu Thr Asp Asn Cys
 275 280 285
 Leu Tyr Tyr Phe Glu Tyr Thr Thr Asp Lys Glu Pro Arg Gly Ile Ile
 290 295 300
 Pro Leu Glu Asn Leu Ser Ile Arg Glu Val Asp Asp Pro Arg Lys Pro
 305 310 315 320
 Asn Cys Phe Glu Leu Tyr Ile Pro Asn Asn Lys Gly Gln Leu Ile Lys
 325 330 335

ES 2 671 895 T3

Ala Cys Lys Thr Glu Ala Asp Gly Arg Val Val Glu Gly Asn His Met
 340 345 350
 Val Tyr Arg Ile Ser Ala Pro Thr Gln Glu Glu Lys Asp Glu Trp Ile
 355 360 365
 Lys Ser Ile Gln Ala Ala Val Ser Val Asp Pro Phe Tyr Glu Met Leu
 370 375 380
 Ala Ala Arg Lys Lys Arg Ile Ser Val Lys Lys Lys Gln Glu Gln Pro
 385 390 395 400

<210> 116
 <211> 399
 <212> PRT
 <213> Humana

5

<400> 116

Met Glu Asp Gly Val Tyr Glu Pro Pro Asp Leu Thr Pro Glu Glu Arg
 1 5 10 15
 Met Glu Leu Glu Asn Ile Arg Arg Arg Lys Gln Glu Leu Leu Val Glu
 20 25 30
 Ile Gln Arg Leu Arg Glu Glu Leu Ser Glu Ala Met Ser Glu Val Glu
 35 40 45
 Gly Leu Glu Ala Asn Glu Gly Ser Lys Thr Leu Gln Arg Asn Arg Lys
 50 55 60
 Met Ala Met Gly Arg Lys Lys Phe Asn Met Asp Pro Lys Lys Gly Ile
 65 70 75 80
 Gln Phe Leu Val Glu Asn Glu Leu Leu Gln Asn Thr Pro Glu Glu Ile
 85 90 95
 Ala Arg Phe Leu Tyr Lys Gly Glu Gly Leu Asn Lys Thr Ala Ile Gly
 100 105 110
 Asp Tyr Leu Gly Glu Arg Glu Glu Leu Asn Leu Ala Val Leu His Ala
 115 120 125
 Phe Val Asp Leu His Glu Phe Thr Asp Leu Asn Leu Val Gln Ala Leu
 130 135 140
 Arg Gln Phe Leu Trp Ser Phe Arg Leu Pro Gly Glu Ala Gln Lys Ile
 145 150 155 160
 Asp Arg Met Met Glu Ala Phe Ala Gln Arg Tyr Cys Leu Cys Asn Pro
 165 170 175
 Gly Val Phe Gln Ser Thr Asp Thr Cys Tyr Val Leu Ser Phe Ala Val

10

ES 2 671 895 T3

	180		185		190
Ile Met	Leu Asn Thr Ser Leu	His Asn Pro Asn Val	Arg Asp Lys Pro		
	195	200	205		
Gly Leu Glu Arg Phe Val	Ala Met Asn Arg Gly	Ile Asn Glu Gly Gly			
	210	215	220		
Asp Leu Pro Glu Glu	Leu Leu Arg Asn Leu	Tyr Asp Ser Ile Arg Asn			
	225	230	235		240
Glu Pro Phe Lys	Ile Pro Glu Asp Asp	Gly Asn Asp Leu Thr	His Thr		
	245	250	255		
Phe Phe Asn Pro Asp Arg Glu Gly	Trp Leu Leu Lys Leu	Gly Gly Arg			
	260	265	270		
Val Lys Thr Trp Lys Arg Arg	Trp Phe Ile Leu Thr	Asp Asn Cys Leu			
	275	280	285		
Tyr Tyr Phe Glu Tyr Thr	Thr Asp Lys Glu Pro	Arg Gly Ile Ile Pro			
	290	295	300		
Leu Glu Asn Leu Ser	Ile Arg Glu Val Asp	Asp Pro Arg Lys Pro Asn			
	305	310	315		320
Cys Phe Glu Leu	Tyr Ile Pro Asn Asn	Lys Gly Gln Leu Ile	Lys Ala		
	325	330	335		
Cys Lys Thr	Glu Ala Asp Gly Arg	Val Val Glu Gly Asn	His Met Val		
	340	345	350		
Tyr Arg	Ile Ser Ala Pro Thr	Gln Glu Glu Lys Asp	Glu Trp Ile Lys		
	355	360	365		
Ser Ile Gln Ala Ala Val	Ser Val Asp Pro Phe	Tyr Glu Met Leu Ala			
	370	375	380		
Ala Arg Lys Lys Arg	Ile Ser Val Lys Lys	Lys Gln Glu Gln Pro			
	385	390	395		

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 <211> 165
 <212> PRT
 <213> Humana

<400> 117

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	20	25 30

ES 2 671 895 T3

Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys Gly Phe Gly Tyr
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Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Met Cys Gln Gly
50 55 60
Gly Asp Phe Thr Arg His Asn Gly Thr Gly Gly Lys Ser Ile Tyr Gly
65 70 75 80
Glu Lys Phe Glu Asp Glu Asn Phe Ile Leu Lys His Thr Gly Pro Gly
85 90 95
Ile Leu Ser Met Ala Asn Ala Gly Pro Asn Thr Asn Gly Ser Gln Phe
100 105 110
Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu Asp Gly Lys His Val Val
115 120 125
Phe Gly Lys Val Lys Glu Gly Met Asn Ile Val Glu Ala Met Glu Arg
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Cys Gly Gln Leu Glu
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<211> 44
<212> PRT
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5

<400> 118

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10

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35 40 45
Pro Leu Pro Asp Pro Gly Leu Pro Thr Ser Leu Leu Ala Ser Ala Thr
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Gly

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35 40 45
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Tyr Arg Val Pro Arg Gly Ser His Ser Pro Pro Pro Arg Ser Pro Gln
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Gly

<210> 121
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<213> Humana
<400> 121

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

ES 2 671 895 T3

Ala Trp Arg Pro Ser Pro Pro Ala Ala Arg Ser Trp Pro Pro Thr Thr
35 40 45

Thr Thr Gly Ala Ala Trp Val Pro Leu Pro Ala Thr Ala Pro Ala Ala
50 55 60

Val Pro Ser Ala Pro Gly Lys Pro Phe Pro Thr Pro Gln Val Ser Pro
65 70 75 80

Arg Leu Thr Arg Val Ile Gly Gly Pro Ala Ser Phe Ser Gly Ser Pro
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Pro Ser Arg Ser Trp Pro Arg Cys Trp Ser Pro Gln Ser Thr Arg Asn
100 105 110

Leu Pro Arg Pro Pro Ala Ala
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<210> 122
<211> 29
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<213> Humana

<400> 122

Trp Thr Cys Ser Pro His Pro Thr Pro Thr Thr Arg Arg Ser Thr Thr
1 5 10 15

Ser Arg Ser Ala Ser Trp Ser Ala Arg Cys Ala Ser Thr
20 25

REIVINDICACIONES

1. Un método *in vitro* de diagnóstico de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α para evaluar la capacidad de respuesta a un tratamiento anti-TNF α antes, durante y/o después del tratamiento anti-TNF α , que comprende:
 - la detección de inmunoglobulina/s contra una o más proteínas biomarcadoras en un fluido corporal o un excremento de dicho paciente, en el que una proteína biomarcadora es un producto de expresión codificado por un gen seleccionado del grupo que comprende RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1,
 - en el que un individuo positivo en al menos una de dichas inmunoglobulinas se clasifica como individuo que NO responde;
 - en el que la/s inmunoglobulina/s es/son IgA.
2. Un método *in vitro* de diagnóstico de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α de acuerdo con la reivindicación 1, en el que el grupo de proteínas biomarcadoras comprende además al menos otro producto de expresión codificado por un gen seleccionado del grupo que comprende PECI, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4, PRC1, NAT6, EEF1AL3, NP_612480.1, PLXNA2, ELMO2 y NDUFS2.
3. Un método *in vitro* de diagnóstico de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α de acuerdo con las reivindicaciones 1 o 2, en el que se detecta/n inmunoglobulina/s contra al menos dos proteínas biomarcadoras.
4. Un método *in vitro* de diagnóstico de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α de acuerdo con cualquiera de las reivindicaciones 1 a 3, en el que el fluido corporal y/o el excremento se pueden seleccionar de un grupo que comprende: sangre, saliva, lágrimas, líquido sinovial o espinal, plasma, orina y heces.
5. Un método *in vitro* de diagnóstico de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α de acuerdo con cualquiera de las reivindicaciones 1 a 4, en el que el individuo padece artritis reumatoide.
6. Uso de un kit para realizar el método de cualquiera de las reivindicaciones 1 a 5 para evaluar la capacidad de respuesta a un tratamiento anti-TNF α de un individuo que se va a someter o que se está sometiendo a un tratamiento anti-TNF α , en el que el kit comprende una o más proteínas biomarcadoras, en el que la proteína biomarcadora es un producto de expresión codificado por un gen seleccionado del grupo que comprende RAB11B, PPP2R1A, KPNB1, COG4 y FDFT1.
7. El uso de acuerdo con la reivindicación 6, en el que el grupo de proteínas biomarcadoras comprende además al menos otro producto de expresión codificado por un gen seleccionado del grupo que comprende PECI, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4, PRC1, NAT6, EEF1AL3, NP_612480.1, PLXNA2, ELMO2 y NDUFS2.
8. El uso de acuerdo con la reivindicación 6, que comprende al menos dos proteínas biomarcadoras seleccionadas del grupo de RAB11B, PPP2R1A, KPNB1, COG4, FDFT1, PECI, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4, PRC1, NAT6, EEF1AL3, NP_612480.1, PLXNA2, ELMO2 y NDUFS2.
9. El uso de acuerdo con una cualquiera de las reivindicaciones 6 a 8, en el que el kit es un ensayo seleccionado del grupo que consiste en un ensayo de tira reactiva, un radioinmunoensayo, inmunoensayo de quimioluminiscencia, inmunoensayo de fluorescencia, ensayo de inmunotransferencia, ELISA, matriz de perlas basadas en Luminex y ensayo de micromatrices de proteínas.
10. El uso de acuerdo con una cualquiera de las reivindicaciones 6 a 9, en el que el kit es un ensayo seleccionado del grupo que consiste en ensayos basados en placas de microtitulación, basados en microplacas, basados en perlas, en los que las proteínas biomarcadoras se pueden unir a la superficie o estar en solución.

Fig. 1

SEQ ID NO: 1

RAB11B

>ENSG00000185236 | 19 | codificante de proteina | ENST00000328024 | ENSP00000333547
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Fig. 2

SEQ ID NO: 2

PPP2R1A

>ENSG00000105568 | 19 | codificante de proteina | ENST00000391791 | ENSP00000375668
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Fig. 3

SEQ ID NO: 3

PPP2R1A

>ENSG00000105568 | 19 | codificante de proteína | ENST00000322088 | ENSP00000324804
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Fig. 4

SEQ ID NO: 4

KPNB1

>ENSG00000108424 | 17 | codificante de proteina | ENST00000290158 | ENSP00000290158

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Fig. 5

SEQ ID NO: 5

COG4

>ENSG00000103051|16| codificante de proteina|ENST00000323786|ENSP00000315775
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Fig. 6**SEQ ID NO: 6**

COG4

>ENSG00000103051 | 16 | codificante de proteína | ENST00000393612 | ENSP00000377236

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 ACCCTGATCAATATCTGCAGGTGGAATGTGACAGACAGGTGGAGAAGGTGGTAGACAAG
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Fig. 7

SEQ ID NO: 7

COG4

>ENSG00000103051 | 16 | codificante de proteína | ENST00000338984 | ENSP00000345047

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 TACTTGTGCTGGACAAGTCGGTCATTGAGCTCAGCCGACAGGGCAAAGAGGGGAGCATG
 ATTGATGCCAACCTGAAATTGCTGCAGGAAGCTGAGCAACGTCTCAAAGCCATTGTGGCA
 GAGAAGTTTGGCATTGCCACCAAGGAAGGTGATCTGCCCCAGGTGGAGCGCTTCTTCAAG
 ATCTTCCCACTGCTGGGTTTGCATGAGGAGGGATTAAGAAAGTTCTCGGAGTACCTTTGC
 AAGCAGGTGGCCAGTAAAGCTGAGGAGAATCTGCTCATGGTGTGGGACAGACATGAGT
 GATCGGAGAGCTGCAGTCATCTTGCAGATACACTTACTCTTCTGTTTGAAGGGATTGCC
 CGCATTGTGGAGACCCACCAGCCAATAGTGGAGACCTATTATGGGCCAGGGAGACTCTAT
 ACCCTGATCAAATATCTGCAGGTGGAATGTGACAGACAGGTGGAGAAGGTGGTAGACAAG
 TTCATCAAGCAAAGGGACTACCACCAGCAGTTCCGGCATGTTTCAAGCAACCTGATGAGA
 AATTCTACAACAGAAAAAATCGAACCAAGAGAACTGGACCCCATCCTGACTGAGGTCAAC
 CTGATGAATGCCCGCAGTGAGCTATACCTACGCTTCCTCAAGAAGAGGATTAGCTCTGAT
 TTTGAGGTGGGAGACTCCATGGCCTCAGAGGAAGTAAAGCAAGAGCACCAGAAGTGTCTG
 GACAACTCCTCAATAACTGCCTTTTGGAGCTGTACCATGCAGGAGCTAATTGGCTTATAT
 GTTACCATGGAGGAGTACTTCATGAGGGAGACTGTCAATAAGGCTGTGGCTCTGGACACC
 TATGAGAAGGGCCAGCTGACATCCAGCATGGTGGATGATGTCTTCTACATTGTTAAGAAG
 TGCATTGGGCGGGCTCTGTCCAGCTCCAGCATTGACTGTCTCTGTGCCATGATCAACCTC
 GCCACCACAGAGCTGGAGTCTGACTTCAGGGATGTTCTGTGTAATAAGCTGCGGATGGGC
 TTCTCTGCCACCACCTTCCAGGACATCCAGCGCGGGGTGACAAGTGCCGTGAACATCATG
 CACAGCAGCCTCCAGCAAGGCAAATTTGACACAAAAGGCATCGAGAGTACTGACGAGGCG
 AAGATGTCTTCTTGGTGAATCTGAACAACGTGGAAGTCTGCAGTGAAAACATCTCCACT
 CTGAAGAAGACACTGGAGAGTGAATGCACCAAGCTCTTCAGCCAGGGCATTGGAGGGGAG
 CAGGCCCAGGCCAAGTTTGACAGCTGCCTTTCTGACTTGGCCGCCGTGTCCAACAAATTC
 CGAGACCTCTTGCAGGAAGGGCTGACGGAGCTCAACAGCACAGCCATCAAGCCACAGGTG
 CAGCCTTGGATCAACAGCTTTTCTCCGTCTCCCAACATCGAGGAGGAAGAATTCAAT
 GACTATGAGGCCAACGACCCTTGGGTACAACAGTTCATCCTTAACCTGGAGCAGCAAATG
 GCAGAGTTCAAGGCCAGCCTGTCCCGGTCTACGACAGCCTAACCAGCCTCATGACT
 AGCCTTGTGCGCTCGAGTTGGAGAAAGTGGTGTGAAATCCACCTTTAACCAGCTGGGT
 GGTCTGCAGTTTGACAAGGAGCTGAGGTGCTCATTTGCCCTACCTTACCACGGTGACCACC
 TGGACCATCCGAGACAAGTTTGCCCGCTCTCCAGATGGCCACCATCCTCAATCTGGAG
 CGGGTGACCGAGATCCTCGATTACTGGGGACCCAATTCCGGCCCATTTGACGTGGCGCCTC
 ACCCTTGCTGAAGTGCGCCAGGTGCTGGCCCTGCGGATAGACTTCCGCAGTGAAGATATC
 AAGAGGCTGCGCCTGTAG

Fig. 8

SEQ ID NO: 8

COG4

>ENSG00000103051 | 16 | codificante de proteina | ENST00000219329 | ENSP00000219329
 ATGGGGACCAAGATGGCGGACCTTGATTGCGCTCCGAAGCTGTCAGGGGTGCAGCAGCCG
 TCTGAGGGGGTGGGAGGTGGCCGCTGCTCCGAAATCTCCGCTGAGCTCATTCCGCTCCCTG
 ACAGAGCTGCAGGAGCTGGAGGCTGTATACGAACGGCTCTGCGGCGAGGAGAAAGTGGTG
 GAGAGAGAGCTGGATGCTCTTTTGGAAACAGCAAAACACCATTGAAAGTAAGATGGTCACT
 CTCCACCGAATGGGTCCCTAATCTGCAGCTGATTGAGGCCAACCTGAAATTGCTGCAGGAA
 GCTGAGCAACGTCTCAAAGCCATTGTGGCAGAGAAGTTTGCCATTGCCACCAAGGAAGGT
 GATCTGCCCCAGGTGGAGCGCTTCTTCAAGATCTTCCACTGCTGGGTTTGCTATGAGGAG
 GGATTAAGAAAGTTCTCGGAGTACCTTTGCAAGCAGGTGGCCAGTAAAGCTGAGGAGAAT
 CTGCTCATGGTGCTGGGGACAGACATGAGTGATCGGAGAGCTGCAGTCATCTTTCAGAT
 AACTTACTCTTCTGTTTGAAGGGATTGCCCGCATTGTGGAGACCCACCAGCCAATAGTG
 GAGACCTATTATGGGCCAGGGAGACTCTATACCCTGATCAATATCTGCAGGTGGAATGT
 GACAGACAGGTGGAGAAGGTGGTAGACAAGTTCATCAAGCAAAGGGACTACCACCAGCAG
 TTCCGGCATGTTCCAGAACACCTGATGAGAAATTCTACAACAGAAAAAATCGAACCAAGA
 GAACTGGACCCCATCTGACTGAGGTCAACCTGATGAATGCCCGCAGTGAGCTATACTTA
 CGCTTCCTCAAGAAGAGGATTAGCTCTGATTTTGAGGTGGGAGACTCCATGGCCTCAGAG
 GAAGTAAAGCAAGAGCACCAGAAGTGTCTGGACAACTCCTCAATAACTGCCTTTTGAGC
 TGTACCATGCAGGAGCTAATTGGCTTATATGTTACCATGGAGGAGTACTTCATGAGGGAG
 ACTGTCAATAAGGCTGTGGCTCTGGACACCTATGAGAAGGGCCAGCTGACATCCAGCATG
 GTGGATGATGTCTTCTACATTGTTAAGAAGTGCATTGGGCGGGCTCTGTCCAGCTCCAGC
 ATTGACTGTCTCTGTGCCATGATCAACCTCGCCACCACAGAGCTGGAGTCTGACTTCAGG
 GATGTTCTGTGTAATAAGCTGCGGATGGGCTTTCTGCCACCACCTTCCAGGACATCCAG
 CGCGGGGTGACAAGTGCCGTGAACATCATGCACAGCAGCCTCCAGCAAGGCAAATTTGAC
 ACAAAGGCATCGAGAGTACTGACGAGGCGAAGATGTCTTCTGGTGACTCTGAACAAC
 GTGGAAGTCTGCAGTGAAAACATCTCCACTCTGAAGAAGACACTGGAGAGTGACTGCACC
 AAGCTCTTCAGCCAGGGCATTGGAGGGGAGCAGGCCAGGCCAAGTTTGACAGCTGCCTT
 TCTGACTTGGCCGCCGTGTCCAACAAATTCCGAGACCTCTTGCAGGAAGGGCTGACGGAG
 CTCAACAGCAGCCATCAAGCCACAGGTGCAGCCTTGGATCAACAGCTTTTTCTCCGTC
 TCCCACAACATCGAGGAGGAAGAATTCAATGACTATGAGGCCAACGACCCTTGGGTACAA
 CAGTTCATCCTTAACCTGGAGCAGCAAATGGCAGAGTTCAGGCCAGCCTGTCCCCGGTC
 ATCTACGACAGCCTAACCGGCCCTCATGACTAGCCTTGTTGCCGTCGAGTTGGAGAAAGTG
 GTGCTGAAATCCACCTTTAACCGGCTGGGTGGTCTGCAGTTTGACAAGGAGCTGAGGTG
 CTCATTGCCCTACCTTACCACGGTGACCACCTGGACCATCCGAGACAAGTTTGCCCGGCTC
 TCCCAGATGGCCACCATCTCAATCTGGAGCGGGTGACCGAGATCCTCGATTACTGGGGA
 CCCAATTCCGGCCCATTGACGTGGCGCCTCACCCCTGCTGAAGTGCGCCAGGTGCTGGCC
 CTGCGGATAGACTTCCGCAGTGAAGATATCAAGAGGCTGCGCCTGTAG

Fig. 9

SEQ ID NO: 9

FDFT1

>ENSG00000079459 | 8 | codificante de proteína | ENST00000220584 | ENSP00000220584

ATGGAGTTTCGTGAAATGCCTTGGCCACCCCGAAGAGTTCTACAACCTGGTGCGCTTCCGG
 ATCGGGGGCAAGCGGAAGGTGATGCCCAAGATGGACCAGGACTCGCTCAGCAGCAGCCTG
 AAAACTTGCTACAAGTATCTCAATCAGACCAGTCGCAGTTTCGCAGCTGTTATCCAGGCG
 CTGGATGGGGAAATGCGCAACGCAGTGTGCATATTTTATCTGGTTCTCCGAGCTCTGGAC
 AACTGGAAGATGACATGACCATCAGTGTGGAAAAGAAGGTCCCGCTGTTACACAACCTTT
 CACTCTTTTCTTTACCAACCAGACTGGCGGTTTCATGGAGAGCAAGGAGAAGGATCGCCAG
 GTGCTGGAGGACTTCCCAACGATCTCCCTTGAGTTTAGAAATCTGGCTGAGAAATACCAA
 ACAGTGATTGCCGACATTTGCCGGAGAATGGGCATTGGGATGGCAGAGTTTTTGGATAAG
 CATGTGACCTCTGAACAGGAGTGGGACAAGTACTGCCACTATGTTGCTGGGCTGGTCGGA
 ATTGGCCTTTCCCGTCTTTTCTCAGCCTCAGAGTTTGAAGACCCCTTAGTTGGTGAAGAT
 ACAGAACGTGCCAACTCTATGGGCCTGTTTTTGCAGAAAACAAACATCATCCGTGACTAT
 CTGGAAGACCAGCAAGGAGGAAGAGAGTTCTGGCCTCAAGAGGTTTGGAGCAGGTATGTT
 AAGAAGTTAGGGGATTTTGCTAAGCCGGAGAATATTGACTTGGCCGTGCAGTGCCTGAAT
 GAACTTATAACCAATGCACTGCACCACATCCCAGATGTCATCACCTACCTTTTCGAGACTC
 AGAACCAGAGTGTGTTTAACTTCTGTGCTATTCCACAGGTGATGGCCATTGCCACTTTG
 GCTGCCTGTTATAATAACCAGCAGGTGTTCAAAGGGGCGAGTGAAGATTTCGGAAAGGGCAA
 GCAGTGACCTTGATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATATATCAG
 TATATGGAAGAGATTTATCATAGAATCCCCGACTCAGACCCATCTTCTAGCAAAACAAGG
 CAGATCATCTCCACCATCCGGACGCAGAATCTTCCCAACTGTCAGCTGATTTCCCGAAGC
 CACTACTCCCCCATCTACCTGTCGTTTGTGTCATGCTTTTGGCTGCCCTGAGCTGGCAGTAC
 CTGACCCTCTCTCCAGGTAACAGAAGACTATGTTTCAGACTGGAGAACACTGA

Fig. 10

SEQ ID NO: 10

PECI

>ENSG00000198721 | 6 | codificante de proteína | ENST00000380125 | ENSP00000369468

ATGAGAGCCAGTCAGAAGGACTTTGAAAATTCATGAATCAAGTGAACTCTTGAAAAAG
 GATCCAGGAAACGAAGTGAAGCTAAAACCTACGCGCTATATAAGCAGGCCACTGAAGGA
 CCTTGTAACATGCCCCAAACCAGGTGTATTTGACTTGATCAACAAGGCCAAATGGGACGCA
 TGGAATGCCCTTGGCAGCCTGCCCAAGGAAGCTGCCAGGCAGAACTATGTGGATTTGGTG
 TCCAGTTTGAGTCCTTCATTGGAATCCTCTAGTCAGGTGGAGCCTGGAACAGACAGGAAA
 TCAACTGGGTTTGAACTCTGGTGGTGACCTCCGAAGATGGCATCACAAAGATCATGTTC
 AACCGGCCCCAAAAGAAAAATGCCATAAACACTGAGATGTATCATGAAATTATGCGTGCA
 CTTAAAGCTGCCAGCAAGGATGACTCAATCATCACTGTTTTAACAGGAAATGGTGACTAT
 TACAGTAGTGGGAATGATCTGACTAATTCATGATATTCCCCCTGGTGGAGTAGAGGAG
 AAAGCTAAAAATAATGCCGTTTTACTGAGGGAATTTGTGGGCTGTTTTATAGATTTTCCT
 AAGCCTCTGATTGCAGTGGTCAATGGTCCAGCTGTGGGCATCTCCGTCACCCCTCCTTGGG
 CTATTTCGATGCCGTGTATGCATCTGACAGGGCAACATTTATACACCATTTAGTCACCTA
 GGCCAAAGTCCGGAAGGATGCTCCTCTTACACTTTTCCGAAGATAATGAGCCAGCCAAG
 GCAACAGAGATGCTTATTTTGGAAAGAAGTTAACAGCGGGAGAGGCATGTGCTCAAGGA
 CTTGTTACTGAAGTTTTCCCTGATAGCACTTTTCAGAAAGAAGTCTGGACCAGGCTGAAG
 GCATTTGCAAAGCTTCCCCCAAATGCCTTGAGAATTTCAAAGAGGTAATCAGGAAAAGA
 GAGAGAGAAAACTACACGCTGTTAATGCTGAAGAATGCAATGTCCTTCAGGGAAGATGG
 CTATCAGATGAATGCACAAATGCTGTGGTGAACCTCTTATCCAGAAAATCAAACCTGTGA

Fig. 11

SEQ ID NO: 11

PECI

>ENSG00000198721 | 6 | codificante de proteína | ENST00000380114 | ENSP00000369457
 ATGTATCATGAAATTTATGCGTGCACTTAAAGCTGCCAGCAAGGATGACTCAATCATCACT
 GTTTTAACAGGAAATGGTGAATATTACAGTAGTGGGAATGATCTGACTAACTTCACTGAT
 ATTCCCCCTGGTGGAGTAGAGGAGAAAGCTAAAAATAATGCCGTTTTACTGAGGGAATTT
 GTGGGCTGTTTTATAGATTTTCCTAAGCCTCTGATTGCAGTGGTCAATGGTCCAGCTGTG
 GGCATCTCCGTCACCCCTCCTTGGGCTATTCGATGCCGTGTATGCATCTGACAGGGCAACA
 TTTCATACACCATTTAGTCACCTAGGCCAAAGTCCGGAAGGATGCTCCTCTTACACTTTT
 CCGAAGATAATGAGCCCAGCCAAGGCAACAGAGATGCTTATTTTTGGAAAGAAGTTAACA
 GCGGGAGAGGCATGTGCTCAAGGACTTGTTACTGAAGTTTTCCCTGATAGCACTTTTCAG
 AAAGAAGTCTGGACCAGGCTGAAGGCATTTGCAAAGCTTCCCCAAATGCCTTGAGAATT
 TCAAAAGAGGTAATCAGGAAAAGAGAGAGAGAGAAAACTACACGCTGTTAATGCTGAAGAA
 TGCAATGTCTTCAGGGAAGATGGCTATCAGATGAATGCACAAATGCTGTGGTGAACCTC
 TTATCCAGAAAAATCAAACTGTGA

Fig. 12

SEQ ID NO: 12

PECI

>ENSG00000198721 | 6 | codificante de proteína | ENST00000380118 | ENSP00000369461
 ATGGCGATGGCGTACTTGGCTTGGAGACTGGCGCGGCGTTTCGTGTCCGAGTTCTCTGCAG
 GTCAGTAGTTTCCCGGTAGTTTCAGCTGCACATGAATAGAACAGCAATGAGAGCCAGTCAG
 AAGGACTTTGAAAATTCAATGAATCAAGTGAACTCTTGAAAAAGGATCCAGGAAACGAA
 GTGAAGCTAAACTCTACGCGCTATATAAGCAGGCCACTGAAGGACCTTGTAACATGCCC
 AAACCAGGTGTATTTGACTTGATCAACAAGGCCAAATGGGACGCATGGAATGCCCTTGGC
 AGCCTGCCCAAGGAAGCTGCCAGGCAGAACTATGTGGATTGGGTGTCCAGTTTGAGTCCT
 TCATTGGAATCCTCTAGTCAGGTGGAGCCTGGAACAGACAGGAAATCAACTGGGTTTGAA
 ACTCTGGTGGTGACCTCCGAAGATGGCATCACAAAGATCATGTTCAACCGGCCCAAAAAG
 AAAAATGCCATAAACACTGAGATGTATCATGAAATTATGCGTGCACTTAAAGCTGCCAGC
 AAGGATGACTCAATCATCACTGTTTTAACAGGAAATGGTGACTATTACAGTAGTGGGAAT
 GATCTGACTAACTTCACTGATATTTCCCTGGTGGAGTAGAGGAGAAAGCTAAAAATAAT
 GCCGTTTTACTGAGGGAATTTGTGGGCTGTTTTATAGATTTTCCTAAGCCTCTGATTGCA
 GTGGTCAATGGTCCAGCTGTGGGCATCTCCGTCACCTCCTTGGGCTATTCGATGCCGTG
 TATGCATCTGACAGGGCAACATTTATACACCATTTAGTCACCTAGGCCAAAGTCCGGAA
 GGATGCTCCTCTTACACTTTTCCGAAGATAATGAGCCCAGCCAAGGCAACAGAGATGCTT
 ATTTTTGGAAAGAAGTTAACAGCGGGAGAGGCATGTGCTCAAGGACTTGTTACTGAAGTT
 TTCCCTGATAGCACTTTTCAGAAAGAAGTCTGGACCAGGCTGAAGGCATTTGCAAGCTT
 CCCCCAATGCCTTGAGAATTTCAAAAGAGGTAATCAGGAAAAGAGAGAGAGAAAACTA
 CACGCTGTTAATGCTGAAGAATGCAATGTCCTTCAGGGAAGATGGCTATCAGATGAATGC
 ACAAATGCTGTGGTGAACCTCTTATCCAGAAAATCAAACTGTGA

Fig. 13

SEQ ID NO: 13

PECI

>ENSG00000198721 | 6 | codificante de proteina | ENST00000361538 | ENSP00000354737
 ATGAATAGAACAGCAATGAGAGCCAGTCAGAAGGACTTTGAAAATTCAATGAATCAAGTG
 AAACCTCTTGAAAAGGATCCAGGAAACGAAGTGAAGCTAAAACCTCTACGCGCTATATAAG
 CAGGCCACTGAAGGACCTTGTAACATGCCCAAACAGGTGTATTTGACTTGATCAACAAG
 GCCAATGGGACGCATGGAATGCCCTTGGCAGCCTGCCCCAAGGAAGCTGCCAGGCAGAAC
 TATGTGGATTTGGTGTCCAGTTTGAGTCCTTCATTGGAATCCTCTAGTCAGGTGGAGCCT
 GGAACAGACAGGAAATCAACTGGGTTTGAAACTCTGGTGGTGACCTCCGAAGATGGCATC
 ACAAAGATCATGTTCAACCGGCCCAAAAAGAAAAATGCCATAAACACTGAGATGTATCAT
 GAAATTATGCGTGCCTTAAAGCTGCCAGCAAGGATGACTCAATCATCACTGTTTTAACA
 GGAAATGGTGACTATTACAGTAGTGGGAATGATCTGACTAACTTCACTGATATTCCCCCT
 GGTGGAGTAGAGGAGAAAGCTAAAAATAATGCCGTTTTACTGAGGGAATTTGTGGGCTGT
 TTTATAGATTTTCTAAGCCTCTGATTGCAGTGGTCAATGGTCCAGCTGTGGGCATCTCC
 GTCACCCTCCTTGGGCTATTGATGCCGTGTATGCATCTGACAGGGCAACATTTTCATACA
 CCAATTTAGTCACCTAGGCCAAAGTCCGGAAGGATGCTCCTCTTACACTTTTCCGAAGATA
 ATGAGCCCAGCCAAGGCAACAGAGATGCTTATTTTTGGAAAGAAGTTAACAGCGGGAGAG
 GCATGTGCTCAAGGACTTGTTACTGAAGTTTTCCCTGATAGCACTTTTCAGAAAGAAGTC
 TGGACCAGGCTGAAGGCATTTGCAAAGCTTCCCCCAAATGCCTTGAGAATTTCAAAGAG
 GTAATCAGGAAAAGAGAGAGAGAAAACTACACGCTGTTAATGCTGAAGAATGCAATGTC
 CTTCAGGGAAGATGGCTATCAGATGAATGCACAAATGCTGTGGTGAACCTCTTATCCAGA
 AAATCAAACTGTGA

Fig. 14

SEQ ID NO: 14

PECI

>ENSG00000198721 | 6 | codificante de proteína | ENST00000380120 | ENSP00000369463

ATGTTCAACCGGCCCAAAAAGAAAAATGCCATAAACACTGAGATGTATCATGAAATTATG
CGTGCACTTAAAGCTGCCAGCAAGGATGACTCAATCATCACTGTTTTAACAGGAAATGGT
GACTATTACAGTAGTGGGAATGATCTGACTAACTTCACTGATATCCCCCTGGTGGAGTA
GAGGAGAAAGCTAAAAATAATGCCGTTTTACTGAGGGAATTTGTGGGCTGTTTTATAGAT
TTTCCTAAGCCTCTGATTGCAGTGGTCAATGGTCCAGCTGTGGGCATCTCCGTCACCCCTC
CTTGGGCTATTCGATGCCGTGTATGCATCTGACAGGGCAACATTTTCATACACCATTTAGT
CACCTAGGCCAAAGTCCGGAAGGATGCTCCTCTTACACTTTTCCGAAGATAATGAGCCCA
GCCAAGGCAACAGAGATGCTTATTTTTGGAAAGAAGTTAACAGCGGGAGAGGCATGTGCT
CAAGGACTTGTTACTGAAGTTTCCCTGATAGCACTTTTCAGAAAGAAGTCTGGACCAGG
CTGAAGGCATTTGCAAAGCTTCCCCCAAATGCCTTGAGAATTTCAAAGAGGTAATCAGG
AAAAGAGAGAGAGAAAACTACACGCTGTTAATGCTGAAGAATGCAATGTCCTTCAGGGA
AGATGGCTATCAGATGAATGCACAAATGCTGTGGTGAACCTCTTATCCAGAAATCAAAA
CTGTGA

Fig. 15

SEQ ID NO: 15

CTNND2

>ENSG00000169862 | 5'codificante de proteína|ENST00000359640 | ENSP00000352661

ATGTTTGCGAGGAAGCCGCGGGCGCGCGCTTTGGGAGCTATGCCTGTTCCAGACCAG
 CCTTCATCAGCCTCAGAGAAGACGAGTTCCCTGAGCCCCGGCTTAAACACCTCCAACGGG
 GATGGCTCTGAAACAGAAACCACCTCTGCCATCCTCGCCTCAGTCAAAGAACAGGAATTA
 CAGTTTGAAAGGCTGACCCGAGAGCTGGAGGCTGAACGGCAGATCGTAGCCAGCCAGCTG
 GAGCGATGCAAGCTCGGATCCGAGACTGGCAGCATGAGCAGCATGAGTTCAGCAGAAGAG
 CAGTTTCAGTGGCAGTCAACAGATGGTCAAAAAGATATCGAAGATGAGCTTACAACAGGT
 CTCGAGCTGGTGGACTCCTGTATTAGGTCACTACAGGAATCAGGAATACTTGACCCACAG
 GATTATTCTACAGGTGAAAGGCCAGCCTGCTCTCCAGAGTGCCTTCAGCTCAATTCC
 AAACCTGAAGGGTCTTTCCAGTATCCGGCCAGCTACCATAGCAACCAGACCTTGGCCCTG
 GGGGAAACCACCCCTTCACAGCTCCCGGCCCGAGGCACACAAGCCCGAGCTACGGGCCAG
 AGCTTCAGCCAGGGCAGCACCAGCCGCGCGGCCACCTGGCGGGGCCGAGCCCGCGCCG
 CCGCCGCGCGCCGCGCGCGGGAGCCGTTTCGCGCCAGCCTGGGCAGCGCCTTCCACCTG
 CCGGACGCGCGCCGCGCGCGCGCGCGCGCTCTACTACTCCAGCTCCACGCTGCC
 GCGCGCGCGCGCGGGGCTCCCGCTGGCGCGCGCCAGGGCGGTTGCGCCACCAAGCTG
 CAGCGCGCGCGCTGGCCCCCGAGGGCGCCACCTACGCGCGCGCGCGCGCTCCTCGCCC
 AAGCAGTCGCCCCAGCCGCTGGCCAGTCTACAGCACCAGCTCGCCCATCAACATCGTC
 GTGTCTCGGCCGGCCTGTCCCGATCCGCGTGACCTCGCCCCCACCCTGTCAGTCCACC
 ATCTCTCTCGCCCATCCACCAGCTGAGCTCCACCATCGGCAGCTACGCCACCTGTCTG
 CCCACCAAGCGCCTGGTCCACGCGTCCGAGCAGTACAGCAAGCACTCGCAGGAGCTGTAT
 GCCACGGCCACCTCCAGAGGCCGGGCAGCCTGGCAGCTGGTTCCCGAGCCTCATACAGC
 AGCCAGCATGGGCACCTGGGCCAGAGTTGCGGGCCCTGCAGTCCCCAGAACACCACATA
 GATCCCATCTATGAAGACCGCGTCTATCAGAAGCCCCCTATGAGGAGTCTCAGCCAGAGC
 CAGGGGGACCCCTCTGCCGCCAGCACACCGGCACCTACCGCAGCAGCAGCCCCATCT
 TCCCTTGGTGTGACTCCGTCCCTTGACGCGCACAGGCAGCCAGCAGCGCCACAGAGT
 GCCCGCGCGCCACCTTCAGAGGGCCAGCTATGCCGCGCGCCAGCCTCCAAATACGCG
 GACCCCTACCGACAGCTGCAGTATTGTCCCTCTGTTGAGTCTCCATACAGCAATCCGGC
 CCTGCTCTCCCGCTGAAGGCACCTTGCGCCAGGTCCCGTCCATGATAGCATTACAGAA
 GATCCAGAGAATTTGGATGGAGAGACCCGGAACGCGGGAAGTGATTAGATGTTGCAG
 CACCACTTTCCCTCGGTCCAGTCTAACGCGGCAGCCTACTTGCAACACCTCTGTTTGA
 GACAACAAATTAAGCCGAGATAAGGAGACAAGGAGGCATCCAGCTCCTGGTGGACCTG
 TTGGATCATCGGATGACCGAAGTCCACCGTAGTGCTGTGGAGCTCTGAGAAACCTGGTG
 TATGGGAAGGCCAACGATGATAACAAATTGCCCTGAAAAACTGTGGTGGCATCCAGCA
 CTGGTGAAGTTACTCCGCAAGACGACTGACCTGGAGATCCGGGAGCTGGTCACAGGAGTC
 CTTTGAACCTCTCCTCATGCGATGCACTCAAAATGCCAATCATCCAGATGCCCTAGCA
 GTACTGACCAACGCGGTGATTATCCCCCACTCAGGCTGGGAAAAATTCGCCTTTCAGGAT
 GATCGGAAAAATACAGCTGCATTTCATCAGGTGCTGCGTAACGCCACCGGGTGCTAAGG
 AATGTTAGTTTCGGCCGAGAGGAGGCCCCGAGAAGGATGAGAGAGTGTGATGGGCTTACG
 GATGCTTGTCTGCTGATCCAGTCTGCGCTGGGAGAGTGTGATGATGATGATGATGATGAT
 GTTGAACCTGTGTGTCATTTTAAGGAACCTCTCGTACCGGCTGGCGGCAGAAACGTCT
 CAGGGACAGCAGATGGGCACGGACGAGCTGGACGGCTACTCTGTGGCGAGGCCAATGGC
 AAGGATGCTGAGAGCTCTGGGTGCTGGGGCAAGAGAAGAGAAAAAGAAATCCCAAGAT
 CAGTGGTCAGTATATATCCGAGCCGCTGTCCGAAAAGAGAAAGGCTGCCCATCTCGTG
 GAGCTGCTCCGAATAGACAATGACCGTGTGGTGTGCGCGGTGGCCACTGCGCTGCGGAAC
 ATGGCCTTGGACGTCAGAAATAAGGAGCTCATCGGCAAAATACGCCATGCGAGACCTAGTC
 CACAGGCTTCCAGGAGGGAACAACAGCAACAACACTGCAAGCAAGGCCATGTCCGATGAC
 ACAGTGACAGCTGTCTGCTGCACACTGCACGAAGTGATTACCAAGAACATGGAGAAGCC
 AAGGCCCTACGGGATCCCGCTGCGATCGAGAAGTGGTGGCATCTCCAAAAGCAAAGGA
 GATAAACACTCTCCAAAAGTGGTCAAGGCTGCATCTCAGGTCTCAACAGCATGTGGCAG
 TACCGAGATCTGAGGAGTCTCTACAAAAAGGATGGATGGTCAACATACCCTTTGTAGCC
 TCGTCTTCAACCATCGAGAGGGACCGGCAAGGCCCTACTCTCTCCCGACGCCCTCC
 ATCTCCCTGTGCGCGTGTCTCCCAACAACCGCTCAGCAAGTGCCCCAGCTTCACCTCGG
 GAAATGATCAGCCTCAAAGAAAGGAAAAACAGACTACGAGTGACCGGCAGCAACGCCACC
 TACCACGGAGCTAAAGGCGAACACACTTCCAGGAAAGATGCCATGACAGCTCAAAACACT
 GGAAATTCACCTTTGTATAGGAATTCCTATGGTGCGCCCGCTGAAGACATCAACACAAC
 CAGGTTTCAGCACAGCCAGTCCACAGGAGCCAGCAGAAAAGATTACGAGACCTACCAG
 CCATTTCAGAATTCACAAGAAATTACGATGAGTCCTTCTTCGAGGACCAGGTCCACCAT
 CGCCCTCCCGCCAGCGAGTACACCATGCACCTGGGTCTCAAGTCCACCGGCAACTACGTT
 GACTTCTACTCAGCTGCCCGTCCCTACAGTGAACCTGAACATGAAACGAGCCACTACCCG
 GCCTCCCCGACTCCTGGGTGTGA

Fig. 16

SEQ ID NO: 16

CTNND2

>ENSG00000169862 | 5qodificante de proteína | ENST00000304623 | ENSP00000307134

ATGTTTGCAGGAAGCCGCCGGGCGCCGCGCTTTGGGAGCTATGCCTGTTCCAGACCAG
 CCTTCATCAGCCTCAGAGAAGACGAGTTCCCTGAGCCCGGCTTAAACACCTCCAACGGG
 GATGGCTCTGAAACAGAAACCACCTCTGCCATCCTCGCCTCAGTCAAAGAACAGGAATTA
 CAGTTTGAAGGCTGACCCGAGAGCTGGAGGCTGAACGGCAGATCGTAGCCAGCCAGCTG
 GAGCGATGCAAGCTCGGATCCGAGACTGGCAGCATGAGCAGCATGAGTTCAGCAGAAGAG
 CAGTTTCAGTGGCAGTCACAAGATGGTCAAAAAGATATCGAAGATGAGCTTACACAGGT
 CTCGAGCTGGTGGACTCCTGTATTAGGTCACTACAGGAATCAGGAATACTTGACCCACAG
 GATTATTCTACAGGTGAAAGGCCAGCCTGCTCTCCAGAGTGCACCTCAGCTCAATTCC
 AAACCTGAAGGGTCTTTCCAGTATCCGGCCAGCTACCATAGCAACCAGACCCTGGCCCTG
 GGGGAAACCACCCCTTCACAGCTCCCGGCCGAGGCACACAAGCCCGAGCTACGGGCCAG
 AGCTTCAGCCAGGGCACGACCAGCCGCGCGGCCACCTGGCGGGGCCGAGCCCGCGCGG
 CCGCGCGCGCGCGCGCGCGCGGAGCCGTTGCGGCCAGCCTGGGCAGCGCCTTCCACCTG
 CCCGACGCGCGCGCGCGCGCGCGCGCGCGCGCTCTACTACTCCAGCTCCACGCTGCCC
 GCGCGCGCGCGCGGGGCTCCCGCTGGCGCGCGCCAGGGCGGTTGCGCCACCAAGCTG
 CAGCGCGCGCGCTCGGCCCGGAGGCGCCACCTACGCGCGCGCGCGCGCTCCTCGCCC
 AAGCAGTCGCCCAGCCGCTGGCCAAGTCTACAGCACCAGCTCGCCCATCAACATCGTC
 GTGTCTCGGCCGCGCTGTCGCCGATCCGCGTGACCTCGCCCCCACCCTGCAGTCCAGC
 ATCTCCTCCTCGCCCATCCACCAGCTGAGCTCCACCATCGGCACGTACGCCACCCTGTG
 CCCACCAAGCGCTGGTCCACGCGTCCGAGCAGTACAGCAAGCACTCGCAGGAGCTGTAT
 GCCACGGCCACCCTCCAGAGGCCGGCAGCCTGGCAGCTGGTTCCCGAGCCTCATACAGC
 AGCCAGCATGGGCACCTGGGCCAGAGTTGCGGGCCCTGAGTCCCGAGAACCACACATA
 GATCCCATCTATGAAGACCGCTCTATCAGAAGCCCCCTATGAGGAGTCTCAGCCAGAGC
 CAGGGGGACCTCTGCCGCCAGCACACACCGGCACCTACCGCACGAGCACAGCCCCATCT
 TCCCTTGGTGTGAGTCCGTCCCCTTGACGCGCACAGGCAGCCAGCAGGCCACAGAAAT
 GCGCGCGCGGCCACCTCCAGAGGGCCAGCTATGCGCGCGGCCAGCCTCCAATTACGCG
 GACCCCTACCGACAGCTGCAGTATTGTCCCTCTGTTGAGTCTCCATACAGCAATCCGGC
 CTTGCTCTCCGCGCTGAAGGCACCTTGGCCAGGTCCCGTCCATTGATAGCATTAGAAA
 GATCCAGAGAATTTGGATGGAGAGACCCGGAAGTCCGGAAGTGATTAGATGTTGACAG
 CACCAGTTTCCCTCGGTCCAGTCTAACGCGGCAGCCTACTTGCAACACCTCTGTTTTGGA
 GACAACAAATTAAGCCAGATAAGGAGACAAGGAGGCATCCAGTCTCTGGTGGACCTG
 TTGGATCATCGGATGACCGAAGTCCACCGTAGTGCCTGTGGAGCTCTGAGAAACCTGGTG
 TATGGGAAGGCCAACGATGATAACAAATTTGCCCTGAAAACTGTGGTGGCATCCAGCA
 CTGGTGAGGTACTCCGCAAGACGACTGACCTGGAGATCCGGGAGCTGGTACAGGAGTCT
 CTTTGGAACTCTCTCTCATGCGATGCACTCAAAATGCCAATCATCCAGGATGCCCTAGCA
 GTACTGACCAACGCGGTGATTATCCCCACTCAGGCTGGGAAAATTCGCTCTTCAGGAT
 GATCGGAAAATACAGCTGCATTATCACAGGTGCTGCGTAACGCCACCGGGTGCCTAAGG
 AATGTTAGTTTCGGCCGGAGAGGAGGCCCGCAGAAGGATGAGAGAGTGTGATGGGCTTACG
 GATGCCTTGTGTACGTGATCCAGTCTGCGCTGGGGAGCAGTGAGATCGATAGCAAGACC
 GTTGAAAAGTGTGTGTGCAATTTAAGGAACCTCTCGTACCAGCTGGCGCGCAGAAACGCTCT
 CAGGGACAGCAGATGGGACCGGACGAGCTGGACGGGCTACTCTGTGGCGAGGCCAATGGC
 AAGGATGCTGAGAGCTCTGGGTGCTGGGGCAAGAAGAAGAAAAAGAAATCCCAAGAT
 CAGTGGGATGGAGTAGGACCTCTTCCAGACTGTGCTGAACCACCAAGGGATCCAGATG
 CTGTGGCACCCTCAATAGTCAAACCTACCTCACACTGCTCTCTGAGTGCTCAAATCCA
 GACAGCTGGGAAGGGGCGGCGAGGCGCCCTGCAGAACTTGGCTGCAGGGAGCTGGAAGTGG
 TCAGTATATATCCGAGCCGCTGTCCGAAAAGAGAAAGGCTGCCATCCTCGTGGAGCTG
 TCCGAAATAGACAATGACCGTGTGGTGTGCGCGGTGGCCACTGCGCTGCGGAACATGGCC
 TTGGACGTGAGAAATAAGGAGCTCATCGGCAATACGCCATGCGAGACCTAGTCCACAGG
 CTTCCAGGAGGGAACAACAGCAACAACACTGCAAGCAAGGCCATGTGCGATGACACAGTG
 ACAGCTGTCTGCTGCACACTGCACGAAGTGATTACCAAGAACATGGAGAACGCCAAGGCC
 TTACGGGATGCCGCTGGCATCGAGAAGTTGGTCGGCATCTCCAAAAGCAAAGGAGATAAA
 CACTCTCCAAAAGTGGTCAAGGCTGCATCTCAGGTCTCAACAGCATGTGGCAGTACCGA
 GATCTGAGGAGTCTCTACAAAAGGATGGATGGTCACAAATACCACTTGTAGCCTCGTCT
 TCAACCATCGAGAGGGACCGGCAAGGCCCTACTCCTCCTCCGCGACGCCCTCCATCTCC
 CCTGTGCGCTGTCTCCCAACAACCGCTCAGCAAGTGCCCCAGCTTCACCTCGGGAAATG
 ATCAGCCTCAAAGAAAGGAAAACAGACTACAGTGCACCGGCAGCAACGCCACCTACCAC
 GGAGCTAAAGGCGAACACACTTCCAGGAAAGATGCCATGACAGCTCAAAACACTGGAATT
 TCAACTTTGTATAGGAATTCTTATGGTGCGCCGCTGAAGACATCAACACAACCAGGTT
 TCAGCACAGCCAGTCCACAGGAGCCAGCAGAAAAGATTACGAGACCTACAGCCATTT
 CAGAATCCACAAGAAATTACGATGAGTCTTCTTCGAGGACCAGTCCACCATCGCCCT

CCCGCCAGCGAGTACACCATGCACCTGGGTCTCAAGTCCACCGGCAACTACGTTGACTTC
TACTCAGCTGCCCCGTCCCTACAGTGAAGTGAAGTATGAAACGAGCCACTACCCGGCCTCC
CCCGACTCCTGGGTGTGA

Fig. 16 (continuación)

Fig. 17

SEQ ID NO: 17

NSMCE1

>ENSG00000169189|16|codificante de proteina|ENST00000358787|ENSP00000351638
 CCGTATCCGCTAGCGCGGTGGGATGCGCTTGGGCTCCCTGTTTCGTTCCCACATGCAGGGC
 AGCACAAAGGAGAATGGGCGTCATGACTGATGTCCACCGGCGCTTCCTCCAGTTGCTGATG
 ACCCATGGCGTGCTAGAGGAATGGGACGTGAAGCGCTTGCAGACGCACTGCTACAAGGTC
 CATGACCGCAATGCCACCGTAGATAAGTTGGAGGACTTCATCAACAACATTAACAGTGTC
 TTGGAGTCCTTGTATATTGAGATAAAGAGAGGAGTCACGGAAGATGATGGGAGACCCATT
 TATGCGTTGGTGAATCTTGCTACAACCTCAATTTCCAAAATGGCTACGGATTTTGCAGAG
 AATGAACTGGATTTGTTTAGAAAAGGCTCTGGAAGTGATTATTGACTCAGAAACCTTGCGT
 CTTCCACAAACATATTGA

Fig. 18

SEQ ID NO: 18

NSMCE1

>ENSG00000169189|16|codificante de proteína|ENST00000361439|ENSP00000355077
 ATGCAGGGCAGCACAAAGGAGAAATGGGCGTCATGACTGATGTCCACCGGCGCTTCCTCCAG
 TTGCTGATGACCCATGGCGTGCTAGAGGAATGGGACGTGAAGCGCTTGCAGACGCACTGC
 TACAAGGTCCATGACCGCAATGCCACCGTAGATAAGTTGGAGGACTTCATCAACAACATT
 AACAGTGTCTTGGAGTCCTTGTATATTGAGATAAAGAGAGGAGTCACGGAAGATGATGGG
 AGACCCATTTATGCGTTGGTGAATCTTGCTACAACCTCAATTTCCAAAATGGCTACGGAT
 TTTGCAGAGAATGAACTGGATTTGTTTAGAAAGGCTCTGGAAGTGAATTATTGACTCAGAA
 ACCGGCTTTGCGTCTTCCACAAACATATTGAACCTGGTTGATCAACTTAAAGGCAAGAAG
 ATGAGGAAGAAGGAAGCGGAGCAGGTGCTGCAGAAGTTTGTTCAAAACAAGTGGCTGATT
 GAGAAGGAAGGGGAGTTCACCCCTGCACGGCCGGGCCATCCTGGAGATGGAGCAATACATC
 CGGGAGACGTACCCCGACGCGGTGAAGATCTGCAATATCTGTCACAGCCTCCTCATCCAG
 GGTCAAAGCTGCGAAACCTGTGGGATCAGGATGCACTTACCCCTGCGTGGCCAAGTACTTC
 CAGTCGAATGCTGAACCGCGCTGCCCCACTGCAACGACTACTGGCCCCACGAGATCCCA
 AAAGTCTTCGACCCTGAGAAGGAGAGGGAGTCTGGTGTCTTGAAATCGAACAAAAAGTCC
 CTGCGGTCCAGGCAGCATTAG

Fig. 19

SEQ ID NO: 19

NSMCE1

>ENSG00000169189 | 16 | codificante de proteína | ENST00000311505 | ENSP00000310853

GTCCACCTTGCGACCGTATCCGCTAGCGCGGCCCTGGGATGCGCTTGGGCTCCCTGTTTCGT
 TCCCACATGCAGGGCAGCACAAGGAGAATGGGCGTCATGACTGATGTCCACCGGCGCTTC
 CTCCAGTTGCTGATGACCCATGGCGTGCTAGAGGAATGGGACGTGAAGCGCTTGCAGACG
 CACTGCTACAAGGTCCATGACCGCAATGCCACCGTAGATAAGTTGGAGGACTTCATCAAC
 AACATTAACAGTGTCTTGGAGTCCTTGTATATPGAGATAAAGAGAGGAGTCACGGAAGAT
 GATGGGAGACCCATTTATGCGTTGGTGAATCTTGCTACAACTTCAATTTCCAAAATGGCT
 ACGGATTTTGCAGAGAATGAACTGGATTTGTTTAGAAAGGCTCTGGAAGTGAATTATTGAC
 TCAGAAACCGGCTTTGCGTCTTCCACAAACATATTGAACCTGGTTGATCAACTTAAAGGC
 AAGAAGATGAGGAAGAAGGAAGCGAGGTGCTGCAGAAGTTTGTTCAAAACAAGTGGCTGA

Fig. 20

SEQ ID NO: 20

KTELC1

>ENSG00000163389 | 3 | codificante de proteína | ENST00000295588 | ENSP00000295588
 ATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTGGCTGCTGTTGTTCTCCTGCCCTCA
 GCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGAAAGTATTTATTGACCAAATTAAC
 AGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAACTGCAGCTGCTACCATGGTGTC
 ATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAGGAAGATGATGGCAGAGGTA
 GTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACAGACTGTACCGGGAAAAT
 GACTGCATGTTCCCCCTCAAGGTGTAGTGGTGTGAGCACTTTATTTTGGAAAGTGATCGGG
 CGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCAGGTTCTTAAATGG
 ATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACCATGATATCATG
 TATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTGGCCAATTTATCCTACAGGT
 CTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTGGCCATGG
 AAAAAGAAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAGATCCT
 CTCATTCTTCTGTCTCGGAAAAACCCAAAACCTGTTGATGCAGAATACACCAAAAACCCAG
 GCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGTG
 GATCACTGCAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTT
 AAACACCTCTTCTGTGTGGCTCACTTGTTCATGTTGGTGATGAGTGGCTAGAATTC
 TTCTATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAAT
 GTCCAAGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAA
 AGGGGAAGCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAG
 AACCTCTTGAGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTAT
 GATCAAATTATTCCCAAATGTTGAAAACCTGAACATAG

Fig. 21

SEQ ID NO: 21

HS6ST1

>ENSG00000136720|2| codificante de proteína| ENST00000259241| ENSP00000259241

ATCGCGCGGCGGCGCGCCGGCGGCGGACGACCATGGTTGAGCGCGCCAGCAAGTTCGTGCTG
GTGGTGGCGGGCTCGGTGTGCTTCATGCTCATCTTGTAACAGTACGCGGGCCCAGGACTG
AGCCTGGGCGCGCCCGGCGGCGCGCGCCGACGACCTGGACCTGTTCCCCACACCC
GACCCCCACTACGAGAAGAAGTACTACTTCCCGGTCCGCGAGCTGGAGCGCTCGCTGCGG
TTCGACATGAAGGGCGACGACGTGATCGTCTTCCTGCACATCCAGAAGACGGGCGGCACC
ACCTTCGGCCGCCACCTCGTG CAGAACGTACGCTCGAGGTGCCGTGCGACTGCCGGCCC
GGCCAGAAGAAGTGCACCTGCTACCGGCCAACCGCCGCGAGACTTGGCTCTTCTCCCGC
TTCTCCACCGGCTGGAGCTGCGGGCTGCACGCCGACTGGACCGAGCTCACCAACTGCGTG
CCGGGCGTGCTGGACCGCGCGACTCCGCGCGCTGCGCACGCCCCAGGAAGTTCTACTAC
ATCACCTGCTACGAGACCCCGTGTCCCGCTACCTGAGCGAGTGGCGGCATGTGCAGAGG
GGTGCCACGTGGAAGACGTGTTGCATATGTGTGATGGGCGCACGCCACGCTGAGGAG
CTGCCGCCCTGCTACGAGGGGCACGGACTGGTCGGGCTGCACGCTACAGGAGTTCATGGAC
TGCCCGTACAACCTGGCCAACAACCGCCAGGTGCGCATGCTGGCCGACCTGAGCCTGGTG
GGCTGCTACAACCTGTCTTCATCCCCGAGGGCAAGCGGGCCAGCTGCTGCTCGAGAGC
GCCAAGAAGAACCTGCGGGGCATGGCCTTCTTCGGCCTGACCGAGTTCAGCGCAAGACG
CAGTACCTGTTGAGCGGACGTTCAACCTCAAGTTCATCCGGCCCTTCATGCAGTACAAT
AGCACGCGGGCGGGCGGCGTGGAGGTGGATGAAGACACCATCCGGCGCATCGAGGAGCTC
AACGACCTGGACATGCAGCTGTACGACTACGCCAAGGACCTCTTCAGCAGCGCTACCG
TACAAGCGGCAGCTGGAGCGCAGGGAGCAGCGCTGAGGAGCCGCGAGGAGCGTCTGCTG
CACC GGCCCAAGGAGGCACTGCCGCGGGAGGATGCCGACGAGCCGGGCCGCGTGCCACC
GAGGACTACATGAGCCACATCATTGAGAAGTGGTAG

Fig. 22**SEQ ID NO: 22****ARMC6**

>ENSG00000105676 | 19 | codificante de proteina | ENST00000379532 | ENSP00000368847

ATGACATCCTGCAGATGCTCAGTGACCTCCAGGAGTCTGTGGCCAGCTCTCGCCCCCAGG
 AGGTGTGAGCATACCTCACCCGCTTCTGCGCAGTGCAAACAGGACAAGGCCTGCCGCTTC
 CTCGCGGCCCCAGAAGGGGGCCTACCCCATCATCTTCACTGCCTGGAAGCTGGCCACTGCA
 GGTGACCAGGGCCTTCTGCTCCAGTCCCTCAATGCCCTGTGCGTGCTGACTGATGGACAG
 CCAGACCTCCTGGATGCCCAGGGCCTGCAGCTCCTAGTGGCCACGCTGACCCAGAATGCT
 GATGAGGCTGACCTGACCTGCTCTGGGATCCGCTGTGTGCGTCACGCTTGCCTGAAACAT
 GAACAGAATCGGCAAGACCTGGTGAAAGCTGGCGTGCTGCCTCTGCTGACTGGTGCCATC
 ACCCATCATGGCCACCACACTGACGTGGTCAGGGAAGCCTGCTGGGCCCTGCGTGTGATG
 ACCTTCGATGACGACATCCGTGTGCCCTTTGGCCATGCCACAACCATGCCAAGATGATT
 GTGCAGGAGAACAAAGGCTTGAAGGTGCTCATCGAAGCCACCAAAGCGTTCCTGGATAAC
 CCTGGCATCCTGAGCGAGCTCTGTGGAACCCCTGTCCCGCCTGGCCATTTCGCAACGAGTTC
 TGCCAGGAGGTGCTCGACCTCGGGGGCCTGAGCATTCTGGTGTCCCTGCTAGCCGACTGC
 AATGACCACCAGATGAGGGACCAGAGCGGCGTTCAGGAGCTCGTGAAGCAAGTGCTGAGC
 ACCCTGCGAGCCATCGCAGGCAACGACGACGTGAAAGATGCTATTGTCCGTGCTGGTGGG
 ACGGAGTCCATCGTGGCTGCTATGACCCAGCATCTGACCAAGCCCCAGGTGTGTGAGCAG
 AGCTGCGCGGCCCTGTGCTTCCTGGCCCTGCGTAAGCCCGACAACAGCCGCATCATCGTG
 GAGGGTGGCGGGGCTGTGGCAGCACTGCAGGCCATGAAGGCACACCCGCAGAAGGCCGGC
 GTGCAGAAACAGGCTTGCATGCTGATCGAAACCTGGTGGCCACAGGCCTTCTCGAAGC
 CCATCCTGGACCTGGGGGCTGAGGCACTCATCATGCAGGCCCGATCTGCCACCGTGACT
 GTGAGGACGTGGCCAAGGCCGCCCTGCGGGACCTGGGTTGTGATGTCGAGCTCCGAGAGC
 TGTGGACAGGCCAGAGGGGCAACCTGGCGCCATGACCCAGGCCAGTCTGGTGACTCTG
 GGTGAGTCGTGTGACTCAGGAATGGGGGTAGATCCATGTCTCCACTGTCCCCCATTAGT
 TCTGTCCCTTACAAATGAGAAGTGTCTTCTGGCAGGCCCTAGGTAAAGGGTCGGGGGAG
 GGGGGAGCCTTGTAAG

Fig. 23

SEQ ID NO: 23

ARMC6

>ENSG00000105676|19|codificante de proteína|ENST00000392335|ENSP00000376147

ATGGTCTCCAAGCGCATTGCCCAGGAGACCTTTGATGCAGCTGTGCGCGAGAACATCGAG
 GAGTTTGCGATGGGGCCAGAGGAGGCAGTGAAAGAGGCCGTGGAGCAGTTTGAATCGCAA
 GGGGTTGATCTGAGCAACATTGTAAAGACGGCACCTAAAGTCTCTGCAGACGGATCCAG
 GAGCCACACATGACATCCTGCAGATGCTCAGTGACCTCCAGGAGTCTGTGGCCAGCTCT
 CGCCCCCAGGAGGTGTCAGCATACCTCACCCGCTTCTGCGACCAGTGCAACAGGACAAG
 GCCTGCCGCTTCTCGCGGCCAGAAAGGGGGCCTACCCCATCATCTTCACTGCCTGGAAG
 CTGGCCACTGCAGGTGACCAGGGCCTTCTGCTCCAGTCCCTCAATGCCCTGTGGGTGCTG
 ACTGATGGACAGCCAGACCTCCTGGATGCCCAGGGCCTGCAGCTCCTAGTGGCCACGCTG
 ACCCAGAATGCTGATGAGGCTGACCTGACCTGCTCTGGGATCCGCTGTGTGCGTCACGCT
 TGCCTGAAACATGAACAGAATCGGCAAGACCTGGTGAAAGCTGGCGTGCTGCCTCTGCTG
 ACTGGTGCCATCACCCATCATGGCCACCACACTGACGTGGTCAGGGAAGCCTGCTGGGCC
 CTGCGTGTGATGACCTTCGATGACGACATCCGTTGCGCCCTTTGGCCATGCCCACAACCAT
 GCCAAGATGATTGTGCAGGAGAACAAGGCTTGAAGGTGCTCATCGAAGCCACCAAGCG
 TTCCTGGATAACCCTGGCATCCTGAGCGAGCTCTGTGGAACCCTGTCCCGCCTGGCCATT
 CGCAACGAGTTCTGCCAGGAGGTGCTCGACCTCGGGGGCCTGAGCATTCTGGTGTCCCTG
 CTAGCCGACTGCAATGACCACCAGATGAGGGACCAGAGCGGCGTTTCAAGGAGCTCGTGAAG
 CAAGTGCTGAGCACCTGCGAGCCATCGCAGGCAACGACGACGTGAAAGATGCTATTGTC
 CGTGCTGGTGGGACGGAGTCCATCGTGGCTGCTATGACCCAGCATCTGACCAGCCCCCAG
 GTGTGTGAGCAGAGCTGCGCGGCCCTGTGCTTCTGGCCCTGCGTAAGCCCGACAACAGC
 CGCATCATCGTGGAGGGTGGCGGGGCTGTGGCAGCACTGCAGGCCATGAAGGCACACCCG
 CAGAAGGCCGGCGTGACAGAAACAGGCTTGATGCTGATCCGAAACCTGGTGGCCACGGC
 CAGGCCCTTCTCGAAGCCCATCCTGGACCTGGGGGCTGAGGCACTCATCATGCAGGCCCGA
 TCTGCCCCACCGTGAATGTGAGGACGTGGCCAAGGCCGCTGCGGGACCTGGGTGTGTCAT
 GTCGAGCTCCGAGAGCTGTGGACAGGCCAGAGGGGCAACCTGGCGCCATGA

Fig. 24

SEQ ID NO: 24

ARMC6

>ENSG00000105676|19|codificante de proteína|ENST00000392336|ENSP00000376148
 ATGAGTGAACGATGTTGCTCTAGATACAGCTCAGGAGCATCTATCGGCTGCACGCCAACA
 TCAACACAGGCGAAGATGGTCTCCAAGCGCATTGCCAGGAGACCTTTGATGCAGCTGTG
 CGCGAGAACATCGAGGAGTTTGCATGGGGCCAGAGGAGGCAGTGAAAGAGGGCCGTGGAG
 CAGTTTGAATCGCAAGGGGTTGATCTGAGCAACATTGTAAAGACGGCACCTAAAGTCTCT
 GCAGACGGATCCCAGGAGCCCACACATGACATCCTGCAGATGCTCAGTGACCTCCAGGAG
 TCTGTGGCCAGCTCTCGCCCCCAGGAGGTGTCAGCATACCTCACCCGCTTCTGCGACCAG
 TGCAAAACAGGACAAGGCCCTGCCGCTTCCTCGCGGGCCAGAAGGGGGCCTACCCCATCATC
 TTCACTGCCCTGGAAGCTGGCCACTGCAGGTGACCAGGGCCTTCTGCTCCAGTCCCTCAAT
 GCCCTGTGGTGCTGACTGATGGACAGCCAGACCTCCTGGATGCCAGGGCCTGCAGCTC
 CTAGTGGCCACGCTGACCCAGAATGCTGATGAGGCTGACCTGACCTGCTCTGGGATCCGC
 TGTGTGCGTCACGCTTGCCCTGAAACATGAACAGAATCGGCAAGACCTGGTGAAAGCTGGC
 GTGCTGCCCTCTGCTGACTGGTGCCATCACCCATCATGGCCACCACACTGACGTGGTCAGG
 GAAGCCTGCTGGGGCCCTGCGTGTGATGACCTTCGATGACGACATCCGTGTGCCCTTTGGC
 CATGCCACAAACCATGCCAAGATGATTGTGAGGAGAACAAAGGCTTGAAGGTGCTCATC
 GAAGCCACCAAGCGTTCCCTGGATAACCCTGGCATCCTGAGCGAGCTCTGTGGAACCCCTG
 TCCCGCCTGGCCATTCGCAACGAGTTCTGCCAGGAGGTGTCGACCTCGGGGGCCTGAGC
 ATTCTGGTGTCCCTGCTAGCCGACTGCAATGACCACCAGATGAGGGACCAGAGCGGCGTT
 CAGGAGCTCGTGAAGCAAGTGTGAGCACCCCTGCGAGCCATCGCAGGCAACGACGACGTG
 AAAGATGCTATTGTCCGTGCTGGTGGGACGGAGTCCATCGTGGCTGCTATGACCCAGCAT
 CTGACCAGCCCCCAGGTGTGTGAGCAGAGCTGCGCGGCCCTGTGCTTCTGGCCCTGCGT
 AAGCCCGACAACAGCCGCATCATCGTGGAGGGTGGCGGGGCTGTGGCAGCACTGCAGGCC
 ATGAAGGCACACCCGCAGAAGGCCGGCGTGCAGAAACAGGCTTGCTGCTGATCCGAAAC
 CTGGTGGCCACGGCCAGGCCCTTCTCGAAGCCATCCTGGACCTGGGGGCTGAGGCACTC
 ATCATGCAGGCCCCGATCTGCCACCGTGACTGTGAGGACGTGGCCAAGGCCGCCCTGCGG
 GACCTGGGTGTGCTGTCGAGCTCCGAGAGCTGTGGACAGGCCAGAGGGGCAACCTGGCG
 CCATGA

Fig. 25

SEQ ID NO: 25

ARMC6

>ENSG00000105676 | 19 | codificante de proteína | ENST00000269932 | ENSP00000269932

ATGGTCTCCAAGCGCATTTGCCAGGAGACCTTTGATGCAGCTGTGCGCGAGAACATCGAG
 GAGTTTGGGATGGGGCCAGAGGAGGCAGTGAAAGAGGCCGTGGAGCAGTTTGAATCGCAA
 GGGGTTGATCTGAGCAACATTGTAAAGACGGCACCTAAAGTCTCTGCAGACGGATCCAG
 GAGCCCACACATGACATCCTGCAGATGCTCAGTGACCTCCAGGAGTCTGTGGCCAGCTCT
 CGCCCCAGGAGGTGTCAGCATACCTCACCCGCTTCTGCGACCAGTGCAAAACAGGACAAG
 GCCTGCCGCTTCCTCGCGGGCCAGAAGGGGGCCTACCCCATCATCTTCACTGCCCTGGAAG
 CTGGCCACTGCAGGTGACCAGGGCCTTCTGCTCCAGTCCCTCAATGCCCTGTGCGTGCTG
 ACTGATGGACAGCCAGACCTCCTGGATGCCCAGGGCCTGCAGCTCCTAGTGGCCACGCTG
 ACCCAGAATGCTGATGAGGCTGACCTGACCTGCTCTGGGATCCGCTGTGTGCGTCACGCT
 TGCCTGAAACATGAACAGAATCGGCAAGACCTGGTGAAAGCTGGCGTGCTGCCTCTGCTG
 ACTGGTGCCATCACCCATCATGGCCACCACACTGACGTGGTCAGGGAAGCCTGCTGGGCC
 CTGCGTGTCATGACCTTCGATGACGACATCCGTGTGCCCTTTGGCCATGCCACAAACCAT
 GCCAAGATGATTGTGCAGGAGAACAAGGCTTGAAGGTGCTCATCGAAGCCACCAAGCG
 TTCCTGGATAACCCCTGGCATCCTGAGCGAGCTCTGTGGAACCCTGTCCCGCCTGGCCATT
 CGCAACGAGTTCTGCCAGGAGGTGTCGACCTCGGGGGCCTGAGCATTTCTGGTGTCCTTG
 CTAGCCGACTGCAATGACCACCAGATGAGGGACCAGAGCGGCGTTTCAAGGAGCTCGTGAAG
 CAAGTGCTGAGCACCCCTGCGAGCCATCGCAGGCAACGACGACGTGAAAGATGCTATTGTC
 CGTGCTGGTGGGACGGAGTCCATCGTGGCTGCTATGACCCAGCATCTGACCAGCCCCAG
 GTGTGTGAGCAGAGCTGCGCGGCCCTGTGCTTCTTGCCCTGCGTAAGCCCGACAACAGC
 CGCATCATCGTGGAGGGTGGCGGGGCTGTGGCAGCACTGCAGGCCATGAAGGCACACCCG
 CAGAAGGCCGGCGTGCAGAAACAGGCTTGATGCTGATCCGAAACCTGGTGGCCCACGGC
 CAGGCCCTTCTCGAAGCCCATCCTGGACCTGGGGGCTGAGGCACTCATCATGCAGGCCCGA
 TCTGCCACCGTGACTGTGAGGACGTGGCCAAGGCCGCCCTGCGGGACCTGGGTTGTCAT
 GTCGAGCTCCGAGAGCTGTGGACAGGCCAGAGGGGCAACCTGGCGCCATGA

Fig. 26

SEQ ID NO: 26

TH1L

>ENSG00000101158 | 20 | codificante de proteina | ENST00000344018 | ENSP00000342300
 ATGGCGGGGGCCGTGCCGGGCGCCATCATGGACGAGGACTACTACGGGAGCGCGGCCGAG
 TGGGGCGACGAGGCTGACGGCGGCCAGCAGGAGGATGATTCTGGAGAAGGAGAGGATGAT
 GCGGAGGTTCAGCAAGAATGCCTGCATAAATTTTCCACCCGGGATTATATCATGGAACCC
 TCCATCTTCAACACTCTGAAGAGGTATTTTCAGGCAGGAGGGTCTCCAGAGAATGTTATC
 CAGCTCTTATCTGAAACTACACCGCTGTGGCCCGAGCTGTGAACCTGCTGGCCGAGTGG
 CTCATTCAGACAGGTGTTGAGCCAGTGCAGGTTTCAGGAACTGTGGAAAATCACTTGAAG
 AGTTTGCTGATCAAACATTTTGACCCCCGCAAAGCAGATTCTATTTTACTGAAGAAGGA
 GAGACCCAGCGTGGCTGGAACAGATGATTGCACATACCACGTGGCGGGACCTTTTTTAT
 AAAGTGGCTGAAGCCCATCCAGACTGTTTGATGCTGAACTTCACCGTTAAGCTTATTTCT
 GACGCAGGGTACCAGGGGGAGATCACCAGTGTGTCCACAGCATGCCAGCAGCTAGAAGTG
 TTCTCGAGAGTGCTCCGGACCTCTCTAGCTACAATTTTAGATGGAGGAGAAGAAAACCTT
 GAAAAAATCTCCCTGAGTTTGCCAAAGATGGTGTGCCACGGGGAGCACACGTACCTGTTT
 GCCCAGGCCATGATGTCCTGCTGGCCAGGAGGAGCAGGGGGGCTCCGCTGTGCGCAGG
 ATCGCCAGGAAGTGCAGCGCTTTGCCAGGAGAAAGGTCATGACGCCAGTCAGATCACA
 CTAGCCTTGGGCGACAGCTGCCTCCTACCCAGGGCCTGCCAGGCTCTCGGGGCCATGCTG
 TCCAAAGGAGCCCTGAACCCTGCTGACATCACCGTCTGTTCAGATGTTTCAAGCATG
 GACCCCTCCCTCCGGTTGAACTTATCCGCGTTCCAGCCTTCCTGGACCTGTTTATGCACTCA
 CTCTTTAAACCAGGGGCTCGGATCAACCAGGACCACAAGCACAAATACATCCACATCTTG
 GCGTACGCAGCAAGCGTGGTTGAGACCTGGAAGAAGAACAAGCGAGTGAGCATCAATAAA
 GATGAGCTGAAGTCAACGTCAAAGCTGTGAAACCGTTCACAATTTGTGTTGCAACGAG
 AACAAAGGGGCTCTGAACTAGTGGCAGAATTGAGCACACTTTATCAGTGTATTAGGTTT
 CCAGTGGTAGCAATGGGTGTGCTGAAGTGGGTGGATTGGACTGTATCAGAACCAGGTAC
 TTTTCAAGCTGCAGACTGACCATAACCCCTGTCCACCTGGCGTTGCTGGATGAGATCAGCACC
 TGCCACCAGCTCCTGCACCCCGAGGTCTGTCAGCTGCTTGTAAAGCTTTTGGAGACTGAG
 CACTCCCAGCTGGACGTGATGGAGCAGCTTGAGTTGAAGAAGACACTGCTGGACAGGATG
 GTTCACCTGCTGAGTCGAGGTTATGTACTTCCTGTTGTGTCAGTTACATCCGAAAGTGTCTG
 GAGAAGCTGGACACTGACATTTCACTCATTTCGCTATTTTGTCACTGAGGTGCTGGACGTC
 ATTGCTCCTCCTTATACCTCTGACTTCGTGCAACTTTTCTCCCATCCTGGAGAATGAC
 AGCATCGCAGGTACCATCAAACGGAAGGCGAGCATGACCCTGTGACGGAGTTTATAGCT
 CACTGCAATCTAACTTCATCATGGTGAATAA

Fig. 27

SEQ ID NO: 27

PSME1

>ENSG00000092010 | 14 | codificante de proteína | ENST00000382708 | ENSP00000372155

ATGGCCATGCTCAGGGTCCAGCCCGAGGCCCAAGCCAAGGTGGATGTGTTTCGTGAAGAC
CTCTGTACCAAGACAGAGAACCTGCTCGGGAGCTATTTCCCAAGAAGATTTCTGAGCTG
GATGCATTTTTAAAGGAGCCAGCTCTCAATGAAGCCAAC TTGAGCAATCTGAAGGCCCA
TTGGACATCCCAGTGCCTGATCCAGTCAAGGAGAAAGAGAAAGAGGAGCGGAAGAAACAG
CAGGAGAAGGAAGACAAGGATGAAAAGAAGAAGGGGGAGGATGAAGACAAAGGTCCTCCC
TGTGGCCCAAGTGAAC TGCAATGAAAAGATCGTGGTCCTTCTGCAGCGCTTGAAGCCTGAG
ATCAAGGATGTCAATTGAGCAGCTCAACCTGGTCACCCACCTGGTTGCAGCTGCAGATACCT
CGGATTGAGGATGGTAACAATTTTGGAGTGGCTGTCCAGGAGAAGGTGTTTGAGCTGATG
ACCAGCCTCCACACCAAGCTAGAAGGCTTCCACACTCAAATCTCTAAGTATTTCTCTGAG
CGTGGTGATGCAGTGACTAAAGCAGCCAAGCAGCCCCATGTGGGTGATTATCGGCAGCTG
GTGCACGAGCTGGATGAGGCAGAGTACCGGGACATCCGGCTGATGGTCATGGAGATCCGC
AATGCTTATGTGAGGAGGCAAGGGCAGGGCAGGGGTGGGCAGAGGCAGCTTTCCCAGGCC
ACCCACTCCCTGACCTGCAGGCTAGGGGTAA

Fig. 28

SEQ ID NO: 28

PSME1

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>ENSG00000092010 | 14 | codificante de proteina | ENST00000206451 | ENSP00000206451
ATGGCCATGCTCAGGGTCCAGCCCGAGGCCCAAGCCAAGGTGGATGTGTTTCGTGAAGAC
CTCTGTACCAAGACAGAGAACCTGCTCGGGAGCTATTTCCCAAGAAGATTTCTGAGCTG
GATGCATTTTTAAAGGAGCCAGCTCTCAATGAAGCCAACCTTGAGCAATCTGAAGGCCCCA
TTGGACATCCCAGTGCCTGATCCAGTCAAGGAGAAAGAGAAAGAGGAGCGGAAGAAACAG
CAGGAGAAGGAAGACAAGGATGAAAAGAAGAAGGGGGAGGATGAAGACAAAGGTCCTCCC
TGTGGCCCAGTGAAGTCAATGAAAAGATCGTGGTCCTTCTGCAGCGCTTGAAGCCTGAG
ATCAAGGATGTCAATTGAGCAGCTCAACCTGGTCACCACTGGTTGCAGCTGCAGATACCT
CGGATTGAGGATGGTAACAATTTTGGAGTGGCTGTCCAGGAGAAGGTGTTTGAGCTGATG
ACCAGCCTCCACACCAAGCTAGAAGGCTTCCACACTCAAATCTCTAAGTATTTCTCTGAG
CGTGGTGATGCAGTGAAGCAAGCAGCCCAAGCAGCCCCATGTGGGTGATTATCGGCAGCTG
GTGCACGAGCTGGATGAGGCAGAGTACCGGGACATCCGGCTGATGGTCATGGAGATCCGC
AATGCTTATGCTGTGTTATATGACATCATCCTGAAGAACTTCGAGAAGCTCAAGAAGCCC
AGGGGAGAAACAAAGGAATGATCTATTGA
```

Fig. 29

SEQ ID NO: 29

GPC1

>ENSG00000063660 | 2 |codificante de proteína | ENST00000264039 | ENSP00000264039
 ATGGAGCTCCGGGCCCCGAGGCTGGTGGCTGCTATGTGCGGCCGCAGCGCTGGTGCCTGC
 GCGCGCGGGGACCCGGCCAGCAAGAGCCGGAGCTGCGCGGAGGTCCGCCAGATCTACGGA
 GCCAAGGGCTTCAGCCTGAGCGACGTGCCCCAGGCGGAGATCTCGGGTGAGCACCTGCGG
 ATCTGTCCCAGGGCTACACCTGCTGCACCAGCGAGATGGAGGAGAACCTGGCCAACCGC
 AGCCATGCCGAGCTGGAGACCGCGCTCCGGGACAGCAGCCGCGTCCTGCAGGCCATGCTT
 GCCACCCAGCTGCGCAGCTTCGATGACCACCTCCAGCACCTGCTGAACGACTCGGAGCGG
 ACGCTGCAGGCCACCTTCCCGGCGCCTTCGGAGAGCTGTACACGCAGAACGCGAGGGCC
 TTCCGGGACCTGTACTCAGAGCTGCGCCTGTACTACCGCGGTGCCAACCTGCACCTGGAG
 GAGACGCTGGCCGAGTTCTGGGCCCCGCTGCTCGAGCGCCTCTTCAAGCAGCTGCACCCC
 CAGCTGCTGCTGCCTGATGACTACCTGGACTGCCCTGGGCAAGCAGGCCGAGGCGCTGCGG
 CCCTTCGGGGAGGCCCCGAGAGAGCTGCGCCTGCGGGCCACCGTGCTTCGTGGCTGCT
 CGCTCCTTTGTGCAGGGCCTGGGCGTGGCCAGCGACGTGGTCCGGAAAGTGGCTCAGGTC
 CCCCTGGGCCCCGAGTGTCTGAGAGCTGTCATGAAGCTGGTCTACTGTGCTCACTGCCTG
 GGAGTCCCCGGCGCCAGGCCCTGCCCTGACTATTGCCGAAATGTGCTCAAGGGCTGCCTT
 GCCAACCAGGCCGACCTGGACGCCGAGTGGAGGAACCTCCTGGACTCCATGGTGTCTATC
 ACCGACAAGTTCTGGGGTACATCGGGTGTGGAGAGTGTATCGGCAGCGTGCACACGTGG
 CTGGCGGAGGCCATCAACGCCCTCCAGGACAACAGGGACACGCTCACGGCCAAGGTATC
 CAGGGCTGCGGGAACCCCAAGGTCAACCCCCAGGGCCCCGGGCCGTGAGGAGAAGCGGCGC
 CGGGGCAAGCTGGCCCCGCGGGAGAGGCCACCTTCAGGCACGCTGGAGAAGCTGGTCTCC
 GAAGCCAAGGCCCCAGCTCCGCGACGTCCAGGACTTCTGGATCAGCCTCCAGGGACACTG
 TGCAGTGAGAAGATGGCCCTGAGCACTGCCAGTGATGACCGCTGCTGGAACGGGATGGCC
 AGAGGCCGGTACCTCCCCGAGGTTCATGGGTGACGGCCTGGCCAACCAGATCAACAACCC
 GAGGTGGAGGTGGACATCACCAGCCGGACATGACCATCCGGCAGCAGATCATGCAGCTG
 AAGATCATGACCAACCGGCTGCGCAGCGCTACAACGGCAACGACGTGGACTTCCAGGAC
 GCCAGTGACGACGGCAGCGGCTCGGGCAGCGGTGATGGCTGTCTGGATGACCTCTGCAGC
 CGGAAGGTGAGCAGGAAGAGCTCCAGCTCCCGGACGCCCTTGACCCATGCCCCCCCAGGC
 CTGTGAGAGCAGGAAGGACAGAAGACCTCGGCTGCCAGCTGCCCCCAGCCCCCGACCTTC
 CTCTGCCCCCTCTCTCTTCTCTGGCCCTTACAGTAGCCAGGCCCCGGTGGCGGTAA

Fig. 30

SEQ ID NO: 30

EDC4

>ENSG00000038358|16|odificante de protein|ENST00000041337|ENSP00000041337

ATGGCCTCCTGCGCGAGCATCGACATCGAGGACGCCACGCAGCACCTGCGGGACATCCTC
 AAGCTGGACCGGCCCCGCGGCGGCCCCAGTGCAGAGAGCCCCACGGCCATCCAGTGCCTAC
 AATGGGGACCTCAATGGACTTCTGGTCCCAGACCCGCTCTGCTCAGGTGATAGTACCTCA
 GCAAACAGACTGGTCTTCGGACCATGCCACCCATTAACTGCAAGAGAAGCAGGTTCATC
 TGTCTCTCAGGAGATGATAGCTCCACCTGCATTGGGATTTTGGCCAAGGAGGTGGAGATT
 GTGGCTAGCAGTGACTCTAGCATTTCAGCAAGGCCCGGGGAAGCAACAAGGTGAAAATT
 CAGCCTGTGCGCAAGTATGACTGGGAACAGAAGTACTACTATGGCAACCTGATTGCTGTG
 TCTAACTCCTTCTTGGCCTATGCCATTTCGGGCTGCCAACAATGGCTCTGCCATGGTGGCG
 GTGATCAGCGTCAGCACTTCGGAGCGGACCTTGCTCAAGGGCTTCACAGGCAGTGTGGCT
 GATCTGGCTTTTCGCGCACCTCAACTCTCCACAGCTGGCTGCTTGGATGAGGCAGGCAAC
 CTGTTCTGTGGCGCTTGGCTCTGGTTAATGGCAAAATTCAAGAAGAGATCTTGGTCCAT
 ATTCGGCAGCCAGAGGGCACGCCACTGAACCACTTCGCGAGGATCATCTGGTGCCTCTC
 ATCCTGTAGGAGAGCGAAGACTGCTGTGAGGAGAGCAGCCCAACAGTGGCCTGCTGCAT
 GAAGACCGGGCTGAGGTGTGGGACCTGGACATGCTCCGCTCCAGCCACAGTACCTGGCCT
 GTGGATGTTAGCCAGATCAAGCAGGGCTTCATTGTGGTAAAGGTCATAGCACGTGCCCTC
 AGTGAAGGAGCCCTCTCTCTGATGGGACTGTGCTGGCTACTGCGAGCCACGATGGCTAT
 GTCAGTTCTTGGCAGATCTACATTGAGGGGCAAGATGAGCCAAAGGTGTCTGCACGAGTGG
 AAACCTCATGATGGGCGGCCCCCTCTCTGCTCCTGTCTCTGTGACAACCATAAAGAAACA
 GACCTGATGTCCCTTTCTGGAGGTTCCTTATTACTGGTGTGACCAAGCCGAGAGTTA
 AAGATGTGGTGTACAGTATCCTGGACCTGCTTGCAGACTATTCGCTTCTCCCGAGATATC
 TTCAGCTCAGTGAGTCTGCCCCCTAGCCTCAAGGTTTGTCTGGACCTCTCAGCAGAATAC
 CTGATTCTCAGCGATGTGCAACGGAAGGTCTCTATGTGATGGAGCTGCTGCAAAACCAG
 GAGGAGGGCCACGCTGCTTCAGCTCCATCTCGGAGTTCCTGCTCACCACCCCTGTGCTG
 AGCTTTGGTATCCAGGTGTGTGAGTTCGCTGCCGGCTACGGCACACTGAGGTGCTGCTGCC
 GAAGAGGAAAATGACAGCCTGGGTGCTGATGGTACCCATGGAGCCGGTGCCATGGAGTCT
 GCGGCCGGTGTGCTCATCAAGCTCTTTTGTGTGCATACTAAGGCACCTGCAAGATGTGCAG
 ATCCGCTTCAGCCACAGCTGAACCTGATGTGGTGGCCCCACTGCCACCCACACTGCC
 CACGAGGACTTCACATTTGGAGAGTCTCGGCCGAACCTGGGCTCTGAGGGCTGGGGTCA
 GCCGCTCAGGCTCCAGCCTGACCTCCGACGAATCGTGGAGCTGCCTGCACCTGCCGAC
 TTCTCAGTCTGAGCAGTGAGACCAAGCCCAAGTTGATGACACCTGACGCTTCATGACA
 CCTAGCGCCTCCTTGACAGCAGTCACTGCCTCTCCAGCAGCAGCAGCGGTAGCAGC
 AGCAGCAGCAGCAGTAGCAGCAGCTCCCTTACAGCTGTGTCTGCCATGAGCAGCACTCA
 GCTGTGGACCCCTCCTTGACAGGCCACCTGAGGAGCTGACCTTGAGCCCCAAGCTGCAG
 CTGGATGGCAGCTGACAATGAGCAGCAGTGGCAGCCTTCAGGCNAGCCCGCGTGGCTC
 CTGCTGGCCTGCTCCAGCCCCAGCTGACAACTGACTCCCAAGGGGCGGGGCCAGGTG
 CCTACTGCCACCTCTGCACTGTCCCTGGAGCTGCAGGAAGTGGAGCCCTGGGGCTACCC
 CAAGCCTCCCTAGCCGCACTCGTTCCCTGTATGTATCTCCTCAGCTTCCACTGCCCTG
 TCCAGGACATCCCTGAGATTGCATCTGAGGCCCTGTCCGTTGGTTTGGCTCCTCTGCA
 CCAGAGGGCCTTGAGCCAGACAGTATGGCTTCAGCCGCTTCGGCACTGCACCTGCTGTCC
 CCACGGCCCCCGCCAGGGCCGAGCTCGGCCCCAGCTCGGGCTTGATGGAGGCCCTGGG
 GATGGAGATCGGCATAATACCCCTCCCTCCTGGAGGCAGCCTTGACCCAGGAGGCCCTCG
 ACTCCTGACAGTCAGGTTTGGCCACAGCACCTGACATTACTCGTGAGACCTGCAGCACC
 CTGGCAGAAAGCCCCAGGAATGGCCTTCAGGAAAAGCACAAGAGCCTGGCCTTCCACCGA
 CCACCATATCACCTGCTGCAGCAACGTGACAGCCAGGATGCCAGTGTGAGCAAGTGAC
 CATGATGATGAGGTGGCCAGCCTTGCTCTGCTTCAGGAGGCTTTGGCACCAAGTTCCT
 GCTCCACGGCTGCTGCCAAGGACTGGAAGACCAAGGGATCCCTCGAACCTCACCCAAAG
 CTCAGAGGAAAAGCAAGAAGGATGATGGGGATGCAGCCATGGGATCCCGCTCACAGAG
 CACAGGTGGCAGAGCCCCCTGAGGACTGGCCAGCACTAATTTGGCAACAGCAGAGAGAG
 CTGGCAGAGCTGCGGCACAGCCAGGAAGAGCTGCTGCAGCGTCTGTGTACCCAACTCGAA
 GGCCTGCAGAGCAGTCAAGGCCACGTAGAACGTGCCCTTGAGACTCGGCACGAGCAG
 GAACAGCGGGCTGGAGCGAGCACTGGCTGAGGGGCAGCAGGGGAGGGCAGCTGCAG
 GAGCAGCTGACACAACAGTTGTCCCAAGCACTGTCTGCTCAGCTGTAGCTGGGCGGCTAGAG
 CGCAGCATACGGGATGAGATCAAGAAGACAGTCCCTCCATGTGTCTCAAGGAGTCTGGAG
 CCTATGGCAGGCCAACTGAGCAACTCAGTGGCTACCAAGCTCACAGCTGTGGAGGGCAGC
 ATGAAAGAGAACATCTCCAAGCTGCTCAAGTCCAAGAACTTGAAGTATGCCATCGCCCGA
 GCAGCTGCAGACACATTACAAGGGCCGATGCAGGCTGCTACCGGGAAGCCTTCCAGAGT
 GTGGTGTGCCGGCCTTTGAGAAAGAGCTGCCAGGCCATGTTCCAGCAATCAATGATAGC
 TTCCGGCTGGGGACACAGGAATACTTGACGAGCTAGAAAGCCACATGAAGAGCCGGAAG
 GCACGGGAACAGGAGGCCAGGGAGCCTGTGCTAGCCAGCTGCGGGGCTGGTACGACA

CTGCAGAGTGCCACTGAGCAGATGCCACCGTGGCCGGCAGTGTTTCGTGCTGAGGTGCAGC
ACCAGCTGCATGTGGCTGTGGGCAGCCTGCAGGAGTCCATTTTAG

Fig. 30 (continuación)

Fig. 31

SEQ ID NO: 31

EDC4

>ENSG00000038358 | 16 | codificante de protein | ENST00000358933 | ENSP00000351811

ATGGCCTCCTGCGCGAGCATCGACATCGAGGACGCCACGCAGCACCTGCGGGACATCCTC
AAGCTGGACCGGCCCGCGGGCGGCCCCAGTGCAGAGAGCCCACGGCCATCCAGTGCCCTAC
AATGGGGACCTCAATGGACTTCTGGTCCCAGACCCGCTCTGCTCAGGTGATAGTACCTCA
GCAAACAAGACTGGTCTTCGGACCATGCCACCCATTAACTGCAAGAGAAGCAGGTGATC
TGTCTCTCAGGAGATGATAGCTCCACCTGCATTGGGATTTTGGCCAAGGAGGTGGAGATT
GTGGCTAGCAGTGAATCTAGCATTTCAAGCAAGGCCCGGGGAAGCAACAAGGTGAAAATT
CAGCCTGTGCGCAAGTATGACTGGGAACAGAAGTACTACTATGGCAACCTGATTGCTGTG
TCTAACTCCTTCTTGGCCTATGCCATTTCGGGCTGCCAACAATGGCTCTGCCATGGTGC GG
GTGATCAGCGTCAGCACTTCGGAGCGGACCTTGCTCAAGGGCTTCACAGGCAGTGTGGCT
GATCTGGCTTTTCGCGCACCTCAACTCTCCACAGCTGGCCTGCCCTGGATGAGGCAGGCAAC
CTGTTCTGTGGCGCTTGGCTCTGGTTAATGGCAAAATTCAAGAAGAGATCTTGGTCCAT
ATTTCGGCAGCGAGGGGACGCCACTGAACCCTTTTCGAGGATCATCTGGTGCCCTTC
ATCCTTGAGGAGAGCGAAGACTGCTGTGAGGAGAGCAGCCCAACAGTGGCCCTGCTGCAT
GAAGACCGGGCTGAGGTGTGGGACCTGGACATGCTCCGCTCCAGCCACAGTACCTGGCCT
GTGGATGTTAGCCAGATCAAGCAGGGCTTCATTGTGGTAAAAGGTGATAGCACGTGCCTC
AGTGAAGGAGCCCTCTCTCCTGATGGGACTGTGCTGGCTACTGCGAGCCACGATGGCTAT
GTCAAGTTCTGGCAGATCTACATTGAGGGGCAAGATGAGCCAAGGTGTCTGCACGAGTGG
AAACCTCATGATGGGCGGCCCTCTCCTGCCCTGTTCTGTGACAACCATAAGAAACAA
GACCTGATGTCCTTTCTGGAGGTTCTTATTAAGTGGTGCTGACCAAGCCGAGGTTA
AAGATGTGGTGTACAGTATCCTGGACCTGCCCTGCAGACTATTCGCTTCTCCCCAGATATC
TTCAGCTCAGTGAATGTGCCCCCTAGCCTCAAGGTTTGGCTTGGACCTCTCAGCAGAATAC
CTGATTCTCAGCGATGTGCAACGGAAGGTCCCTATGTGATGGAGCTGCTGCAAAACAG
GAGGAGGGCCACGCCTGCTTCAGCTCCATCTCGGAGTTCTGCTCAACCCACCTGTGCTG
AGCTTTGGTATCCAGGTTGTGAGTCTGCTGCCGGCTACGGCACACTGAGGTGCTGCCTGCC
GAAGACGAAAATGACAGCCTGGGTGCTGATGGTACCCATGGAGCCGCTGCCATGGAGTCT
GCGGCCGCTGTGCTCATCAAGCTCTTTTGTGTGCATACTAAGGCACTGCAAGATGTGCAG
ATCCGCTTCCAGCCACAGCTGAACCTGATGTGGTGGCCCCACTGCCACCCACACTGCC
CACGAGGACTTCACATTTGGAGAGTCTCGGCCCGAAGTGGGCTCTGAGGGCTTGGGGTCA
GCCGCTCACGGCTCCCAGCTGACCTCCGACGAATCGTGGAGCTGCCTGCACCTGCCGAC
TTCCTCAGTCTGAGCAGTGAACCAAGCCCAAGTTGATGACACCTGACGCCTTCATGACA
CCTAGCGCCTCCTTGACAGCAGATCACTGCCCTCTCCAGCAGCAGCAGCAGCGGTAGCAGC
AGCAGCAGCAGCAGTAGCAGCAGCTCCCTTACAGCTGTGTCTGCCATGAGCAGCACCTCA
GCTGTGGAGCTCCCTTACAGGCTTACAGGCTGAGGAGCTGACCTTGAAGCCCAAGCTGCAG
CTGGATGGCAGCCTGACAATGAGCAGCAGTGGCAGCCTTCAGGCAAGCCCGCGTGGCCTC
CTGCCTGGCCTGCTCCCAGCCCCAGCTGACAACTGACTCCCAAGGGGCGGGCCAGGTG
CCTACTGCCACCTCTGCACTGTCCCTGGAGCTGCAGGAAGTGGAGCCCTGGGGCTACCC
CAAGCCTCCCCTAGCCGCACTCGTTCCCCTGATGTGATCTCCTCAGCTTCCACTGCCCTG
TCCCAGGACATCCCTGAGATTGCATCTGAGGCCCTGTCCCGTGGTTTGGCTCCTCTGCA
CCAGAGGGCCTTGAGCCAGACAGTATGGCTTCAGCCGCTCGGCACTGCACCTGCTGTCC
CCAGGGCCCCGGCCAGGGCCGAGCTCGGCCCCAGCTCGGGCTTGATGGAGGGCTTGGG
GATGGAGATCGGCATATACCCCTCCCTCCTGGAGGCAGCCTTGACCCAGGAGGCTCG
ACTCCTGACAGTCAAGTTTGGCCCCACAGCACCTGACATTACTCGTGAGACCTGCAGCACC
CTGGCAGAAAGCCCAAGGAATGGCCTTCAGGAAAAGCACAAGAGCCTGGCCTTCCACCGA
CCACCATATCACCTGCTGCAGCAACGTGACAGCCAGGATGCCAGTGTGAGCAAGTGAC
CATGATGATGAGGTGGCCAGCCTTGCTCTGCTTCAGGAGGCTTGGCACCAAGTTCTCT
GCTCCACGGCTGCTGCCAAGGACTGGAAGACCAAGGGATCCCTCGAACCCTACCCCAAG
CTCAAGAGGAAAAGCAAGAGGATGATGGGATGCAGCCATGGGATCCCGCTCACAGAG
CACCAGTGGCAGAGCCCCCTGAGGACTGGCCAGCACTAATTTGGCAACAGCAGAGAGAG
CTGGCAGAGCTGCGGCACAGCCAGGAAGAGCTGCTGCAGCGTCTGTGTACCCAACTCGAA
GGCCTGCAGAGCACAGTACAGGCCACGTAGAACGTGCCCTTGAGACTCGGCACGAGCAG
GAACAGCGCGGCTGGAGCGAGCACTGGCTGAGGGGCGAGCAGCGGGGAGGGCAGCTGCAG
GAGCAGCTGACACAACAGTTGTCCCAAGCACTGTGCTCAGCTGTAGCTGGGCGGCTAGAG
CGCAGCATACGGGATGAGATCAAGAGACAGTCCCTCCATGTGTCTCAAGGAGTCTGGAG
CCTATGGCAGGCCAACTGAGCAACTCAGTGGCTACCAAGCTCACAGCTGTGGAGGGCAGC
ATGAAGAGAACATCTCCAAGCTGCTCAAGTCCAAGAACTTGACTGATGCCATCGCCCGA
GCAGCTGCAGACACATTACAAGGGCCGATGCAGGCTGCCCTACCGGGAAGCCTTCCAGAGT
GTGGTGTGCGGGCTTTGAGAAGAGCTGCCAGGCCATGTTCCAGCAATCAATGATAGC
TTCGGCTGGGGACACAGGAATACTTGCAGCAGCTAGAAAGCCACATGAAGAGCCGGAAG
GCACGGGAACAGGAGGCCAGGGAGCCTGTGCTAGCCAGCTGCGGGGCTGGTTCAGCACA

CTGCAGAGTGCCACTGAGCAGATGGCAGCCACCGTGGCCGGCAGTGTTTCGTGCTGAGGTG
 CAGCACCAGCTGCATGTGGCTGTGGGCAGCCTGCAGGAGTCCATTTTAGCACAGGTACAG
 CGCATCGTTAAGGGTGAGGTGAGTGTGGCGCTCAAGGAGCAGCAGGCCGCCGTACCTCC
 AGCATCATGCAGGCCATGCGCTCAGCTGCTGGCACACCTGTCCCCCTCTGCCACCTTGAC
 TGCCAGGCCCAGCAAGCCCATATCCTGCAGCTGCTGCAGCAGGGCCACCTCAATCAGGCC
 TTCCAGCAGGCGCTGACAGCTGCTGACCTGAACCTGGTGCTGTATGTGTGTGAAACTGTG
 GACCCAGCCCAGGTTTTTGGGCAGCCACCCTGCCCGCTCTCCAGCCTGTGCTCCTTTCC
 CTCATCCAGCAGCTGGCATCTGACCTTGGCACTCGAACTGACCTCAAGCTCAGCTACCTG
 GAAGAGGCCGTGATGCACCTGGACCACAGTGACCCCATCACTCGGGACCACATGGGCTCC
 GTTATGGCCCAGGTGCGCCAAAAGCTTTTTTCAGTTCCTGCAGGCTGAGCCACACAACCTCA
 CTTGGCAAAGCAGCTCGGCGTCTCAGCCTCATGCTGCATGGCCTCGTGACCCCCAGCCTC
 CCTTAG

Fig. 31 (continuación)

Fig. 32

SEQ ID NO: 32

PRC1

>ENSG00000198901 | 15 | codificante de proteina | ENST00000361188 | ENSP00000354679
 ACGAGGCTTCGCCCCGTGGCGCGGTTTGAATTTTGCGGGGCTCAACGGCTCGCGGAGCG
 GCTACGCGGAGTGACATCGCCGGTGTTTGCGGGTGGTTGTTGCTCTCGGGGCCGTGTGGA
 GTAGGTCTGGACCTGGACTCACGGCTGCTTGGAGCGTCCGCCATGAGGAGAAGTGAGGTG
 CTGGCGGAGGAGTCCATAGTATGTCTGCAGAAAGCCCTAAATCACCTTCGGGAAATATGG
 GAGCTAATTGGGATTCCAGAGGACCAGCGGTTACAAAGAACTGAGGTGGTAAAGAAGCAT
 ATCAAGGAACTCCTGGATATGATGATTGCTGAAGAGGAAAGCCTGAAGGAAAGACTCATC
 AAAAGCATATCCGTCTGTCTAGAAAGAGCTGAACACTCTGTGCAGCGAGTTACATGTTGAG
 CCATTTTCAGGAAGAAGGAGAGACGACCATCTTGCAACTAGAAAAAGATTTGCGCACCCAA
 GTGGAATTGATGCGAAAACAGAAAAAGGAGAGAAAAACAGGAAGTGAAGCTACTTCAAGAG
 CAAGATCAAGAAGTGTGCGAAATTCCTTTGTATGCCCCACTATGATATTGACAGTGCCTCA
 GTGCCCAGCTTAGAAGAGCTGAACCAAGTTGAGGCAACATGTGACAACCTTGAGGGAAACA
 AAGGCTTCTAGGCGTGAGGAGTTTGTCTAGTATAAAGAGACAGATCATACTGTGTATGGAA
 GCATTAGACCACACCCAGACACAAGCTTTGAAAGAGATGTGGTGTGTGAAGACGAAGAT
 GCCTTTTGTGTTGTCTTTGGAGAATATTGCAACACTACAAAAGTTGCTACGGCAGCTGGAA
 ATGCAGAAATCACAAAATGAAGCAGTGTGTGAGGGGCTGCGTACTCAAATCCGAGAGCTC
 TGGGACAGGTTGCAAAATACCTGAAGAAGAAAGAGAAGCTGTGGCCACCATTATGTCTGGG
 TCAAAGGCCAAGGTCCGGAAGCGCTGCAATTAGAAGTGGATCGGTTGGAAGAACTGAAA
 ATGCAAAACATGAAGAAAGTGATTGAGGCAATTGAGTGGAGCTGGTTGAGTACTGGGAC
 CAGTGCTTTTATAGCCAGGAGCAGAGACAAGCTTTTGGCCCTTTCTGTGCTGAGGACTAC
 ACAGAAAGTCTGCTCCAGCTCCACGATGCTGAGATTGTGCGGTTAAAAAACTACTATGAA
 GTTCACAAGGAACTCTTTGAAGGTGTCCAGAAGTGGGAAGAAACCTGGAGGCTTTTCTTA
 GAGTTTGAGAGAAAAGCTTCAGATCCAAATCGATTTACAAACCGAGGAGGAAATCTTCTA
 AAAGAAGAAAAACAACGAGCCAAGCTCCAGAAAATGCTGCCCAAGCTGGAAGAAGAGTTG
 AAGGCACGAATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAG
 AAATTCATGGAGTATGTGGCAGAACAAATGGGAGATGCATCGATTGGAGAAAGAGAGAGCC
 AAGCAGGAAAGACAACCTGAAGAACAAAAACAGACAGAGACAGAGATGCTGTATGGCAGC
 GCTCCTCGAACACCTAGCAAGCGGCGAGGACTGGCTCCCAATACACCGGGCAAAGCACGT
 AAGCTGAACACTACCACCATGTCCAATGCTACGGCCAATAGTAGCATTCGGCCTATCTTT
 GGAGGGACAGTCTACCACTCCCCCGTGTCTCGACTTCCTCCTTCTGGCAGCAAGCCAGTC
 GCTGCTTCACCTGTTTCAGGGAAGAAAAACACCCCGTACTGGCAGGCATGGAGCCAAACAAG
 GAGAACCCTGGAGCTCAACGGCAGCATCCTGAGTGGTGGGTACCCTGGCTCGGCCCCCTC
 CAGCGCAACTTCAGCATTAATTCTGTTGCCAGCACCTATTCTGAGTTTGCGCGAGAAGTT
 TCAAAGGCTTCCAAATCTGATGCTACTTCTGGAATCCTCAATTCAACCAACATCCAGTCC
 TGA

Fig. 33

SEQ ID NO: 33

PRC1

>ENSG00000198901 | 15 | codificante de proteína | ENST00000394249 | ENSP00000377793
 ACGAGGCTTCGCCCCGTGGCGCGGTTTGAAATTTTGGGGGCTCAACGGCTCGCGGAGCG
 GCTACGCGGAGTGACATCGCCGGTGTGCGGGTGGTTGTTGCTCTCGGGGCCGTGTGGA
 GTAGGTCTGGACCTGGACTCACGGCTGCTTGGAGCGTCCGCCATGAGGAGAAGTGAGGTG
 CTGGCGGAGGAGTCCATAGTATGCTGCGAGAAAGCCCTAAATCACCTTCGGGAAATATGG
 GAGCTAATTGGGATTCCAGAGGACCAGCGGTTACAAAGAACTGAGGTGGTAAAGAAGCAT
 ATCAAGGAACTCCTGGATATGATGATTGCTGAAGAGGAAAGCCTGAAGGAAAGACTCATC
 AAAAGCATATCCGTCTGTCAGAAAGAGCTGAACACTCTGTGCAGCGAGTTACATGTTGAG
 CCATTTTCAGGAAGAAGGAGAGACGACCATCTTGCAACTAGAAAAAGATTTGCGCACCCAA
 GTGGAATTGATGCGAAAACAGAAAAAGGAGAGAAAAACAGGAACTGAAGCTACTTCAAGAG
 CAAGATCAAGAACTGTGCGAAATTCCTTTGTATGCCCCACTATGATATTGACAGTGCCTCA
 GTGCCCAGCTTAGAAGAGCTGAACCAAGTTCAGGCAACATGTGACAACCTTTGAGGGAAACA
 AAGCCTTCTAGGCGTGAAGAGTTTGTTCAGTATAAAGAGACAGATCATACTGTGTATGGAA
 GCATTAGACCACACCCAGACACAGCTTTGAAAGAGATGTGGTGTGTGAAGACGAAGAT
 GCCTTTTGTGTTGTCTTTGGAGAATATTGCAACACTACAAAAGTTGCTACGGCAGCTGGAA
 ATGCAGAAATCACAAAATGAAGCAGTGTGTGAGGGGCTGCGTACTCAAATCCGAGAGCTC
 TGGGACAGGTTGCAATACCTGAAGAAGAAAGAGAAGCTGTGGCCACCATTATGTCTGGG
 TCAAAGGCCAAGGTCCGGAAGCGCTGCAATTAGAAGTGGATCGGTTGGAAGAAGTGA
 ATGCAAAACATGAAGAAAGTGATTGAGGCAATTCGAGTGGAGCTGGTTCAGTACTGGGAC
 CAGTGCTTTTATAGCCAGGAGCAGAGACAAGCTTTTGCCCCCTTCTGTGCTGAGGACTAC
 ACAGAAAGTCTGCTCCAGCTCCACGATGCTGAGATTGTGCGGTTAAAAAAGTACTATGAA
 GTTCACAAGGAACTCTTTGAAGGTGTCCAGAAGTGGGAAGAAACCTGGAGGCTTTTCTTA
 GAGTTTGAGAGAAAAGCTTCAGATCCAAATCGATTTACAAACCGAGGAGGAAATCTTCTA
 AAAGAAGAAAAACAACGAGCCAAGCTCCAGAAAATGCTGCCCAAGCTGGAAGAAGAGTTG
 AAGGCACGAATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAG
 AAATTCATGGAGTATGTGGCAGAACAAATGGGAGATGCATCGATTGGAGAAAGAGAGAGCC
 AAGCAGGAAAGACAACCTGAAGAACAACAAACAGACAGAGACAGAGATGCTGTATGGCAGC
 GCTCCTCGAACACCTAGCAAGCGGCGAGGACTGGCTCCCAATACACCGGGCAAAGCACGT
 AAGCTGAACACTACCACCATGTCCAATGCTACGGCCAATAGTAGCATTCGGCCCTATCTTT
 GGAGGGACAGTCTACCACTCCCCGTGTCTCGACTTCCTCCTTCTGGCAGCAAGCCAGTC
 GCTGCTTCCACCTGTTTCAGGGAAGAAAACACCCCGTACTGGCAGGCATGGAGCCAACAAG
 GAGAACCTGGAGCTCAACGGCAGCATCCTGAGTGGTGGGTACCTGGCTCGGCCCCCTC
 CAGCGCAACTTCAGCATTAAATCTGTGTCAGCACCTATTCTGAGTTTGCGAAGGATCCG
 TCCCTCTCTGACAGTTCACCTGTTGGGCTTCAGCGAGAACTTTCAAAGGCTTCCAAATCT
 GATGCTACTTCTGGAATCCTCAATTCAACCAACATCCAGTCTCTGA

Fig. 34

SEQ ID NO: 34

PRC1

>ENSG00000198901 | 15 | codificante de proteina | ENST00000361919 | ENSP00000354618
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 CACCTTCGGGAAATATGGGAGCTAATTGGGATTCCAGAGGACCAGCGGTTACAAAGAACT
 GAGGTGGTAAAGAAGCATATCAAGGAACCTCTGGATATGATGATTGCTGAAGAGGAAAGC
 CTGAAGGAAAGACTCATCAAAGCATATCCGTCCTGTCAGAAAGAGCTGAACACTCTGTGC
 AGCGAGTTACATGTTGAGCCATTTAGGAAGAAGGAGAGACGACCATCTTGCAACTAGAA
 AAAGATTTGCGCACCCCAAGTGGAATTGATGCGAAAACAGAAAAAGGAGAGAAAAACAGGAA
 CTGAAGCTACTTCAAGAGCAAGATCAAGAACTGTGCGAAATTCTTTGTATGCCCCACTAT
 GATATTTGACAGTGCCTCAGTGCCTCAGCTTAGAAGAGCTGAACCAGTTGAGCAACATGTG
 ACAACTTTGAGGGAAACAAAGGCTTCTAGGCGTGAGGAGTTTGTGAGTATAAAGAGACAG
 ATCATACTGTGTATGGAAGCATTAGACCACACCCAGACACAAGCTTTGAAAGAGATGTG
 GTGTGTGAAGACGAAGATGCCTTTTGTGTTGCTTTGGAGAATATTGCAACACTACAAAAG
 TTGCTACGGCAGCTGGAATGCAGAAATCACAATGAAGCAGTGTGTGAGGGGCTGCGT
 ACTCAAATCCGAGAGCTCTGGGACAGGTTGCAATACCTGAAGAAGAAAGAGAAGCTGTG
 GCCACCATATGTCTGGGTCAAAGGCCAAGGTCGGAAAGCGCTGCAATTAGAAGTGGAT
 CGGTTGGAAGAACTGAAAATGCAAAACATGAAGAAAGTGATTGAGGCAATTCGAGTGGAG
 CTGGTTGAGTACTGGGACCAAGTCTTTTATAGCCAGGAGCAGAGACAAGCTTTTGCCCCCT
 TTCTGTGCTGAGGACTACACAGAAAGTCTGCTCCAGCTCCACGATGCTGAGATTGTGCGG
 TTAATAAATACTATGAAGTTCACAAGGAACCTCTTGAAGGTGTCCAGAAGTGGGAAGAA
 ACCTGGAGGCTTTTCTTAGAGTTTGAGAGAAAAGCTTCAGATCCAAATCGATTTACAAAC
 CGAGGAGGAAATCTTCTAAAAGAAGAAAAACAACGAGCCAAGCTCCAGAAAATGCTGCCC
 AAGCTGGAAGAAGAGTTGAAGGCACGAATTGAATTGTGGGAACAGGAACATTCAAAGGCA
 TTTATGGTGAATGGGCAGAAATTCATGGAGTATGTGGCAGAACAAATGGGAGATGCATCGA
 TTGGAGAAAGAGAGAGCCAAGCAGGAAAGACAACCTGAAGAACAAAAACAGACAGAGACA
 GAGATGCTGTATGGCAGCGCTCCTCGAACACCTAGCAAGCGGCGAGGACTGGCTCCCAAT
 ACACCGGGCAAAGCACGTAAGCTGAACACTACCACCATGTCCAATGCTACGGCCAATAGT
 AGCATTCGGCCTATCTTTGGAGGGACAGTCTACCACTCCCCCGTGTCTCGACTTCCTCCT
 TCTGGCAGCAAGCCAGTCTGCTTCCACCTGTTGAGGGAAGAAAACACCCCGTACTGGC
 AGGCATGGAGCCAACAAGGAGAACCTGGAGCTCAACGGCAGCATCCTGAGTGGTGGGTAC
 CTTGGCTCGGCCCCCTCCAGCGCAACTTCAGCATTAATTCTGTTGCCAGCACCTATTCT
 GAGTTTGCGAAGGATCCGTCCCTCTCTGACAGTTCCACTGTTGGGCTTCAGCGAGAACTT
 TCAAAGGCTTCAAATCTGATGCTACTTCTGGAATCCTCAATTCAACCAACATCCAGTCC
 TGA

Fig. 35

SEQ ID NO: 35

NAT6

>ENSG00000186792 | 3 | |codificante de proteína| ENST00000359051 | ENSP00000351946

ATGACCACGCAACTGGGCCCAGCCCTGGTGCTGGGGGTGGCCCTGTGCCTGGGTTGTGGC
 CAGCCCCTACCACAGGTCCCTGAACGCCCCCTTCTCTGTGCTGTGGAATGTACCCTCAGCA
 CACTGTGAGGCCCCGCTTTGGTGTGCACCTGCCACTCAATGCTCTGGGCATCATAGCCAAC
 CGTGGCCAGCATTTCACGGTCAGAACATGACCATTTCCTACAAGAACCAACTCGGCCTC
 TATCCCTACTTTGGACCCAGGGGCACAGCTCACAAATGGGGGCATCCCCAGGCTTTGCCC
 CTTGACCGCCACCTGGCACTGGCTGCCTACCAGATCCACCACAGCCTGAGACCTGGCTTF
 GCTGGCCAGCAGTGCTGGATTGGGAGGAGTGGTGTCCACTCTGGGCTGGGAACTGGGGC
 CGCCGCCGAGCTTATCAGGCAGCCTCTTGGGCTTGGGCACAGCAGGTATTCCCTGACCTG
 GACCCTCAGGAGCAGCTCTACAAGGCCTATACTGGCTTTGAGCAGGCGGCCCGTGCACTG
 ATGGAGGATACGCTGCGGGTGGCCCAGGCACCTACGGCCCCATGGACTCTGGGGCTTCTAT
 CACTACCCAGCCTGTGGCAATGGCTGGCATAGTATGGCTTCCAACTATACCGGCCGCTGC
 CATGCAGCCACCCCTTGCCCGCAACACTCAACTGCATTGGCTCTGGGCCGCTCCAGTGCC
 CTCTTCCCCAGCATCTACCTCCCACCCAGGCTGCCACCTGCCACCACCAGGCCTTTGTC
 CGACATCGCCTGGAGGAGGCCTTCCGTGTGGCCCTTGTGGGCACCGACATCCCCTGCCT
 GTCTGGCCTATGTCCGCCTCACACACCGGAGATCTGGGAGGTTCCCTGTCCAGGAGGAG
 TGCTGGCATCTCCATGACTACCTGGTGGACACCTTGGGCCCTATGTGATCAATGTGACC
 AGGGCAGCGATGGCCTGCAGTCACCAGCGGTGCCATGGCCACGGGCGCTGTGCCCGGCGA
 GATCCAGGACAGATGGAAGCCTTTCTACACCTGTGGCCAGACGGCAGCCTTGAGATTGG
 AAGTCCTTCAGCTGCCACTGTTACTGGGGCTGGGCTGGCCCCACCTGCCAGGAGCCAGG
 CCTGGGCCTAAAGAAGCAGTATAA

Fig. 36**SEQ ID NO: 36****NAT6**

>ENSG00000186792 | 3 | codificante de proteina | ENST00000066014 | ENSP00000066014
 ATGACCACGCAACTGGGCCCAGCCCTGGTGCTGGGGGTGGCCCTGTGCCTGGGTTGTGGC
 CAGCCCCTACCACAGGTCCCTGAACGCCCCTTCTCTGTGCTGTGGAATGTACCCTCAGCA
 CACTGTGAGGCCCCGCTTTGGTGTGCACCTGCCACTCAATGCTCTGGGCATCATAGCCAAC
 CGTGGCCAGCATTTTCACGGTCAGAACATGACCATTTTCTACAAGAACCAACTCGGCCTC
 TATCCCTACTTTGGACCCAGGGGCACAGCTCACAAATGGGGGCATCCCCAGGCTTTGCCC
 CTTGACCGCCACCTGGCACTGGCTGCCTACCAGATCCACCACAGCCTGAGACCTGGCTTT
 GCTGGCCAGCAGTGCTGGATTGGGAGGAGTGGTGTCCACTCTGGGCTGGGAACTGGGGC
 CGCCGCCGAGCTTATCAGGCAGCCTCTTGGGCTTGGGCACAGCAGGTATTCCCTGACCTG
 GACCCTCAGGAGCAGCTCTACAAGGCCTATACTGGCTTTGAGCAGGCGGCCCGTGCCTG
 ATGGAGGATACGCTGCGGGTGGCCCAGGCACTACGGCCCCATGGACTCTGGGGCTTCTAT
 CACTACCCAGCCTGTGGCAATGGCTGGCATAGTATGGCTTCCAACATATACCGGCCGCTGC
 CATGCAGCCACCCCTGCCCCGCAACACTCAACTGCATTGGCTCTGGGCCGCCCTCAGTGCC
 CTCTTCCCCAGCATCTACCTCCCACCCAGGCTGCCACCTGCCACCACCAGGCCTTTGTC
 CGACATCGCCTGGAGGAGGCCTTCCGTGTGGCCCTTGTTGGGCACCGACATCCCCTGCCT
 GTCCTGGCCTATGTCCGCCTCACACACCGGAGATCTGGGAGGTTCCCTGTCCAGGATGAC
 CTTGTGCAGTCCATTGGTGTGAGTGCAGCACTAGGGGCAGCCGGCGTGGTGCTCTGGGGG
 GACCTGAGCCTCTCCAGCTCTGAGGAGGAGTGCTGGCATCTCCATGACTACCTGGTGGAC
 ACCTTGGGCCCCCTATGTGATCAATGTGACCAGGGCAGCGATGGCCTGCAGTCACCAGCGG
 TGCCATGGCCACGGGCGCTGTGCCCGGCGAGATCCAGGACAGATGGAAGCCTTTCTACAC
 CTGTGGCCAGACGGCAGCCTTGGAGATTGGAAGTCCTTCAGCTGCCACTGTTACTGGGGC
 TGGGCTGGCCCCACCTGCCAGGAGCCCCCTGGGCCTAAAGAAGCAGTATAAAGCCAGGGCC
 CCTGCCACTGCCTCTTCTTTTCCCTGCTGCCACTTTTCCAGTCTTGGAACTACTCTGTCC
 CACTCTTGCTCTATTTCAGTTTACAGTCAACCCTCCCAAGCACACACCCCGCTTCCCTTGG
 AATCCCTGA

Fig. 37**SEQ ID NO: 37**

NAT6

>ENSG00000186792 | 3 | codificante de proteína | ENST00000336307 | ENSP00000337425

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 CAGCCCCTACCACAGGTCCCTGAACGCCCCTTCTCTGTGCTGTGGAATGTACCCTCAGCA
 CACTGTGAGGCCCGCTTTGGTGTGCACCTGCCACTCAATGCTCTGGGCATCATAGCCAAC
 CGTGGCCAGCATTTTCACGGTCAGAACATGACCATTTTCTACAAGAACCAACTCGGCCTC
 TATCCCTACTTTGGACCCAGGGGCACAGCTCACAATGGGGGCATCCCCAGGCTTTGCC
 CTTGACCGCCACCTGGCACTGGCTGCCTACCAGATCCACCACAGCCTGAGACCTGGCTTT
 GCTGGCCCAGCAGTGCTGGATTGGGAGGAGTGGTGTCCACTCTGGGCTGGGAACTGGGGC
 CGCCGCCGAGCTTATCAGGCAGCCTCTTGGGCTTGGGCACAGCAGGTATTCCCTGACCTG
 GACCCTCAGGAGCAGCTCTACAAGGCCTATACTGGCTTTGAGCAGGCGGCCCCGTGCACTG
 ATGGAGGATACGCTGCGGGTGGCCCAGGCACTACGGCCCCATGGACTCTGGGGCTTCTAT
 CACTACCCAGCCTGTGGCAATGGCTGGCATAGTATGGCTTCCAATATAACCGCCCGCTGC
 CATGCAGCCACCCTTGCCCGCAACACTCAACTGCATTGGCTCTGGGCGCCTCCAGTGCC
 CTCTTCCCCAGCATCTACCTCCCACCCAGGCTGCCACCTGCCACCACCAGGCCTTTGTC
 CGACATCGCCTGGAGGAGGCCCTTCCGTGTGGCCCTTGTTGGGCACCGACATCCCTGCCT
 GTCCTGGCCTATGTCCGCCTCACACACCGGAGATCTGGGAGGTTCTGTCCCAGGATGAC
 CTTGTGCAGTCCATTGGTGTGAGTGCAGCACTAGGGGCAGCCGGCGTGGTGTCTGGGGG
 GACCTGAGCCTCTCCAGCTCTGAGGAGGAGTGTGGCATCTCCATGACTACCTGGTGGAC
 ACCTTGGGGCCCTATGTGATCAATGTGACCAGGGCAGCGATGGCCTGCAGTCACCAGCGG
 TGCCATGGCCACGGGCGCTGTGCCCGGCGAGATCCAGGACAGATGGAAGCCTTTCTACAC
 CTGTGGCCAGACGGCAGCCTTGGAGATTGGAAGTCCTTCAGCTGCCACTGTTACTGGGGC
 TGGGCTGGCCCCACCTGCCAGGAGCCCAGGCCTGGGCCATAAGAAGCAGTATAA

Fig. 38

SEQ ID NO: 38

EEF1A1L3

>ENSG00000185637 | 9 | codificante de proteina | ENST00000329018 | ENSP00000332874
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 TCCACCACTACTGGCCATCTGATCTATAAATGCGGTGGCATCGACAAAAGAACCATTGAA
 AAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCCTGGGTCTTG
 GATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTT
 GAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTCATCAAA
 AACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCTGATTGTTGCTGCTGGTGT
 GGTGAATTTGAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCT
 TACACACTGGGTGTGAAACAATAATTGTCGGTGTAAACAAAATGGATTCCACTGAGCCA
 CCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAAGTCAGCACTTACATTAAGAAA
 ATTGGCTACAACCCCGACACAGTAGCATTTGTGCCAATTTCTGGTTGGAATGGTGACAAC
 ATGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCGTAAGGAT
 GGCAATGCCAGTGGAACACGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGC
 CCAACTGACAAGCCCTTGCGCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGT
 ACTGTTCTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACCTTT
 GCTCCAGTCAACGTTACAACGGAAGTAAAATCTGTGGAATGCACCATGAAGCTTTGAGT
 GAAGCTCTTCCTGGGGACAATGTGGGCTTCAAGGTCAAGAATGTGTCTGTCAAGGATGTT
 CGTCGTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTC
 ACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGT
 TTGGATTGCCACATGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGAT
 CGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCC
 ATTGTTGATATGGTTCTTGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCT
 TTGGGTGCTTTGCTGTTCTGTGATATGAGACAGACAGTTGCGGTGGGTGTCAATCAAGCA
 GTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAG
 GCTAAATGA

Fig. 39

SEQ ID NO: 39

NP_612480.1

>ENSG00000168005 | 11 | codificante de proteína | ENST00000294244 | ENSP00000294244

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 CTCAGAGTGACCCAACAGGAGAAGACCCACCGCTAGACCCAGCCCGCTAGAGGCAGGC
 AGTGATGGCTGTGAGGAGCCGAAGCAGCAGGTGTCTTGGGAGCAGGAGTTCCTGGTGGGC
 AGCAGCCCAGGAGGCAGCGGGCGGGCACTGTGCATGGTGTGTGGCGCTGAGATCCGGGCA
 CCTCGGCCGACACAGCTCGCTCGCACATCTTGGAGCAGCACCTCACACCTTGGACCTG
 AGCCCTTCTGAGAAGAGCAATATCCTGGAGGCCCTGGAGTGAAGGGGTGGCCCTCTTGCAA
 GACGTGAGAGCTGAGCAGCCGTCCCCACCCAACCTCAGACTCGGGCCAGGATGCCCCCCA
 GACCCAGACGCCAACCCAGACGCTGCCAGAATGCCAGCCGAAATCGTCGTTCTCCTTGAC
 TCTGAGGATAACCCATCCCTCCCTAAAAGGAGCCGGCCAGGGGACTCCGCCCCCTCGAG
 CTTCTCTGCTGTCCCTGCCACAGAGCCAGGAAATAAGAAGCCCCGTGGTCAGAGATGGAAG
 GAACCCCCAGGGGAAGAGCCAGTCAGAAAGAAAAGAGGCAGACCTATGACCAAAAACCTG
 GACCTTGACCCAGAGCCCCCATCGCCAGACTCGCCACGGAGACTTTCGCAGCACCAGCC
 GAGGTCCGACACTTCACTGACGGCAGCTTCCCCGCCGGCTTCGTCTTGACAGCTCTTCTCC
 CACACCCAGCTCAGGGGCCAGACAGCAAGGACTCACCCAAAGACAGGGAAGTGGCAGAA
 GGAGGCCTTCCCCGGGCGGAGAGCCCTCTCCAGCTCCCCCTCCGGGGCTCCGCGGGACA
 CTGGATCTCCAGGTATCCGCGTGCGGATGGAGGAGCCCCAGCGGTGAGCCTCCTGCAA
 GACTGGTCCAGGCACCCCAAGCGTGTGGGAGCAGGTGACACCTCAGACTGG
 CCCACAGTTCTGTCAGAATCCAGCACCACTGTGGCAGGGAAGCCGGAAGGGGAATGGA
 GTGTAA

Fig. 40

SEQ ID NO: 40

PLXNA2

>ENSG00000076356|1|podificante de proteína|ENST00000321063|ENSP00000323194

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 GTGCTGTGGCCCCCCCCAGCAGCCGGCATGCCCTCAGTTCAGCACCTTCCACTCTGAGAAT
 CGTGA CTGGACCTTCAACCCTTGACCGTCCACCAAGGGACGGGGGCCGTCTATGTGGGG
 GCCATCAACCGGGTCTATAAGCTGACAGGCAACCTGACCATCCAGGTGGCTCATAAGACA
 GGGCCAGAAGAGGACAACAAGTCTTGTACCCGCCCTCATCGTGCAGCCCTGCAGCGAA
 GTGCTCACCTCACCAACAATGTCAACAAGCTGCTCATCTGACTACTCTGAGAACC GC
 CTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTC
 TTCATCCTGGTGGAGCCATCCACAAGAAGGAGCACTACCTGTCCAGTGTCAACAAGACG
 GGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGATGGCAAGCTCTTCATCGGC
 ACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCAGCCGGAAGCTGCCCGA
 GACCCTGAGTCTCTCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCTCTCTC
 ATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTAC
 GGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGACCCCTGAGGGT
 GTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCAGCATCGTGGGCTCTGCAAG
 GATGACCCCAAGTTCCTACTCATACGTGTCCTGCGCTTCCGCTGCGGCTGCACCCGGGCCGGGGTG
 GAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCAGGCC
 TTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAGCAG
 TATCACCACCCGCCCGATGACTCTGCCCTGTGTGCTTCCCTATCCGGGCCATCAACTTG
 CAGATCAAGGAGCGCCTGCAGTCTGTCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGG
 CTGCTGGGGAGGACGCTCCAGTGCACCAAGGCGCCTGTCCCATCGATGATAACTTCTGT
 GGACTGGACATCAACAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCTGTAC
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 CCTCACTGTGGCTGGTGTGCCCTGCACAACATGTGCTCCCGCAGGGACAAATGCCAACAG
 GCTTGGGAACCTAATCGATTGTCTGCCAGCATCAGCCAGTGTGTGAGCCTTGCAGTGCAT
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 GTGTCCGGGAGCCAGGTCTCTGCATCTCACCTGGGCCCAAGGATGTCCCTGTCTATCCCG
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 GCCATCCACCGGGTCCCGCTCTGCGCTTCAACAGCTCCAGCGTTTCACTGTGAGAACAGC
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 CTGGATGTCAATTAGGAGCCAAGGATCCGAGTCAATTCATGGCAAGAATCTGTCAAT
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 TACCGCCTGCGCTGACACTGTGGAACGCCAGATGAGTTTGGATTGTCTTTAACAAT
 GTCCAATCCTTGCTAATTTACAACGACACCAAGTTTATCTACTACCCCAACCCGACCTTT
 GAACTGCTTAGCCCTACTGGAGTCTTGGATCAAAGCCAGGATCGCCCATCATTTCTGAAG

GGCAAAAACCTCTGCCCTCCTGCCTCTGGAGGGGCCAACTCAACTACACTGTGCTCATC
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 CTCACCGGGCAGCACAAGGTCATGGTTACGTGGGCGGGATGGTGTCTCGCCTGGCTCG
 GTGAGTGTCTCATCTCAGACAGCTTGCTGACCCTGCCAGCCATCGTCAGCATCGCGGCCGGC
 GGCAGCCTCCTCCTCATCATCGTCATCATCGTCCTCATTCGCTACAAGCGCAAGTCTCGA
 GAAAATGACCTCACTCTCAAGCGGCTGCAAATGCAGATGGACAATCTGGAGTCCCGTGTG
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 GACCTGGACCGCTCAGGAATCCCTTACCTGGACTATCGTACCTACGCTATGCGAGTCCTG
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 AAGCAGCTGCTCTCTGACCTCATCGATAAGAACCTGGAGAACAAGAACCACCCCAAGCTG
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 AACCTTGACAACGAGAACAGTCCAGAGATCCCAGTGAAGGTGTTAACTGTGACACCATC
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 GGTGACCGGGGCAGCAAGATGGTGTCCGAGATCTACCTGACCCGGCTACTGGCCACCAAG
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 AGGCACAGCATCCATGACACAGATGTGCGGCACACCTGGAAAAGCAACTGCCTCCCTCTG
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 GAGCACCGGTGGGCAAGGACTCCCCCTCCAACAAGCTGCTCTATGCCAAGGACATCCCC
 AGCTACAAGAGCTGGGTGGAGAGATACTACGCAGACATCGCCAAGCTCCCAGCCATCAGT
 GACCAGGACATGAATGCCTACCTCGCCGAGCAGTCCCGCCTGCACGCCGTGGAGTTCAAC
 ATGCTGAGTGCCTCAATGAGATCTACTCCTATGTGAGCAAGTATAGTGAGGAGCTCATC
 GGGGCCCTAGAGCAGGATGAGCAGGCACGGCGGCAGCGGCTGGCTTATAAGGTGGAGCAG
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Fig. 40 (continuación)

Fig. 41

SEQ ID NO: 41

FLXNAZ

>ENSG00000076356|1|modificante de proteina|ENST00000367033|ENSP00000356000

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 TTCCACTCTGAGAACTCGTGACTGGACCTTCAACCCTTGACCGTCCACCAAGGGACGGGG
 GCCGTCTATGTGGGGGCCATCAACCGGTCTATAAGCTGACAGGCAACCTGACCATCCAG
 GTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTTGTACCCGCCCCCTCATCGTG
 CAGCCCTGCAGCGAAGTGCTCACCTCACCACCAATGTCAACAAGCTGCTCATCATTTGAC
 TACTCTGAGAACCCTGCTGGCCTGTGGGAGCCTTACCAGGGGTCTGCAAGCTGCTG
 CGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCACACAAGAGGAGCACTACCTGTCC
 AGTGTCAACAAGACGGGCACCATGTACGGGGTGATTTGTGCGCTCTGAGGGTGAGGATGGC
 AAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCCTGTCCAGC
 CGGAAGCTGCCCGAGACCTTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
 TTTGTCTCCTCTCATCAAGATCCCTTCAGACACCTGGCCCTGGTCTCCCACTTTGAC
 ATCTTTACATCTACGGCTTTGTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCC
 GAGACCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATC
 GTGCGGCTCTGCAAGGATGACCCCAAGTTCACCTCATACGTGTCCCTGCCCTTCGGCTGC
 ACCCGGGCCGGGTGGAATACCGCTCTCTGCAGCTGCTTACCTGGCCAAGCTGGGGAC
 TCACTGGCCAGGCTTCAATATCACCAGCCAGGAGCATGTACTCTTTGCCATCTTCTCC
 AAAGGGCAGAAGCAGTATCACCACCGCCCGATGACTCTGCCCTGTGTGCCCTTCCCTATC
 CGGGCCATCAACTTGCAGATCAAGGAGCGCCTGCAGTCTGCTACAGGGCGAGGGCAAC
 CTGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGCACCAAGGCGCTGTCCCATC
 CATGATAACTTCTCTGCACTCCACATCAACCAGCCCCGAGGAGCTCAACTCCAGTGGAG
 GGCTGACCCCTGACACCACAGCAGGGACCGCATGACCTCTGTGGCTCTCTACGTTTAC
 AACGGCTACAGCGTGGTTTTTGTGGGACTAAGAGTGGCAAGCTGAAAAAGATTTCGGGCC
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 TGCATCTATGACCCACACCTGCTCCTTCCAGGAGGGCCGGATCAATATTTAGAGGAC
 TGTCGCCAGCTGGTGCCACAGAGGAGATCTTGATTCCAGTGGGGAGGTAAAGCCAATC
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 TTTGAGTGTGGCTGGTGCAGCGGCGAGCGCAGGTGCACCTCCACAGCACTGTACAGC
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 ATCAGAGCTTCAACCTGGATGTCAATTAGGAGCCAAGGATCCGAGTCAAAATCAATGGC
 AAGAATCTGTCAATGTGTGTAAAGTTGTGAACACAACCACCTCACCTGCCTGGCACCC
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TACACTGTGCTCATCGGAGAGACCCCTTGTGCTGTACCCGTATCTGAGACCCAGCTTCTC
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 ATCCTGAACTGCGTCAACCCTGACAACGAGAACAGTCCAGAGATCCAGTGAAGGTGTTA
 AACTGTGACACCATCACACAGGTCAAGGAGAAGATTCTTGATGCCGTGTATAAGAATGTG
 CCTATTCCCAGCGGCCGAGGGCAGTGGACATGGACTTGGAGTGGCGCCAAGGCCGGATC
 GCGCGGTCTGTGCTGCAAGATGAGGACATCACCACCAAGATTGAGGGTGAAGGAGCGG
 CTCACACACTGATGCATTATCAGGTGTGAGACAGGTGCGTGGTGGCTCTGGTCCCCAA
 CAGACCTCCTCCTACAACATCCCTGCCTCTGCCAGCATCTCCCGGACGTCCATCAGCAGA
 TACGACTCCTCCTTCAGGTATACGGGCAGCCCCGACAGCCTGCGGTCCCGGGCCCCGATG
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 AGCACTGTGCACCGGGGCAGCGCTCTCCCCCTGGCCATCAAGTACATGTTTGATTTCTTA
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 TCTTGTTCAACGTGAGAGCACGGGCTGGGCAAGGACTCCCCCTCCAACAAGCTGCTCTAT
 GCCAAGGACATCCCCAGCTACAAGAGCTGGGTGGAGAGATACTACGCAGACATCGCCAAG
 CTCCCAGCCATCAGTGACCAGGACATGAATGCCTACCTCGCCGAGCAGTCCCGCCTGCAC
 GCCGTGGAGTTCAACATGCTGAGTGCCCTCAATGAGATCTACTCCTATGTCAGCAAGTAT
 AGTGAGGAGCTCATCGGGGCCCTAGAGCAGGATGAGCAGGCACGGCGGCAGCGGCTGGCT
 TATAAGGTGGAGCAGCTCATTAAATGCCATGTCCATTGAGAGCTGA

Fig. 41 (continuación)

Fig. 42

SEQ ID NO: 42

ELMO2

>ENSG00000062598 | 20 | codificante de proteina | ENST00000290246 | ENSP00000290246
 ATGCCACCACCGTCAGACATTGTCAAAGTGGCCATTGAGTGGCCAGGTGCTAACGCCCAG
 CTCCTTGAAATCGACCAGAAACGGCCCCTGGCATCCATTATCAAGGAAGTTTGTGATGGG
 TGGTCGTTGCCAAACCCAGAGTATTATACCCCTCCGTTATGCAGATGGTCCTCAGCTGTAC
 ATCACCGAACAGACTCGCAGTGACATTAAGAATGGGACAATCTTACAACCTGGCTATCTCC
 CCGTCCCGGGCTGCACGCCAGCTGATGGAGAGGACCCAGTCATCCAACATGGAGACCCGG
 CTGGATGCCATGAAGGAGCTGGCCAAGCTCTCTGCCGACGTGACTTTGCTACTGAGTTC
 ATCAACATGGATGGCATCATTGTGCTGACAAGGCTCGTGGAAAGTGGAACCAAGCTCTTG
 TCCCACTACAGTGAGATGCTGGCATTACCCCTGACTGCCCTTCCTAGAGCTCATGGACCAT
 GGCATTGTCTCCTGGGACATGGTTTCAATCACCTTTATTAAGCAGATTGCAGGGTATGTG
 AGCCAGCCCATGGTGGACGTGTCAATCCTTCAGAGGTCCTGGCCATCCTGGAGAGCATG
 GTCTTGAACAGCCAGAGTCTGTACCAGAAGATAGCCGAGGAAATCACCGTGGGACAGCTC
 ATCTCACACCTCCAGGTCTCCAACCAGGAGATTACAGACCTACGCCATTGCACTGATTAAT
 GCACTTTTTCTGAAGGCTCCTGAGGACAAACGACAGGATATGGCAAATGCATTTCACAG
 AAGCATCTCCGGTCTATAATCCTGAATCATGTGATCCGAGGGAACCGCCCCATCAAACT
 GAGATGGCCCATCAGCTATATGTCTTCAAGTCTTAACCTTTAACCTTCTGGAAGAAAGG
 ATGATGACCAAGATGGACCCCAATGACCAGGCTCAAAGGGACATCATATTTGAAGTGAAG
 AGGATTGCATTTGACGCAGAGTCTGATCCTAGCAATGCCCTGGGAGTGGGACCGAAAA
 CGCAAAGCCATGTACACAAAGGACTACAAAATGCTGGGATTTACCAACCACATCAATCCA
 GCCATGGACTTTACCCAGACTCCTCCTGGAATGCTGGCCTTGGACAACATGCTGTACTTG
 GCTAAAGTCCACCAGGACACCTACATCCGGATTGTCTTGGAGAACAGTAGCCGGGAAGAC
 AAACATGAATGCCCCCTTGGCCGCAGTGCCATTGAGCTCACCAAAATGCTCTGTGAAATC
 CTGCAGGTTGGGGAACCTACCAAATGAAGGACGCAATGACTACCACCCGATGTTCTTTACC
 CATGACCGAGCCTTTGAAGAGCTCTTTGGAATCTGCATCCAGCTGTTGAACAAGACCTGG
 AAGGAGATGAGGGCAACAGCAGAGGACTTCAACAAGGTTATGCAAGTCGTCCGAGAGCAA
 ATCACTCGAGCTTTGCCCTCCAAACCCAACTCTTTGGATCAGTTCAAGAGCAAATTGCGT
 AGCCTGAGTTACTCTGAGATTCTACGACTGCGCCAGTCTGAGAGGATGAGTCAGGATGAC
 TTCCAGTCCCCGCCAATTGTGGAGCTGAGGGAGAAGATCCAGCCCGAGATCCTTGAGCTG
 ATCAAGCAGCAGCGCCTGAACCGGCTCTGTGAGGGCAGCAGCTTCCGAAAGATTGGGAAC
 CGCCGAAGGCAAGAACGGTCTGCTACTGCCGCTTGGCACTGAACCACAAGGTCCTTCAC
 TATGGTGAAGTTGGATGACAACCCACAAGGGGAGGTGACATTTGAATCCCTGCAGGAGAAA
 ATTCTGTGTCAGACATTAAGGCCATTGTCACTGGGAAAGATTGTCCCACATGAAAGAG
 AAAAGTGCTCTGAAACAGAACAAAGGAGGTGTTGGAATTGGCCTTCTCCATCCTGTATGAC
 CCTGATGAGACCTTAACTTCATCGCACCTAATAAATATGAGTACTGCATCTGGATTGAT
 GGCTCAGTGCCCTTCTGGGGAAGGACATGTCCAGTGAGCTGACCAAGAGTGACCTGGAC
 ACCCTGCTGAGCATGGAGATGAAGCTGCGGCTCCTGGACCTGGAGAACATCCAGATTCCC
 GAGCCCCACCCCCCATCCCCAAGGAGCCCAGCAGCTATGACTTTGTCTATCACTATGGC
 TGA

Fig. 43

SEQ ID NO: 43

ELM02

>ENSG00000062598 | 20 | codificante de proteína | ENST00000396391 | ENSP00000379673
 ATGCCACCACCGTCAGACATTGTCAAAGTGGCCATTGAGTGGCCAGGTGCTAACGCCCAG
 CTCCTTGAAATCGACCAGAAACGGCCCCCTGGCATCCATTATCAAGGAAGTTTGTGATGGG
 TGGTCGTTGCCAAACCCAGAGTATTATACCCCTCCGTTATGCAGATGGTCCTCAGCTGTAC
 ATCACCGAACAGACTCGCAGTGACATTAAGAATGGGACAATCTTACAACCTGGCTATCTCC
 CCGTCCCGGGCTGCACGCCAGCTGATGGAGAGGACCCAGTCATCCAACATGGAGACCCGG
 CTGGATGCCATGAAGGAGCTGGCCAAGCTCTCTGCCGACGTGACTTTCGCTACTGAGTTC
 ATCAACATGGATGGCATCATTGTGCTGACAAGGCTCGTGGAAAGTGGAAACCAAGCTCTTG
 TCCCACTACAGTGAGATGCTGGCATTACCCCTGACTGCCTTCCTAGAGCTCATGGACCAT
 GGCATTGTCTCCTGGGACATGGTTTCAATCACCTTTATTAAGCAGATTGCAGGGTATGTG
 AGCCAGCCCATGGTGGACGTGTCAATCCTTCAGAGGTCCCTGGCCATCCTGGAGAGCATG
 GTCTTGAAACAGCCAGAGTCTGTACCAGAAGATAGCCGAGGAAATCACCGTGGGACAGCTC
 ATCTCACACCTCCAGGTCTCCAACCAGGAGATTGAGACCTACGCCATTGCACTGATTAAT
 GCACCTTTTCTGAAGGCTCCTGAGGACAAACGACAGGATATGGCAAATGCATTTGCACAG
 AAGCATCTCCGGTCTATAATCCTGAATCATGTGATCCGAGGGAACCGCCCCATCAAAACT
 GAGATGGCCCATCAGCTATATGTCTTCAAGTCTTAACCTTTAACCTTCTGGAAGAAAGG
 ATGATGACCAAGATGGACCCCAATGACCAGGCTCAAAGGGACATCATATTTGAAGTGGG
 AGGATTGCATTTGACGCAGAGTCTGATCCTAGCAATGCCCTGGGAGTGGGACCGAAAAA
 CGCAAAGCCATGTACACAAAGGACTACAAAATGCTGGGATTTACCAACCACATCAATCCA
 GCCATGGACTTTACCCAGACTCCTCCTGGAATGCTGGCCTTGGACAACATGCTGTACTTG
 GCTAAAGTCCACCAGGACACCTACATCCGGATTGTCTTGAGAACAGTAGCCGGGAAGAC
 AAACATGAATGCCCCCTTTGGCCGCACTGCCATTGAGCTCACCAAAATGCTCTGTGAATC
 CTGCAGGTTGGGGAACTACCAATGAAGGACGCAATGACTACCACCCGATGTTCTTTACC
 CATGACCGAGCCTTTGAAGAGCTCTTTGGAATCTGCATCCAGCTGTTGAACAAGACCTGG
 AAGGAGATGAGGGCAACAGCAGAGGACTTCAACAAGGTTATGCAAGTCGTCCGAGAGCAA
 ATCACTCGAGCTTTGCCCTCCAAACCCAACTCTTTGGATCAGTTCAAGAGCAAATTCGCT
 AGCCTGAGTTACTCTGAGATTCTACGACTGCGCCAGTCTGAGAGGATGAGTCAGGATGAC
 TTCCAGTCCCCGCCAATTGTGGAGCTGAGGGAGAAGATCCAGCCCGAGATCCTTGAGCTG
 ATCAAGCAGCAGCGCCTGAACCGGCTCTGTGAGGGCAGCAGCTTCCGAAAGATTGGGAAC
 CGCCGAAGGCAAGAACGGTTCTGGTACTGCCGGTTGGCACTGAACCACAAGGTCTTTCAC
 TATGGTGACTTGGATGACAACCCACAAGGGGAGGTGACATTTGAATCCCTGCAGGAGAAA
 ATTCTGTGTCAGACATTAAGGCCATTGTCACTGGGAAAGATTGTCCCCACATGAAAGAG
 AAAAGTGTCTGAAACAGAACAAAGGAGGTGTTGGAATTGGCCTTCTCCATCCTGTATGAC
 CCTGATGAGACCTTAAACTTCATCGCACCTAATAAATATGAGTACTGCATCTGGATTGAT
 GGCCTCAGTGCCCTTCTGGGGAAGGACATGTCCAGTGAGCTGACCAAGAGTGACCTGGAC
 ACCCTGCTGAGCATGGAGATGAAGCTGCGGCTCCTGGACCTGGAGAACATCCAGATTTCC
 GAAGCCCCACCCCCCATCCCCAAGGAGCCAGCAGCTATGACTTTGTCTATCACTATGGC
 TGA

Fig. 44

SEQ ID NO: 44

ELM02

>ENSG00000062598 | 20 | codificante de proteína | ENST00000372176 | ENSP00000361249
 ATGGAGAGGACCCAGTCATCCAACATGGAGACCCGGCTGGATGCCATGAAGGAGCTGGCC
 AAGCTCTCTGCCGACGTGACTTTCGCTACTGAGTTCATCAACATGGATGGCATCATTGTG
 CTGACAAGGCTCGTGGAAAGTGGAAACCAAGCTCTTGTCCCACTACAGTGAGATGCTGGCA
 TTCACCCTGACTGCCTTCTAGAGCTCATGGACCATGGCATTGTCTCCTGGGACATGGTT
 TCAATCACCTTTATTAAGCAGATTGTCAGGGTATGTGAGCCAGCCCATGGTGGACGTGTCA
 ATCCTTCAGAGGTCCTGGCCATCCTGGAGAGCATGGTCTTGAACAGCCAGAGTCTGTAC
 CAGAAGATAGCCGAGGAAATCACCGTGGGACAGCTCATCTCACACCTCCAGGTCTCCAAC
 CAGGAGATTGAGACCTACGCCATTGCACTGATTAATGCACCTTTTCTGAAGGCTCCTGAG
 GACAAACGACAGGATATGGCAAATGCATTTGCACAGAAGCATCTCCGGTCTATAATCCTG
 AATCATGTGATCCGAGGGGAACCGCCCCATCAAACTGAGATGGCCCATCAGCTATATGTC
 CTTCAAGTCTTAACCTTTAACCTTCTGGAAGAAAGGATGATGACCAAGATGGACCCCAAT
 GACCAGGCTCAAAGGGACATCATATTTGAACTGAGGAGGATTGCATTTGACGCAGAGTCT
 GATCCTAGCAATGCCCTGGGAGTGGGACCGAAAAACGCAAAGCCATGTACACAAAGGAC
 TACAAAATGCTGGGATTTACCAACCACATCAATCCAGCCATGGACTTTACCCAGACTCCT
 CCTGGAATGCTGGCCTTGGACAACATGCTGTACTTGGCTAAAGTCCACCAGGACACCTAC
 ATCCGGATTGTCTTGGAGAACAGTAGCCGGGAAGACAAACATGAATGCCCCTTTGGCCGC
 AGTGCCATTGAGCTCACCAAAATGCTCTGTGAAATCCTGCAGGTTGGGGAACCTACCAAT
 GAAGGACGCAATGACTACCACCCGATGTTCTTTACCCATGACCGAGCCTTTGAAGAGCTC
 TTTGGAATCTGCATCCAGCTGTTGAACAAGACCTGGAAGGAGATGAGGGCAACAGCAGAG
 GACTTCAACAAGGTTATGCAAGTCGTCCGAGAGCAAATCACTCGAGCTTTGCCCTCCAAA
 CCAACTCTTTGGATCAGTTCAAGAGCAAATGCGTAGCCTGAGTTACTCTGAGATTCTA
 CGACTGCGCCAGTCTGAGAGGATGAGTCAGGATGACTTCCAGTCCCCGCCAATTGTGGAG
 CTGAGGGAGAAGATCCAGCCCGAGATCCTTGAGCTGATCAAGCAGCAGCGCCTGAACCGG
 CTCTGTGAGGGCAGCAGCTTCCGAAAGATTGGGAACCGCCGAAGGCAAGAACGGTTCTGG
 TACTGCCGGTTGGCACTGAACCACAAGGTCCTTCACTATGGTGACTTGGATGACAACCCA
 CAAGGGGAGGTGACATTTGAATCCCTGCAGGAGAAAATTCCTGTTGCAGACATTAAGGCC
 ATTGTCACTGGGAAAGATTGTCCCCACATGAAGAGAGAAAAGTGCTCTGAAACAGAACAAAG
 GAGGTGTTGGAATTGGCCTTCTCCATCCTGTATGACCTGATGAGACCTTAAACTTCATC
 GCACCTAATAAATATGAGTACTGCATCTGGATTGATGGCCTCAGTGCCCTTCTGGGGAAG
 GACATGTCCAGTGAGCTGACCAAGAGTGACCTGGACACCCTGCTGAGCATGGAGATGAAG
 CTGCGGCTCCTGGACCTGGAGAACATCCAGATTCCCGAAGCCCCACCCCCCATCCCCAAG
 GAGCCAGCAGCTATGACTTTGTCTATCACTATGGCTGA

Fig. 45

SEQ ID NO: 45

ELM02

>ENSG00000062598 | 20 | codificante de proteína | ENST00000352077 | ENSP00000326172

ATGCCACCACCGTCAGACATTGTCAAAGTGGCCATTGAGTGGCCAGGTGCTAACGCCCAG
 CTCTTGAAATCGACCAGAAACGGCCCCCTGGCATCCATTATCAAGGAAGTTTGTGATGGG
 TGGTCGTTGCCAAACCCAGAGTATTATACCTCCGTTATGCAGATGGTCCTCAGCTGTAC
 ATCACCAGACAGACTCGCAGTGACATTAAGAATGGGACAATCTTACAACCTGGCTATCTCC
 CCGTCCCGGGCTGCACGCCAGCTGATGGAGAGGACCCAGTCATCCAACATGGAGACCCGG
 CTGGATGCCATGAAGGAGCTGGCCAAGCTCTCTGCCGACGTGACTTTCGCTACTGAGTTC
 ATCAACATGGATGGCATCATTGTGCTGACAAGGCTCGTGGAAAGTGGAAACCAAGCTCTTG
 TCCCATGAGATGCTGGCATTACCCCTGACTGCCCTCCCTAGAGCTCATGGACCATGGCATT
 GTCTCTTGGGACATGGTTTCAATCACCTTTATTAAAGCAGATTGCAGGGTATGTGAGCCAG
 CCCATGGTGGACGTGTCAATCCTTCAGAGGTCCCTGGCCATCCTGGAGAGCATGGTCTTG
 AACAGCCAGAGTCTGTACCAGAAGATAGCCGAGGAAATCACCGTGGGACAGCTCATCTCA
 CACCTCCAGGTCTCCAACCAGGAGATTGAGACCTACGCCATTGCACTGATTAATGCACTT
 TTTCTGAAGGCTCCTGAGGACAAACGACAGGATATGGCAAATGCATTTGCACAGAAGCAT
 CTCCGGTCTATAATCCTGAATCATGTGATCCGAGGGAAACCGCCCCATCAAACTGAGATG
 GCCCATCAGCTATATGTCCTTCAAGTCCTAACCTTTAACCTTCTGGAAGAAAGGATGATG
 ACCAAGATGGACCCCAATGACCAGGCTCAAAGGGACATCATATTTGAACTGAGGAGGATT
 GCATTTGACGCAGAGTCTGATCCTAGCAATGCCCTGGGAGTGGGACCGAAAAACGCAAA
 GCCATGTACACAAAGGACTACAAAATGCTGGGATTTACCAACCACATCAATCCAGCCATG
 GACTTTACCCAGACTCCTCCTGGAATGCTGGCCTTGGACAACATGCTGTACTTGGCTAAA
 GTCCACCAGGACACCTACATCCGGATTGTCTTGGAGAACAGTAGCCGGGAAGACAAACAT
 GAATGCCCCCTTTGGCCGAGTGCCATTGAGCTACCAAAAATGCTCTGTGAAATCCTGCAG
 GTTGGGGAACCTACCAAATGAAGGACGCAATGACTACCACCCGATGTTCTTTACCCATGAC
 CGAGCCTTTGAAGAGCTCTTTGGAATCTGCATCCAGCTGTTGAACAAGACCTGGAAGGAG
 ATGAGGGCAACAGCAGAGGACTTCAACAAGGTTATGCAAGTCGTCCGAGAGCAAATCACT
 CGAGCTTTGCCCTCCAAACCCAACCTCTTTGGATCAGTTCAAGAGCAAATGCGTAGCCTG
 AGTTACTCTGAGATTCTACGACTGCGCCAGTCTGAGAGGATGAGTCAGGATGACTTCCAG
 TCCCCGCCAATTGTGGAGCTGAGGGAGAAGATCCAGCCCAGATCCTTGAGCTGATCAAG
 CAGCAGCGCCTGAACCGGCTCTGTGAGGGCAGCAGCTTCCGAAAGATTGGGAACCGCCGA
 AGGCAAGAACGGTTCTGGTACTGCCGGTTGGCACTGAACCACAAGGTCCCTTCACTATGGT
 GACTTGGATGACAACCCACAAGGGGAGGTGACATTTGAATCCCTGCAGGAGAAAATTCCT
 GTTGCAGACATTAAAGGCCATTGTCACTGGGAAAGATTGTCCCCACATGAAAGAGAAAAGT
 GCTCTGAACAGAAACAAGGAGGTGTTGGAATTGGCCTTCTCCATCCTGTATGACCCGTGAT
 GAGACCTTAAACTTCATCGCACCTAATAAATATGAGTACTGCATCTGGATTGATGGCCTC
 AGTGCCCTTCTGGGGAAAGGACATGTCCAGTGAGCTGACCAAGAGTGACCTGGACACCCTG
 CTGAGCATGGAGATGAAGCTGCGGCTCCTGGACCTGGAGAACATCCAGATTCCCGAAGCC
 CCACCCCCCATCCCCAAGGAGCCAGCAGCTATGACTTTGTCTATCACTATGGCTGA

Fig. 46

SEQ ID NO: 46

NDUFS2

>ENSG00000158864 | 1 | codificante de proteina | ENST00000367993 | ENSP00000356972

ATGGCGGGCGCTGAGGGCTTTGTGCGGGCTTCCGGGGCGTCGCGGGCCAGGTGCTGCGGGCT
 GGGGCTGGAGTCCGATTGCCGATTTCAGCCCAGCAGAGGTGTTGCGGCAGTGGCAGCCAGAT
 GTGGAATGGGCACAGCAGTTTGGGGGAGCTGTTATGTACCCAAGCAAAGAAACAGCCCAC
 TGGAAGCCTCCACCTTGGAATGATGTGGACCTCCAAAGGACACAATTGTGAAGAACATT
 ACCCTGAACCTTTGGGGCCCCAACACCCAGCAGCGCATGGTGTCTGCGACTAGTGATGGAA
 TTGAGTGGGGAGATGGTGGGAAGTGTGATCCTCACATCGGGCTCCTGCACCGAGGCACT
 GAGAAGCTCATTGAATACAAGACCTATCTTCAGGCCCTCCATACTTTGACCGGCTAGAC
 TATGTGTCCATGATGTGTAACGAACAGGCCTATTCTCTAGCTGTGGAGAAGTTGCTAAAC
 ATCCGGCCTCCTCCTCGGGCACAGTGGATCCGAGTGTCTGTTGGAGAAATCACACGTTTG
 TTGAACCACATCATGGCTGTGACCACACATGCCCTGGACCTTGGGGCCATGACCCCTTTC
 TTCTGGCTGTTTGAAGAAAGGGAGAAAGATGTTTGAGTTCTACGAGCGAGTGTCTGGAGCC
 CGAATGCATGCTGCTTATATCCGGCCAGGAGGAGTGCACCAGGACCTACCCCTTGGGCTT
 ATGGATGACATTTATCAGTTTTCTAAGAACTTCTCTCTTCGGCTTGATGAGTTGGAGGAG
 TTGCTGACCAACAATAGGATCTGGCGAAATCGGACAATTGACATTGGGGTTGTAACAGCA
 GAAGAAGCACTTAACCTATGGTTTTAGTGGAGTGTGCTTCGGGGCTCAGGCATCCAGTGG
 GACCTGCGGAAGACCCAGCCCTATGATGTTTACGACCAGGTTGAGTTTGATGTTCTGTT
 GGTCTCGAGGGGACTGCTATGATAGGTACCTGTGCCGGGTGGAGGAGATGCGCCAGTCC
 CTGAGAATTATCGCACAGTGTCTAAACAAGATGCCTCCTGGGGAGATCAAGGTTGATGAT
 GCCAAAGTGTCTCCACCTAAGCGAGCAGAGATGAAGACTTCCATGCAGTCACTGATTCAT
 CACTTTAAGTTGTATACTGAGGGCTACCAAGTTCTCAGGAGCCACATATACTGCCATT
 GAGGCTCCCAAGGGAGAGTTTGGGGTGTACCTGGTGTCTGATGGCAGCAGCCGCCCTTAT
 CGATGCAAGATCAAGGCTCCTGGTTTTGCCCATCTGGCTGGTTTGGACAAGATGTCTAAG
 GGACACATGTTGGCAGATGTCGTTGCCATCATAGGTACCCAAGATATTGTATTTGGAGAA
 GTAGATCGGTGA

Fig. 47**SEQ ID NO: 47**

NDUF82

>ENSG00000158864 | 1 | codificante de proteína | ENST00000392179 | ENSP00000376018

ATGGCGGCGCTGAGGGCTTTGTGCGGGCTTCCGGGGCGTCGCGGGCCAGGTGCTGCGGCCT
 GGGGCTGGAGTCCGATTGCCGATTCAGCCCAGCAGAGGTGTTCCGGCAGTGGCAGCCAGAT
 GTGGAATGGGCACAGCAGTTTGGGGGAGCTGTTATGTACCCAAGCAAAGAAACAGCCCAC
 TGGGAAGCCTCCACCTTGAATGATGTGGACCCTCCAAAGGACACAATTGTGAAGAACATT
 ACCCTGAACTTTGGGCCCCAACACCCAGCAGCGCATGGTGTCTTGC GACTAGTGATGGAA
 TTGAGTGGGGAGATGGTGC GGAAGTGTGATCCTCACATCGGGCTCCTGCACCGAGGCACT
 GAGAAGCTCATTGAATACAAGACCTATCTTCAGGCCCTTCCATACTTTGACCGGCTAGAC
 TATGTGTCCATGATGTGTAACGAACAGGCCTATTCTCTAGCTGTGGAGAAGTTGCTAAAC
 ATCCGGCCTCCTCCTCGGGCACAGTGGATCCGAGTGCTGTTTGGAGAAATCACACGTTTG
 TTGAACCACATCATGGCTGTGACCACACATGCCCTGGACCTTGGGGCCATGACCCCTTTC
 TTCTGGCTGTTTGAAGAAAGGGAGAAGATGTTTGAGTTCTACGAGCGAGTGTCTGGAGCC
 CGAATGCATGCTGCTTATATCCGGCCAGGAGGAGTGCACCAGGACCTACCCCTTGGGCTT
 ATGGATGACATTTATCAGTTTCTAAGAACTTCTCTCTCGGCTTGATGAGTTGGAGGAG
 TTGCTGACCAACAATAGGATCTGGCGAAATCGGACAATTGACATTGGGGTTGTAACAGCA
 GAAGAAGCACTTAACATATGGTTTTAGTGGAGTGTGCTTCGGGGCTCAGGCATCCAGTGG
 GACCTGCGGAAGACCCAGCCCTATGATGTTTACGACCAGGTTGAGTTTGATGTTCTTGTT
 GGTCTCGAGGGGACTGCTATGATAGGTACCTGTGCCGGGTGGAGGAGATGCGCCAGTCC
 CTGAGAATTATCGCACAGTGTCTAAACAAGATGCCTCCTGGGGAGATCAAGGTTGATGAT
 GCCAAAGTGTCTCCACCTAAGCGAGCAGAGATGAAGACTTCCATGGAGTCACTGATTCAT
 CACTTTAAGTTGTATACTGAGGGCTACCAAGTTCTCCAGGAGCCACATATACTGCCATT
 GAGGCTCCCAAGGGAGAGTTTGGGGTGTACCTGGTGTCTGATGGCAGCAGCCGCCCTTAT
 CGATGCAAGATCAAGGCTCCTGGTTTTGCCCATCTGGCTGGTTTGGACAAGATGTCTAAG
 GGACACATGTTGGCAGATGTGTTGCCATCATAGGTACCCAAGATATTGTATTTGGAGAA
 GTAGATCGGTGA

Fig. 48

SEQ ID NO: 48

IRAK1

>ENSG00000184216 | X | codificante de proteina | ENST00000369980 | ENSP00000358997

ATGGCCGGGGGGCCGGGCCCCGGGGAGCCCCGAGCCCCGGCGCCAGCACTTCTTGAC
 GAGGTGCCGCCCTGGGTCTATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCCGCC
 GACTGGTGCCAGTTCCGCCCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTGCGAG
 CGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTG
 GCCGACCTCGTGACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACA
 GCCTGGCACCCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCGAGGCCAGCAGC
 ATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAGTTGCCATCCTCAGCCTCC
 ACCTTCCCTCTCCCGAGCTTTTCCAGGCTCCAGACCCATTCCAGGGCCTGAGCTCGGCCTG
 GTCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCAGCCCTTCTTCTACCAAG
 CCAGGCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCCCCTTCCGTTTTGCTGG
 CCCCTCTGTGAGATTTCCCGGGGCACCCACAACCTTCTCGGAGGAGCTCAAGATCGGGGAG
 GGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACGGTGTATGCTGTGAAGAGG
 CTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCCCTGACCGAGGTG
 GAGCAGCTGTCCAGGTTTTCGTCACCCAAACATTGTGGACTTTGCTGGCTACTGTGCTCAG
 AACGGCTTCTACTGCCTGGTGTACGGCTTCCCTGCCCAACGGCTCCCTGGAGGACCGTCTC
 CACTGCCAGACCCAGGCCTGCCACCTCTCTCCTGGCCTCAGCGACTGGACATCCTTCTG
 GGTACAGCCCCGGGCAATTCACTTTCTACATCAGGACAGCCCCAGCCTCATCCATGGAGAC
 ATCAAGAGTTCCAACGTCTTCTGGATGAGAGGCTGACACCCAAGCTGGGAGACTTTGGC
 CTGGCCCCGTTTCCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAGCAGCATGGTGGCCCCG
 ACACAGACAGTGCAGGGGCACCCCTGGCCTACCTGCCCCAGGAGTACATCAAGACGGGAAGG
 CTGGCTGTGGACACGGACACCTTCACTTGGGGTGGTAGTGCTAGAGACCTTGGCTGGT
 CAGAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGAAAGACCTGGTGGGAAGAG
 GAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAGCACACTGCAAGCAGGTCTG
 GCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTACAAGAAGCACCTGGACCCC
 AGGCCCCGGGCCCTGCCACCTGAGCTGGGCCTGGGCCTGGGCCAGCTGGCCTGCTGCTGC
 CTGCAACCGCCGGGCCAAAAGGAGGCCTCCTATGACCCAGGTGTACGAGAGGCTAGAGAAG
 CTGCAGGCAGTGGTGGCGGGGGTGGCCGGGCATTCCGAGGCCGCCAGCTGCATCCCCCTT
 TCCCCGAGGAGAACTCCTACGTGTCCAGCACTGGCAGAGCCCACAGTGGGGCTGCTCCA
 TGGCAGCCCCCTGGCAGCGCCATCAGGAGCCAGTGGCCAGGCAGCAGAGCAGCTGCAGAGA
 GGCCCCAACCCAGCCCGTGGAGAGTGACGAGAGCCTAGGCGGCCTCTCTGCTGCCCTGCGC
 TCCTGGCACTTGACTCCAAGCTGCCCTCTGGACCCAGCACCCCTCAGGGAGGCCGGCTGT
 CCTCAGGGGGACACGGCAGGAGAATCGAGCTGGGGGAGTGGCCAGGATCCCGGCCACA
 GCCGTGGAAGGACTGGCCCTTGGCAGCTCTGCATCATCGTCTCAGAGCCACCGCAGATT
 ATCATCAACCTGCCCGACAGAAGATGGTCCAGAAGCTGGCCCTGTACGAGGATGGGGCC
 CTGGACAGCCTGCAGCTGCTGTCTGTCAGCTCCCTCCAGGCTTGGGCCTGGAACAGGAC
 AGGCAGGGGCCCGAAGAAAGTGATGAATTTCAAGAGCTGA

Fig. 49

SEQ ID NO: 49

IRAK1

>ENSG00000184216 | X | codificante de proteína | ENST00000369973 | ENSP00000358990

ATGGCCGGGGGGCGGGCCCGGGGGAGCCCGCAGCCCCCGGCGCCAGCACTTCTTGTTAC
 GAGGTGCCGCCCTGGGTTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC
 GACTGGTGCCAGTTCTGGTGGGTGGCGGCGGGCTGCCGGGGGGCGGGAGGCGCGCGGGCTC
 CTGGCGCCGACGCCTGACGCCCCCGCCCCGCGAGCCGCCCTGATCGTGCGCGACCAGACC
 GAGCTGCGGCTGTGCGAGCGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATC
 AACCGCAACGCCCGTGTGGCCGACCTCGTGACATCCTCACGCACCTGCAGCTGCTCCGT
 GCGCGGGACATCATCACAGCCTGGCACCCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACT
 GCCCCGAGGCCAGCAGCATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAG
 TTGCCATCCTCAGCCTCCACCTTCTCTCCCCAGCTTTTCCAGGCTCCAGACCCATTCA
 GGGCCTGAGCTCGGCCTGGTCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCA
 GCCCCCTTCTTCTACCAAGCCAGGCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGC
 CCTTTCCGTTTGTGGCCCTCTGTGAGATTTCCCGGGGCACCCACAACCTTCTCGGAG
 GAGCTCAAGATCGGGGAGGGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACG
 GTGTATGCTGTGAAGAGGCTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAG
 AGCTTCCTGACCGAGGTGGAGCAGCTGTCCAGGTTTCGTACCCAAACATTGTGGACTTT
 GCTGGCTACTGTGCTCAGAACGGCTTCTACTGCCCTGGTGTACGGCTTCTGCCCCAACGGC
 TCCCTGGAGGACCGTCTCCACTGCCAGACCCAGGCCCTGCCACCTCTCTCCTGGCCTCAG
 CGACTGGACATCCTTCTGGGTACAGCCCGGGCAATTCAGTTTCTACATCAGGACAGCCCC
 AGCCTCATCCATGGAGACATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCC
 AAGCTGGGAGACTTTGGCCTGGCCCGGTTTCAAGCCGCTTTGCCGGGTCCAGCCCCAGCCAG
 AGCAGCATGGTGGCCCGGACACAGACAGTGCAGGGGCACCCCTGGCCTACCTGCCCGAGGAG
 TACATCAAGACGGGAAGGCTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTG
 CTAGAGACCTTGGCTGGTTCAGAGGGCTGTGAAGACGCACGGTGGCAGGACCAAGTATCTG
 AAAGACCTGGTGAAGAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAGC
 AACTGCAAGCAGGTCTGGCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTAC
 AAGAAGCACCTGGACCCAGGCCCGGGCCCTGCCACCTGAGCTGGGCCTGGGCCTGGGC
 CAGCTGGCCTGCTGCTGCCTGCACCGCCGGGCCAAAAGGAGGCTCCTATGACCCAGGAG
 AACTCCTACGTGTCCAGCACTGGCAGAGCCACAGTGGGGCTGCTCCATGGCAGCCCCCTG
 GCAGCGCCATCAGGAGCCAGTGGCCAGGCAGCAGAGCAGTGCAGAGAGGCCCAACCCAG
 CCCGTGGAGAGTGACGAGAGCCTAGGCGGCCTCTCTGCTGCCCTGCGCTCCTGGCACTTG
 ACTCCAAGCTGCCCTCTGGACCCAGCACCCCTCAGGGAGGCGCGCTGTCTCAGGGGGAC
 ACGGCAGGAGAATCGAGCTGGGGGAGTGGCCAGGATCCCGGCCACAGCCGTGGAAGGA
 CTGGCCCTTGGCAGCTCTGCATCATCGTCTCAGAGCCACCGCAGATTATCATCAACCTT
 GCCCGACAGAAGATGGTCCAGAAGCTGGCCCTGTACGAGGATGGGGCCCTGGACAGCCTG
 CAGCTGCTGTCTCAGCTCCCTCCAGGCTTGGGCCTGGAACAGGACAGGCAGGGGGCC
 GAAGAAAGTGATGAATTCAGAGCTGA

Fig. 50

SEQ ID NO: 50

IRAK1

>ENSG00000184216|X|codificante de proteína|ENST00000369974|ENSP00000358991
 ATGGCCGGGGGGCCGGGCCCCGGGGGAGCCCGCAGCCCCCGGCGCCCAGCACTTCTTGTAC
 GAGGTGCCGCCCTGGGTTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCCGCC
 GACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTGCGAG
 CGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTG
 GCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACA
 GCCTGGCACCCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCGAGGCCAGCAGC
 ATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAGTTGCCATCCTCAGCCTCC
 ACCTTCCTCTCCCCAGCTTTTCCAGGCTCCAGACCCATTCCAGGGCCTGAGCTCGGCCTG
 GTCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCAGCCCCCTTCTTCTACCAAG
 CCAGGCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCCCCTTCCGTTTTGCTGG
 CCCCTCTGTGAGATTTCCCGGGGCACCCACAACCTCTCGGAGGAGCTCAAGATCGGGGAG
 GGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACGGTGTATGCTGTGAAGAGG
 CTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCTGACCGAGGTG
 GAGCAGCTGTCCAGGTTTCGTCAACCAACATTGTGGACTTTGCTGGCTACTGTGCTCAG
 AACGGCTTCTACTGCTGGTGTACGGCTTCTGCCCCAACGGCTCCCTGGAGGACCGTCTC
 CACTGCCAGACCCAGGCCTGCCACCTCTCTCCTGGCCTCAGCGACTGGACATCCTTCTG
 GGTACAGCCCCGGGAATTTCAGTTTCTACATCAGGACAGCCCCAGCCTCATCCATGGAGAC
 ATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAAGCTGGGAGACTTTGGC
 CTGGCCCCGTTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAGCAGCATGGTGGCCCCG
 ACACAGACAGTGCAGGGGCACCCCTGGCTTACCTGCCCCAGGAGTACATCAAGACGGGAAGG
 CTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGACCTTGGCTGGT
 CAGAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGGTGTACGAGAGGCTAGAG
 AAGCTGCAGGCAGTGGTGGCGGGGGTGGCCGGGCATTCCGAGGCCCGCCAGCTGCATCCCC
 CCTTCCCCGCAGGAGAACTCCTACGTGTCCAGCACTGGCAGAGCCCACAGTGGGGCTGCT
 CCATGGCAGCCCCCTGGCAGCGCCATCAGGAGCCAGTGCCAGGCAGCAGAGCAGCTGCAG
 AGAGGCCCCAACCCAGCCCGTGGAGAGTGACGAGAGCCTAGGCGGCCTCTCTGCTGCCCTG
 CGCTCCTGGCACTTGACTCCAAGCTGCCCTCTGGACCCAGCACCCCTCAGGGAGGCGGGC
 TGTCTCAGGGGGACACGGCAGGAGAATCGAGCTGGGGGAGTGGCCCAGGATCCCGGGCC
 ACAGCCGTGGAAGGACTGGCCCTTGGCAGCTCTGCATCATCGTCGTGAGAGCCACCGCAG
 ATTATCATCAACCTGCCCGACAGAAGATGGTCCAGAAGCTGGCCCTGTACGAGGATGGG
 GCCCTGGACAGCTGCAGCTGTGTCGTCCAGCTCCCTCCAGGCTTGGGCCTGGAACAG
 GACAGGCAGGGGCCCGAAGAAAGTGATGAATTTTCAGAGCTGA

Fig. 51

SEQ ID NO: 51

IRAK1

>ENSG00000184216|X|codificante de proteína|ENST00000393682|ENSP00000377287

ATGGCCGGGGGGCCGGGCGGGGGAGCCCGCAGCCCCGGCGCCAGCACTTCTTGTAC
 GAGGTGCCGCCCTGGGTGATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC
 GACTGGTGCCAGTTGCGTGGGTGGCGGGGGCTGCCGGGGGGCGGGAGGCGCGGGGCTC
 CTGGCGCCGACGCTGACGCCCCCGCCCCGCAGCCGCCCTGATCGTGCGCGACCAGACC
 GAGCTGCGGCTGTGCGAGCGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATC
 AACCGCAACGCCCGTGTGGCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGT
 GCGCGGGACATCATCACAGCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACT
 GCCCCGAGGCCAGCAGCATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAG
 TTGCCATCCTCAGCCTCCACCTTCTCTCCCCAGCTTTTCCAGGCTCCCAGACCCATTCA
 GGGCCTGAGCTCGGCCTGGTCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCA
 GCCCCCTTCTTCTACCAAGCCAGGCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGC
 CCCTTTCCGTTTTTGCTGGCCCCCTCTGTGAGATTTCCCGGGGCACCCACAACCTTCTCGGAG
 GAGCTCAAGATCGGGGAGGGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACG
 GTGTATGCTGTGAAGAGGCTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAG
 AGCTTCTGACCGAGGTGGAGCAGCTGTCCAGGTTTCGTACCCAAACATTGTGGACTTT
 GCTGGCTACTGTGCTCAGAACGGCTTCTACTGCCTGGTGTACGGCTTCTGCCCCAACGGC
 TCCCTGGAGGACCGTCTCCACTGCCAGACCAGGCCTGCCACCTCTCTCTTGGCCTCAG
 CGACTGGACATCCTTCTGGGTACAGCCCGGGCAATTTCAGTTTCTACATCAGGACAGCCCC
 AGCCTCATCCATGGAGACATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCC
 AAGCTGGGAGACTTTGGCCTGGCCCGGTTTCAAGCGCTTTGCCGGGTCCAGCCCCAGCCAG
 AGCAGCATGGTGGCCCGGACACAGACAGTCCGGGGCACCTGGCCTACCTGCCCCAGGAG
 TACATCAAGACGGGAAGGCTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTG
 CTAGAGACCTTGGCTGGTCCAGAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTG
 AAAGACCTGGTGGGAAGAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAGC
 ACACTGCAAGCAGGTCTGGCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTAC
 AAGAAGCACCTGGGCCAGCTGGCCTGCTGCTGCCTGCACCGCCGGGCCAAAAGGAGGCCT
 CCTATGACCCAGGAGAACTCCTACGTGTCCAGCACTGGCAGAGCCCACAGTGGGGCTGCT
 CCAATGGCAGCCCCCTGGCAGCGCCATCAGGAGCCAGTGCCCAGGCAGCAGAGCAGCTGCAG
 AGAGGGCCCCAACCAGCCCGTGGAGAGTGACGAGAGCCTAGGCGGCCTCTCTGCTGCCCTG
 CGCTCCTGGCACTTGACTCCAAGCTGCCCTCTGGACCCAGCACCCCTCAGGGAGGCCGGC
 TGTCTCAGGGGGACACGGCAGGAGAATCAGAGCTGGGGGAGTGGCCAGGATCCCGGGCC
 ACAGCCGTGGAAGGACTGGCCCTTGGCAGCTCTGCATCATCGTCGTGAGAGCCACCGCAG
 ATTATCATCAACCCTGCCCGACAGAAGATGGTCCAGAAGCTGGCCCTGTACGAGGATGGG
 GCCCTGGACAGCCTGCAGCTGCTGTCGTCCAGCTCCCTCCCAGGCTTGGGCCTGGAACAG
 GACAGGCAGGGGGCCGAAGAAAGTGATGAATTTACAGAGCTGA

Fig. 52**SEQ ID NO: 52****TRAK1**

>ENSG00000184216|X|codificante de proteína|ENST00000393687|ENSP00000377291
 ATGGCCGGGGGGCCGGGCCCGGGGAGCCCGCAGCCCCGGCGCCAGCACTTCTTGTTAC
 GAGGTGCCGCCCTGGGTTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC
 GACTGGTGCCAGTTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTGCGAG
 CGCTCCGGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTG
 GCCGACCTCGTGACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACA
 GCCTGGCACCCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGAGGCCCGAGCAGC
 ATCCCTGCACCCGCGAGGCCGAGGCCCTGGAGCCCCCGGAAGTTGCCATCCTCAGCCTCC
 ACCTTCCTCTCCCCAGCTTTTCCAGGCTCCAGACCCATTGAGGGCCTGAGCTCGGCCTG
 GTCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCAGCCCCCTTCTTCTACCAAG
 CCAGGCCCGAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCCGCCCTTTCCGTTTGTCTGG
 CCCCTCTGTGAGATTTCCCGGGGCACCCACAACCTTCTCGGAGGAGCTCAAGATCGGGGAG
 GGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACGGTGTATGCTGTGAAGAGG
 CTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCTGACCGAGGTG
 GAGCAGCTGTCCAGTTTTCGTACCCAAACATTGTGGACTTTGCTGGCTACTGTGCTCAG
 AACGGCTTCTACTGCCTGGTGTACGGCTTCTGCCCCAACGGCTCCCTGGAGGACCGTCTC
 CACTGCCAGACCCAGGCCTGCCACCTCTCTCCTGGCCTCAGCGACTGGACATCCTTCTG
 GGTACAGCCCGGGCAATTTCAGTTTCTACATCAGGACAGCCCCAGCCTCATCCATGGAGAC
 ATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAAGCTGGGAGACTTTGGC
 CTGGCCCCGGTTCAGCCGCTTTGCGGGGTCCAGCCCCAGCCAGAGCAGCATGGTGGCCCCGG
 ACACAGACAGTGCGGGGCACCCCTGGCCTACCTGCCCGAGGAGTACATCAAGACGGGAAGG
 CTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGACCTTTGGCTGGT
 CAGAGGGCTGTGAAGACGCACGGTGGCAGGACCAAGTATCTGAAAGACCTGGTGGGAAGAG
 GAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAGCACACTGCAAGCAGGTCTG
 GCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTACAAGAAGCACCTGGACCCC
 AGGCCCGGGCCCTGCCACCTGAGCTGGGCCTGGGCCTGGGCCAGCTGGCCTGCTGCTGC
 CTGCACCGCCGGGGCCAAAAGGAGGCCTCCTATGACCCAGGAGAACTCCTACGTGTCCAGC
 ACTGGCAGAGCCCACAGTGGGGCTGCTCCATGGCAGCCCCTGGCAGCGCCATCAGGAGCC
 AGTGCCCAGGCAGCAGAGCAGCTGCAGAGAGGCCCCAACAGCCCGTGGAGAGTGACGAG
 AGCCTAGGCGGCCTCTCTGCTGCCCTGCGCTCCTGGCACTTGACTCCAAGCTGCCCTCTG
 GACCCAGCACCCCTCAGGGAGGCCGGCTGTCTCAGGGGGACACGGCAGGAGAATCGAGC
 TGGGGGAGTGGCCAGGATCCCGGCCACAGCCGTGGAAGGACTGGCCCTTGGCAGCTCT
 GCATCATCGTCGTGAGAGCCACCGCAGATTATCATCAACCCTGCCCGACAGAAGATGGTC
 CAGAAGCTGGCCCTGTACGAGGATGGGGCCCTGGACAGCCTGCAGCTGCTGTGCTCCAGC
 TCCCTCCAGGCTTGGGCCTGGAACAGGACAGGCAGGGGGCCGAAGAAAGTGATGAATTT
 CAGAGCTGA

Fig. 53

SEQ ID NO: 53

C20orf149

>ENSG00000125534 | 20 | codificante de proteína | ENST00000370177 | ENSP00000359196

ATGGCGGCCATCCCCCTCCAGCGGCTCGCTCGTGGCCACCCACGACTACTACCGGCGCCGC
CTGGGTTCCACTTCCAGCAACAGCTCCTGCAGCAGTACCGAGTGGCCCGGGGAAGCCATT
CCCCACCCCCCAGGTGAGTGCAGGATCGCCCCCTTCTCCCCCGCTCCTCCAGGAGCTGG
CAGCATCAAGACCCCACTTCGCTTCTCTCAGGTCTCCCCAAGGCTGACCCGGGTCAATTGG
TGGGCCAGCTTCTTTTTCGGGAAGTCCACCCTCCCGTTCATGGCCACGGTGTGGAGTCC
GCAGAGCACTCGGAACCTCCCAGGCCTCCAGCAGCATGACCGCCTGTGGCCTGGCTCGG
GACGCCCCGAGGAAGCAGCCCGGCGGTTCAGTCCAGCACAGCCAGCGCTGGGCCCCCGTCC
TGA

Fig. 54

SEQ ID NO: 54

C20orf149

>ENSG00000125534 | 20 | codificante de proteína | ENST00000370178 | ENSP00000359197
ATGGCGGCCATCCCTCCAGCGGCTCGCTCGTGGCCACCCACGACTACTACCGGCGCCGC
CTGGGTTCCACTTCCAGCAACAGCTCCTGCAGCAGTACCGAGTGCCCCGGGGAAGCCATT
CCCCACCCCCCAGGTCTCCCAAGGCTGACCCGGGTCATTGGTGGGCCAGCTTCTTTTTC
GGGAAGTCCACCCTCCCACCCCCCACCCTGTAA

Fig. 55

SEQ ID NO: 55

C20orf149

>ENSEG00000125534 | 20 | codificante de proteina | ENST00000370179 | ENSP00000359198
 ATGGCGGCCATCCCCCTCCAGCGGCTCGCTCGTGGCCACCCACGACTACTACCGGCGCCGC
 CTGGGTTCCTTCCAGCAACAGCTCCTGCAGCAGTACCGAGTGCCCCGGGGAAGCCATT
 CCCCACCCCCCAGGTCTCCCCAAGGCTGACCCGGGTCAATTGGTGGGCCAGCTTCTTTTTC
 GGGGAAGTCCACCCCTCCCGTTTCATGGCCACGGTGTGGAGTCCGCAGAGCACTCGGAACCT
 CCCCAGGCCTCCAGCAGCATGACCGCCTGTGGCCTGGCTCGGGACGCCCCGAGGAAGCAG
 CCCGGCGGTCAGTCCAGCACAGCCAGCGCTGGGCCCCCGTCCTGA

Fig. 56

SEQ ID NO: 56

PSCD2L

>ENSG00000105443 | 19 | codificante de proteína | ENST00000325139 | ENSP00000314566

ATGGAGGACGGCGTCTATGAACCCCGAGACCTGACTCCGGAGGAGCGGATGGAGCTGGAG
 AACATCCGGCGGCGGAAGCAGGAGCTGCTGGTGGAGATTGAGCGCCTGCGGGAGGAGCTC
 AGTGAAGCCATGAGCGAGGTGGAGGGGCTGGAGGCCAATGAGGGCAGTAAGACCTTGCAA
 CGGAACCGGAAGATGGCAATGGGCAGGAAGAAGTTCAACATGGACCCCAAGAAGGGGATC
 CAGTTCTTGGTGGAGAATGAACTGCTGCAGAACACACCCGAGGAGATCGCCCGCTTCCTG
 TACAAGGGCGAGGGGCTGAACAAGACAGCCATCGGGGACTACCTGGGGGAGAGGGAAGAA
 CTGAACCTGGCAGTGCTCCATGCTTTTGTGGATCTGCATGAGTTCACCGACCTCAATCTG
 GTGCAGGCCCTCAGGCAGTTTCTATGGAGCTTTTCGCCTACCCGGAGAGGCCAGAAAATT
 GACCGGATGATGGAGGCCCTTCGCCCAGCGATACTGCCTGTGCAACCCTGGGGTTTTCCAG
 TCCACAGACACGTGCTATGTGCTGTCCTTCGCCGTCATCATGCTCAACACCAGTCTCCAC
 AATCCCAATGTCCGGGACAAGCCGGGCCTGGAGCGCTTTGTGGCCATGAACCGGGGCATC
 AACGAGGGCGGGGACCTGCCTGAGGAGCTGCTCAGGAACCTGTACGACAGCATCCGAAAT
 GAGCCCTTCAAGATTCTTGAGGATGACGGGAATGACCTGACCCACACCTTCTTCAACCCG
 GACCGGGAGGGCTGGCTCCCTGAAGCTGGGTAGGGGCGGGTGAAGACGTGGAAGCGGCGC
 TGGTTTATCCTCACAGACAACCTGCCTCTACTACTTTGAGTACACCACGGACAAGGAGCCC
 CGAGGAATCATCCCCCTGGAGAATCTGAGCATCCGAGAGGTGGACGACCCCCGGAACCG
 AACTGCTTTGAACTTTACATCCCCAACAAAGGGGCAGCTCATCAAAGCCTGCAAACT
 GAGGCGGACGGCCGAGTGGTGGAGGGAAACCACATGGTGTACCGGATCTCGGCCCCACG
 CAGGAGGAGAAGGACGAGTGGATCAAGTCCATCCAGGCGGCTGTGAGTGTGGACCCCTTC
 TATGAGATGCTGGCAGCGAGAAAGAAGCGGATTTTCAGTCAAGAAGAAGCAGGAGCAGCCC
 TGA

Fig. 57**SEQ ID NO: 57****PSCD2L**

>ENSG00000105443 | 19 | codificante de proteina | ENST00000391881 | ENSP00000375753
 ATGGAGGACGGCGTCTATGAACCCCAAGACCTGACTCCGGAGGAGCGGATGGAGCTGGAG
 AACATCCGGCGGCGGAAGCAGGAGCTGCTGGTGGAGATTGAGCGCCTGCGGGAGGAGCTC
 AGTGAAGCCATGAGCGAGGTGGAGGGGCTGGAGGCCAATGAGGGCAGTAAGACCTTGCAA
 CGGAACCGGAAGATGGCAATGGGCAGGAAGAAGTTCAACATGGACCCCAAGAAGGGGATC
 CAGTTCTTGGTGGAGAATGAACTGCTGCAGAACACACCCGAGGAGATCGCCCGCTTCCTG
 TACAAGGGCGAGGGGCTGAACAAGACAGCCATCGGGGACTACCTGGGGGAGAGGGAAGAA
 CTGAACCTGGCAGTGCTCCATGCTTTTGTGGATCTGCATGAGTTCACCGACCTCAATCTG
 GTGCAGGCCCTCAGGCAGTTTCTATGGAGCTTTCGCCCTACCGGAGAGGCCAGAAAATT
 GACCGGATGATGGAGGCCCTTCGCCAGCGATACTGCCTGTGCAACCCTGGGGTTTTCCAG
 TCCACAGACACGTGCTATGTGCTGCTCCTTCGCCGTATCATGCTCAACACAGTCTCCAC
 AATCCCAATGTCCGGGACAAGCCGGGCTGGAGCGCTTGTGGCCATGAACCGGGGCATC
 AACGAGGGCGGGGACCTGCCTGAGGAGCTGCTCAGGAACCTGTACGACAGCATCCGAAAT
 GAGCCCTTCAAGATTCTTGAGGATGACGGGAATGACCTGACCCACACCTTCTTCAACCCG
 GACCGGGAGGGCTGGCTCCTGAAGCTGGGGGGCCGGGTGAAGACGTGGAAGCGGCGCTGG
 TTTATCCTCACAGACAACCTGCCCTCTACTACTTTGAGTACACCACGGACAAGGAGCCCCGA
 GGAATCATCCCCCTGGAGAATCTGAGCATCCGAGAGGTGGACGACCCCCGGAACCGAAC
 TGCTTTGAACTTTACATCCCCAACAACAAGGGGCAGCTCATCAAAGCTGCAAAACTGAG
 GCGGACGGCCGAGTGGTGGAGGGAACACATGGTGTACCGGATCTCGGCCCCACGCAG
 GAGGAGAAGGACGAGTGGATCAAGTCCATCCAGGCGGCTGTGAGTGTGGACCCCTTCTAT
 GAGATGCTGGCAGCGAGAAAGAAGCGGATTTCAAGTCAAGAAGAAGCAGGAGCAGCCCTGA

Fig. 58

SEQ ID NO: 58

PPIA

>ENSG00000198618 | 21 | codificante de proteina | ENST00000358455 | ENSP00000351238
 ATGGTCAACCCACCGTGTTCTTCGACATTGCCGTCGACGGCGAGCCCTTGGGCCGCGTC
 TCCTTTGAGCTGTTTGCAGACAAGGTCCCAAAGACAGCAGAAAATTTTCGTGCTCTGAGC
 ACTGGAGAGAAAGGATTTGGTTATAAGGGTTCCCTGCTTTCACAGAATTATTCCAGGGTTT
 ATGTGTCAGGGTGCTGACTTCACACGCCATAATGGCACTGGTGGCAAGTCCATCTATGGG
 GAGAAAATTTGAAGATGAGAACTTCATCCTAAAGCATACAGGTCCTGGCATCTTGTCCATG
 GCAAATGCTGGACCCAACACAAATGGATCCCAGTTTTTCATCTGCACTGCCAAGACTGAG
 TGGTTGGATGGCAAGCATGTGGTGTGTTGGCAAAGTGAAAGAAGGCATGAATATTGTGGAG
 GCCATGGAGCGCTTTGGGTCCAGGAATGGCAAGACCAGCAAGAAGATCACCATTGCTGAC
 TGTGGACAACCTCGAATAA

Fig. 59

SEQ ID NO: 59

MGTRDDEYDYLEFKVVLIGDSGVGKSNLLSRFTRNEFNLESKSTIGVEFATRSIQVDGKTI
KAQIWDTAGQERYRAITSAYYRGAVGALLVYDIAKHLTYENVERWLKELRDHADSNIIVIM
LVGNKSDLRHLRAVPTDEARAFAEKNNLSFIETSALDSTNVEEAFKNILTEIYRIVSQKQ
IADRAAHDESPGNNVVDISVPPTTDGQKPNKLQCCQNL*

Fig. 60**SEQ ID NO: 60**

MAAADGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSTIALALGVERTRSELLPFLTDTIY
 DEDEVLLALAEQLGTFTTLVGGPEYVHCLLPPLSLATVEETVVRDKAVESLRAISHEHS
 PSDLEAHFVPLVKRLAGGDWFTSRTSACGLFSVCYPRVSSAVKAELRQYFRNLCSDDTPM
 VRRAAASKLGEFAKVLLELDNVKSEIIPMFSNLASDEQDSVRLAVEACVNIAQLLPQEDL
 EALVMPTLRQAAEDKSWRVRYMVADKFTELQKAVGPEITKTDLVPAFQNLMKDCEAEVRA
 AASHKVKEFCENLSADCENVIMSQILPCIKELVSDANQHVKSALASVIMGLSPILGKDN
 TIEHLLPLFLAQLKDECPEVRLNIISNLDCVNEVIGIRLSQSLPAIVELAEDAKWRVR
 LAIEYMPLLAGQLGVEFFDEKLNSLCMAWLVDHVYAIREAATSNLKKLVEKFGKEWAHA
 TIIPKVLAMSGDPNYLHRMTTLFCINVLSEVCGQDITTKHMLPTVLRMAGDFVANVRFNV
 AKSLQKIGPILDNSTLQSEVKPILEKLTQDQDQDVVKYFAQEALTVLSLA*

Fig. 61

SEQ ID NO: 61

MRTFSFASTASRSCPPSPFWPLGLKGPEVSFCLSLQIPSMKMRSSWPWQNSWEPSLPWWE
 AQTCTACCLFSVCYPRVSSAVKAELRQYFRNLCSDDTPMVRRAAASKLGEFAKVLDELN
 VKSEIIPMFSNLASDEQDSVRLlaveacvnIAQLLPQEDLEALVMPTLRQAAEDKSWRVR
 YMVADKFTELQKAVGPEITKTDLVPAFQNLMKDCEAEVRAAASHKVKEFCENLSADCREN
 VIMSQILPCIKELVSDANQHVKSALASVIMGLSPILGKDNTIEHLLPLFLAQLKDECPEV
 RLNIISNLDCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIEYMPLLAGQLGVEFFD
 EKLNSLCMAWLVDHVYAIREAATSNLKKLVEKFGKEWAHATII PKVLAMSGDPNYLHRMT
 TLF CINVLSEVCGQDITTKHMLPTVLRMAGDPVANVRFNVAKSLQKIGPILDNSTLQSEV
 KPILEKLTQDQDQDVVKYFAQEALTVLSLA*

Fig. 62

SEQ ID NO: 62

MELITILEKTVSPDRLELEAAQKFLERA AVENLPTFLVELSRVLANPGNSQVARVAAGLO
 IKNSLTSKDPDIKAQYQQRWL AIDANARREVKNYVLQTLGTETYPSSASQCVAGIACAE
 IPVNQWPELIPQLVANVTNPNSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTAI IQG
 MRKEEPSNNVLAATNALLNSLEFTKANFDKESERHFIMQVVCEATQCPDTRVRVAALON
 LVKIMSLYYQYMETYMGPALFAITIEAMKSDIDEVALQGIEFWSNVCDEEMDLAIEASEA
 AEQGRPPEHTSKFYAKGALQYLVPILTQTLTKQDENDDDDWNPCKAAGVCLMLLATCCE
 DDIVPHVLPFIKEHIKNPDWRYRDAAVMAFGCILEGPEPSQLKPLVIQAMPTLIELMKDP
 SVVVRDTAAWTVGRICELLPEAAINDVYLAPLLQCLIEGLSAEPRVASNVCWAFSSLAEA
 AYEAADVADDQEEPATYCLSSSFELIVQKLETTDRPDGHQNNLRSSAYESIMEIVKNSA
 KDCYPAVQKTTLVIMERLQQVLQMESHIQSTSDRIQFNDLQSLLCATLQNVLRKVQHQDA
 LQISDVVMASLLRMFQSTAGSGGVQEDALMAVSTLVEVLGGEFLKYMEAFKPFGLGIGLKN
 YAEYQVCLAAVGLVGDLCRALQSNII PFCDEVMQLLENLGNENVHRSVKPQILSVFGDI
 ALAIGGEFKKYLEVVLNTLQQASQAQVDKSDYDMVDYLNELRESCLEAYTGIVQGLKGDQ
 ENVHPDVMLVQPRVEFILSFIDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDV LKLV EAR
 PMIHELLTEGRRSKTNKAKTLATWATKELRKLKNQA*

Fig. 64**SEQ ID NO: 64**

MGTKMADLDSPPKLSGVQQPSEGVGGGRCSEISAELIRSLTELQELEAVYERLCGEEKVV
 ERELDALLEQQNTIESKMVTLHRMGPNLQLIEGDAKQLAGMITFTCNLAENVSSKVRQLD
 LAKNRLYQAIQRADDILDLKFCMDGVQTALRSEDYEQAAAHTRYLCCLKSVIELSRQ GK
 EGSMIDANLKLQAEQRLKAIVAEKFATKEGDL PQVERFFKIFPLLGLHEEGLRKFS
 EYLCKQVASKAEENLLMVLGTDMSDRRAAVIFADTLTLLFEGIARIVETHQPIVETYYGP
 GRLYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNSTTEKIEPRELDPIL
 TEVTLMNARSELYLRFLKKRISSDFEVGDSMASEEVKQEHQKCLDKLLNNCLLSCTMQEL
 IGLYVTMEEYFMRETVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSSIDCLCA
 MINLATTELESDFRDVLCNKLRMGFPATTFQDIQRGVTSAVNIMHSSLQQGKFDTKGIES
 TDEAKMSFLVTLNNVEVCSENISTLKKTLES DCTKLFSQGIGGEQAQAKFDSCLSDLA AV
 SNKFRDLLQEGLTELNSTAIKPQVQPWINSFFSVSHNIEEEEFNDYEANDPWVQQFILNL
 EQQMAEFKASLSPVIYDSL TGLMTSLVAVELEKVVLKSTFNRLGGLQFDKELRSLIAYLT
 TVTTWTIRDKEARLSQMATILNLERVTEILDYWGPN SGPLTWRLTPAEVRQVLALRIDFR
 SEDIKRLRL*

Fig. 65

SEQ ID NO: 65

MADLDSPPKLSGVQQPSEGVGGGRCSEISAELIRSLTELQELEAVYERLCGEEKVVEREL
 DALLEQQNTIESKMVTLHRMGPNLQLIEGDAKQLAGMITFTCNLAENVSSKVRQLDLAKN
 RLYQAIQRADDILDLKFCMDGVQTALRSEDYEQAAAHTRYLCCLKSVIELSRQGKEGSM
 IDANLKLQEAQRLKAIVAEKFAIATKEGDLQVERFFKIFPLLGLHEEGLRKFSEYLC
 KQVASKAEENLLMVLGTDMSDRRAAVIFADTLTLFEGIARIVETHQPIVETYYGPGRLY
 TLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNSTTEKIEPRELDPILTEVT
 LMNARSELYLRFLKKRISSDFEVGDSMASEEVKQEHQKCLDKLLNNCLLSCTMQELIGLY
 VTMEEFYFMRETVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSIDCLCAMINL
 ATTELESDFRDVLCNKLRMGFPATTFQDIQRGVTSAVNIMHSSLQQGKFDTKGIESTDEA
 KMSFLVTLNNVEVCSENISTLKKTLES DCTKLFSQGIGGEQAQAKFDSCLSDLA AVSNKF
 RDLLQEGLTELNSTAIKPQVQPWINSFFSVSHNIEEEEFNDYEANOPWVQQFILNLEQQM
 AEFKASLSPVIYDSL TGLMTSLVAVELEKVVLKSTFNRLGGLQFDKELRSLIAYLTTVTT
 WTIRDKFARLSQMATILNLERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDI
 KRLRL*

Fig. 66

SEQ ID NO: 66

MADLDSPPKLSGVQQPSEGVGGGRCSEISAELIRSLTELQELEAVYERLCGEEKVVEREL
DALLEQQNTIESKMVTLHRMGPNLQLIEGDAKQLAGMITFTCNLAENVSSKVRQLDLAKN
RLYQAIQRADDILDLKFCMDGVQTALRSEDYEQAAAHTHRYLCLDKSVIELSRQGKEGSM
IDANLKLQEAQRLKAIVAEKFATKEGDLPQVERFFKIFPLLGLHEEGLRKFSEYLC
KQVASKAEENLLMVLGTDMSDRRAAVIFADTLTLLEGIARIVETHQPIVETYYGPGRLY
TLIKYLQVECDRQVEKVVDKFIKQRDYHQQNFVFSFF*

Fig. 67

SEQ ID NO: 67

MGTKMADLDSPPKLSGVQQPSEGVGGGRCSEISAELIRSLTELQELEAVYERLCGEEKVV
 ERELDALLEQQNTIESKMVTLHRMGPNLQLIEANLKLQEAQRLKAIVAEEKFAIATKEG
 DLPQVERFFKIFPLLGLHEEGLRKFSEYLCKQVASKAEENLLMVLGTDMSDRRAAVIFAD
 TLTLLEFEGIARIVETHQPIVETYYGPGRLYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQ
 FRHVQNNLMRNSTTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSDFEVGDSMASE
 EVKQEHQKCLDKLLNNCLLSCTMQELIGLYVTMEEFYFMRETVNKAVALDTYEKGQLTSSM
 VDDVFYIVKKCIGRALSSSSIDCLCAMINLATTELESDFRDVLCNKLRMGFPATTFQDIQ
 RGVTSAVNIMHSSLQQGKFDTKGIESTDEAKMSFLVTLNNVEVCSENISTLKKTLES DCT
 KLFSQIGIGGEQAQAKFDSCLSDLA AVSNKFRDLLQEGLTELNSTAIKPQVQPWINSFFSV
 SHNIEEEEFNDYEANDPWVQQFILNLEQQMAEFKASLSPVIYDSL TGLMTSLVAVELEKV
 VLKSTFNRLGGLQFDKELRSLIAYLTTVTTWTIRDKFARLSQMATILNLERVTEILDYWG
 PNSGPLTWRLTPAEVRQVLALRIDFRSEDIKRLRL*

Fig. 68

SEQ ID NO: 68

MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA
LDGEMRNAVCI FYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRO
VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG
IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV
KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCALPQVMAIATL
AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRI PDS DPSSSKTR
QIISTIRTQNL PNCQLISRSHYSPIYLSFVMLLAALSWQYLTTLSQVTEDYVQTGEH*

Fig. 69

SEQ ID NO: 69

MRASQKDFENSMNQVKLLKKDPGNEVKLKYALYKQATEGPCNMPKPGVFDLINKAKWDA
WNALGSLPKEAARQNYVDLVSSLSPSLESSSQVEPGTDRKSTGFETLVVTSEDGITKIMF
NRPKKKNAINTEMYHEIMRALKAASKDDSIITVLTGNGDYYSSGNDLTNFTDIPPGGVEE
KAKNNAVLLREFVGCFIDFPKPLIAVVNGPAVGISVTLLGLFDAVYASDRATFHTPFSHL
GQSPEGCSSYTFFPKIMSPAKATEMLIFGKKLTAGEACAQGLVTEVFPDSTFQKEVWTRLK
AFAKLPPNALRISKEVIRKREREKLHAVNAEECNVLQGRWLSDECTNAVVNFLSRKSKL*

Fig. 70

SEQ ID NO: 70

MYHEIMRALKAASKDDSIITVLTGNGDYSSGNDLTNFTDIPPGGVEEKAKNNAVLLREF
VGCFIDFPKPLIAVVNGPAVGISVTLLGLEDAVYASDRATFHTPFSLGQSPEGCSSYTF
PKIMSPAKATEMLIFGKKLTAGEACAQGLVTEVFPDSTFQKEVWTRLKAFKLPNALRI
SKEVIRKREREKLAHVNAEECNVLQGRWLSDECTNAVVNFLSRKSKL*

Fig. 71

SEQ ID NO: 71

MAMAYLAWRLARRSCPSSLQVTSFPPVQLHMNRTAMRASQKDFENSMNQVKLLKKDPGNE
 VKLKLYALYKQATEGPCNMPKPGVFDLINKAKWDANALGSLPKEAARQNYVDLVSSLSP
 SLESSSQVEPGTDRKSTGFETLVVTSEDGITKIMFNRPKKKNAINTEMYHEIMRALKAAS
 KDDSIITVLTGNGDYSSGNDLTNFTDIPGGVEEKAKNNAVLLREFVGCFLDFPKPLIA
 VVNGPAVGISVTLLGLEDAVYASDRATFHTPFSLHLSQSPGCSSTFPKIMSPAKATEML
 IFGKKLTAGEACAQGLVTEVFPDSTFQKEVWTRLKAFKLPPNALRISKEVIRKREREKL
 HAVNAEECNVLQGRWLSDECTNAVVNFLSRKSKL*

Fig. 72

SEQ ID NO: 72

MNRTAMRASQKDFENSMNQVKLLKKDPGNEVKLKLYALYKQATEGPCNMPKPGVFDLINK
 AKWDAWNALGSLPKEAARQNYVDLVSSLSPSLESSSQVEPGTDRKSTGFETLVVTSEDGI
 TKIMFNRPKKKNAINTEMYHEIMRALKAASKDDSIITVLTGNGDYSSGNDLTNFTDIPP
 GGVEEKAKNNAVLLREFVGCFIDFPKPLIAVNGPAVGISVTLLGLFDVAVYASDRATFHT
 PFSHLGQSPEGCSSYTFPKIMSPAKATEMLIFGKKLTAGEACAQGLVTEVFPDSTFQKEV
 WTRLKAFAKLPPNALRISKEVIRKREREKLHAVNAEECNVLQGRWLSDECTNAVVNFLSR
 KSKL*

Fig. 73

SEQ ID NO: 73

MFNRPKKKNAINTEMYHEIMRALKAASKDDSIITVLTGNGDYYSSGNDLTNFTDIPPGGV
EEKAKNNAVLLREFVGCFIDFPKPLIAVVNGPAVGISVTLLGLFDAVYASDRATFHTPFS
HLGQSPEGCSSYTFFPKIMSPAKATEMLIFGKKLTAGEACAQGLVTEVFPDSTFQKEVWTR
LKAFAPLPPNALRISKEVIRKREREKLHAVNAEECNVLQGRWLSDECTNAVVNFLSRKSK
L*

Fig. 74

SEQ ID NO: 74

MFARKPPGAAPLGAMPVPDQPSSASEKTSSLSPLGNTSNGDGSETETTSAILASVKEQEL
 QFERLTRELEAERQIVASQLERCKLGSETGSMSSMSSAEEQFQWQSQDGQKDIEDELTG
 LELVDSCIRSLQESGILDPQDYSTGERPSLLSQSALQLNSKPEGSFQYPASYHSNQTAL
 GETTPSQLPARGTQARATGQSFSQGTTSRAGHLAGPEPAPPPPPPPREPFAPSLGSAFHL
 PDAPFAAAAAALYYSSSTLPAPPRGGSPLAAPQGGSPTKLQRGGSAPEGATYAAPRGSSP
 KQSPSRLAKSYSTSSPINIVVSSAGLSPIRVTSPTVQSTISSSPIHQLSSTIGTYATLS
 PTKRLVHASEQYSKHSQELYATATLQRPGLAAGSRASYSSQHGHGLPELRLALQSPHEHI
 DPIYEDRVYQKPPMRSLSQSQGDPLPPANTGTYRTSTAPSSPGVDSVPLQRTGSQHGPON
 AAAATFORASYAAGPASNYADPYROLOYCPSVESPYSKSGPALPPEGTLARSPSIDSIOK
 DPREFGWRDPELPEVIQMLQHQQFPSVQSNAAAYLQHLFCFGDNKIKAEIRROGGIQLLVDL
 LDHRMTEVHRSACGALRNLYVGKANDDNKIALKNCGGIPALVRLLRKTTDLEIRELVTGV
 LWNLSSCDALKMPIIQDALAVLTNAVIIPHSGWENSPLQDDRKIQLHSSQVLRNATGCLR
 NVSSAGEEARRRMRECDGLTDALLYVIQSALGSSEIDSKTVENCVCILRNLSYRLAETS
 QGQHMGTDELDGLLCGEANGKDAESSGCWGKKKKKKKSQDQWDGVGPLPDCAEPPKGIQM
 LWHPSIVKPYLTLLSECSNPDTLEGAAGALQNLAAAGSWKWSVYIRAAVRKEKGLPILVEL
 LRIDNDRVCAVATALRNMALDVRNKEKIGKYAMRDLVHRLPGGNNNSNTASKAMSDDTV
 TAVCCTLHEVITKNMENAKALRDAGGIEKLVGISKSGDKHSPKVKAASQVLNSMWQYR
 DLRSLYKKDGWSQYHFVASSSTIERDRQRPYSSSRTPSISPVRVSPNNRSASAPASPREM
 ISLKERKTDYECTGSNATYHGAKGEHTSRKDAMTAQNTGISTLYRNSYGAPAEDIKHNQV
 SAQVPVQEPSRKDYETYQPFQNSTRYDESEFFEDQVHHRPPASEYTMHLGLKSTGNYVDF
 YSAARPYSELNYETSHYPASPDV*

Fig. 75

SEQ ID NO: 75

MFARKPPGAAPLGAMFVPDQPSASEKTSSLSPLGNTSNGDGSETETTSAILASVKEQEL
 QFERLTRELEAERQIVASQLERCKLGSETGSMSSMSSAEEQFQWQSQDQKDIEDLTG
 LELVDSCIRSLQESGILDPQDYSTGERPSLLSQSALQLNSKPEGSFQYPASYHSNQTAL
 GETTPSQLPARGTQARATGQSFSQGTTSRAGHLAGEPAPPPPPPPREFFAPSLGSAFHL
 PDAPPAAAAAALYYSSSTLPAPPRGGSPLAAPQGGSPTKLQRGGSAPGATYAAPRGSSP
 KQSPSRLAKSYSTSSPINIVSSAGLSPIRVTSPTTVQSTISSSPIHQLSSTIGTYATLS
 PTKRLVHASEQYSKHSQELYATATLQRPGSLAAGSRASYSSQHGHLPGLRALQSPEHHI
 DPIYEDRVYQKPPMRSLSQSQGDPLPPAHTGTYRTSTAPSSPGVDSVPLQRTGSQHGPQN
 AAAATFQRASYAAGPASNYADPYRQLQYCPSVESPYSKSGPALPPEGLARSPSIDSIQK
 DPREFGWRDPQLPEVIQMLQHQPFSVQSNAAAYLQHLCFGDNKIKAEIRROGGIQLLVDL
 LDHRMTEVHRSACGALRNLYVGKANDDNKIALKNCGGIPALVRLLRKTTDLIELVTVG
 LWNLSSCDALKMPIIQDALAVLTNAVII PHSGWENSPLQDDRKIQLHSSQVLRNATGCLR
 NVSSAGEEARRRMRECDGLTDALLYVIQSALGSSEIDSKTVENCVCILRNLSYRLAETS
 QGQHMGTDELDGLLCGEANGKDAESSGCWGKKKKKKKSQDQWSVYIRAAVRKEKGLPILV
 ELLRIDNDRVCAVATALRNMALDVRNKEKLGKYAMRDLVHRLPGGNNNNNTASKAMSDD
 TVTAVCCTLHEVITKNMENAKALRDAGGIEKLVGISKSKGDKHSPKVKAASQVLNSMWQ
 YRDLRSLYKKDGWSQYHFASSSTIERDRQRPYSSSRTPSISPVRVSPNNRSASAPASPR
 EMISLKERKTDYECTGSNATYHGAKGEHTSRKDAMTAQNTGISTLYRNSYGAPAEDIKHN
 QVSAQPVPPQEPSRKDYETYQPFQNSTRYNDESFFEDQVHHRPPASEYTMHLGLKSTGNYV
 DFYSAARPYSELNYETSHYPASPDWV*

Fig. 76

SEQ ID NO: 76

MQGSTRRMGVMTDVHRRFLQLLMTHGVLEEWDVKRLQTHCYKVHDRNATVDKLEDFINNI
NSVLESLEYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLFRKALELIIDSE
TGFASTNIIILNLDQLKGKKMRKKEAEQVLQKFVQNKWLIEKEGEFTLHGRAILEMEQYI
RETYPDAVKICNICHSLIIQGQSCETCGIRMHLPCVAKYFQSNAEPRCPHCNDYWPHEIP
KVFDPKERESEGLKSNKSLRSRQH*

Fig. 77

SEQ ID NO: 77

PYPLARWDALGLPVRSHMQGSTRRMGVMTDVHRRFLQLLMTHGVLEEWDVKRLQTHCYKV
HDRNATVDKLEDFINNINSVLESLEYIEIKRGVTEDDGRPIYALVNLATTSSKMATDFAE
NELDLFRKALELIIDSETLRLPQTY*

Fig. 78

SEQ ID NO: 78

VHLATVSASAAWDALGLPVRSHMQGSTRRMGVMTDVHRRFLQLLMTHGVLEEWDVKRLQT
HCYKVHORNATVDKLEDFINNINSVLESLEYIEIKRGVTEDDGRPIYALVNLATTSISKMA
TDFAENELDLFRKALELIIDSETGFASSTNILNLVDQLKGKKMRKKEARCCRSLFKTS*

Fig. 79

SEQ ID NO: 79

MEWWASSFLRLWLLLFLPSAQGRQKESGSKWKVFIDQINRSLENYEPCSSQNCSCYHGV
 IEEDLTPFRGGISRKMMAEVVRKLGTHYQITKNRLYREND CMFPSRCSGVEHFILEVIG
 RLPDMEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPITYPTG
 LGRWDLFREDLVRSAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVD AEYTKNQ
 AWKSMKDTLGKPAAKDVHLVDHCKYKYLNFNFRGVAASFRFKHLFLCGSLVFHVGVDEWLEF
 FYPQLKFWVHYIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWE
 NLLSEYSKFLSYNVTRRKG YDQIIPKMLKTEL*

Fig. 80

SEQ ID NO: 80

MRRRRAGGRTMVERASKFVLVVAGSVCFMLILYQYAGPGLSLGAPGGRAPPDDLDFPTF
DPHYEKKYYFPVRELESLRFDMKGDDVIVFLHIQKTGGTTFGRHLVQNRLEVPCDCRP
GQKKCTCYRPNRRETWLFSTRFSTGWSCGLHADWTELNCVPGVLDRRDSAALRTPRKYY
ITLLRDPVSRYLSEWRHVQRGATWKTSLHMC DGRTPTPEELPPCYEGTDWSGCTLQEFMD
CPYNLANNRQVRMLADLSLVGCYNLSFIPEGKRAQLLES AKKNLRGMAFFGLTEFQRKT
QYLFERTFNLFIRPFMQYNSTRAGGVEVDEDTIRRIEELNDLDMQLYDYAKDLFQQRYQ
YKRQLERREQRLRSREERLLHRAKEALPREDADEPGRVPTEDYMSHIEKW*

Fig. 81

SEQ ID NO: 81

MTSCRCSVTSRSLWFPALAPRRQCQHTSPASAQCKQDKACRFLAAQKGAYPIIFTANKLATA
 GDQGLLLQSLNALSVLTDGQPDLLDAQGLQLLVATLTQNADEADLTCSGIRCVRHACLKH
 EQNRQDLVKAGVLP LLTGAI THHGHTDVVREACWALRVMTFDDDIRVPFGHAHNHAKMI
 VQENKGLKVLIEATKAFLDNPGILSEL CGTLSRLAIRNEFCQEVVDLGGLSILVSLADC
 NDHQM RDQSGVQELVKQVLSTLRAIAGNDDVKDAIVRAGGTESIVAAMTQHLTSPQVCEQ
 SCAALCFLALRKPDNSRIIVEGGGAVAALQAMKAHPQKAGVQKQACMLIRNLVAHRPSRS
 PSWTWGLRHSSCRPDLP T V T V R T W P R P P C G T W V M S S S E S C G Q A R G A T W R H D P R P S L V T L
 GESCDSGMGVDPCPPLSPISSVPFTMRSVFWQALGKGS GEGGAL*

Fig. 82

SEQ ID NO: 82

MSERCCSRYSSGASIGCTPTSTQAKMVSKRIAQETFDAVRENIEEFAMGPPEEAVKEAVE
 QFESQGVDSLNI VKTAPKVSADGSQEPTHDILOMLSDLQESVASSRPQEV SAYLTRFCDQ
 CKQDKACRFLAAQKGAYPI IFTAWKLATAGDQGLLLQSLNALSVLTDGQPDLLDAQGLQL
 LVATLTQNADEADLTCSGIRCVRHACLKHEQNRQDLVKAGVLP LLTGAITHHGHHTDVVR
 EACWALRVMTFDDDIRVPFGHAHNHAKMIVQENKGLKVLIEATKAFLDNPGILSEL CGTL
 SRLAIRNEFCQEVVDLGGLSILVSL LADCNDHQMRDQSGVQELVKQVLSTLR A IAGNDDV
 KDAIVRAGGTESIVAAMTQHLTSPOVCEQSCAALCFLALRKPDNSRIIVEGGGAVAALQA
 MKAHPQKAGVQKQACMLIRNLVAHGQAFSKPILDLGAELIMQARS AHRDCEDVAKAALR
 DLGCHVELRELWTGQRGNLAP*

Fig. 83

SEQ ID NO: 83

MVSKRIAQETFDAAVRENIEEFAMGPPEEAVKEAVEQFESQGVDSLNI VKTAPKVSADGSQ
 EPTHDLQMLSDLQESVASSRPQEV SAYLTRFCDQCKQDKACRFLAAQKGAYPIIFTANK
 LATAGDQGLLLQSLNALSVLTDGQPDLLDAQGLQLLVATLTQNADEADLTCSGIRCVRHA
 CLKHEQNRQDLVKAGVLP LLTGAI THHGHTDVVREACWALRVMTFDDDIRVPFGHAHNH
 AKMIVQENKGLKVLI EATKAFLDNPGILSEL CGTLSRLAIRNEFCQEVVDLGGLSILVSL
 LADCNDHQMRDQSGVQELVKQVLSTLRAIAGNDDVKDAIVRAGGTESIVAAMTQHLTSPQ
 VCEQSCAALCFLALRKPDNSRIIVEGGGAVAALQAMKAHPQKAGVQKQACMLIRNLVAHG
 QAFSKPILDLGAEALIMQARSAHRDCEDVAKAALRDLGCHVELRELWTGQRGNLAP*

Fig. 84

SEQ ID NO: 84

MVSKRIAQETFDAAVRENIEEFAMGPPEEAVKEAVEQFESQGVDSLNI VKTAPKVSADGSQ
 EPTHDIQMLSDLQESVASSRPQEV SAYLTRFCDQCKQDKACRFLAAQKGAYPIIFTAWK
 LATAGDQGLLLQSLNALS VLTGQPDLLDAQGLQLLVATLTQNADEADLTC SGIRCVRHA
 CLKHEQNRQDLVKAGVLP LLTGAI THHGHTDVVREACWALRVMTFDDDIRVPFGHAHNNH
 AKMIVQENKGLKVLIEATKAFLDNPGILSEL CGTLSRLAIRNEFCQEVVDLGGLSILVSL
 LADCNDHQMRDQSGVQELVKQVLSTLR A IAGNDDVKDAIVRAGGTESIVAAMTQHLTSPQ
 VCEQSCAALCFLALRKPDNSRIIVEGGGAVAALQAMKAHPQKAGVQKQACMLIRNLVAHG
 QAFSKPILDLGAEALIMQARS AHRDCEDVAKAALRDLGCHVELRELWTGQRGNLAP*

Fig. 85

SEQ ID NO: 85

MAGAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGEDDAEVQQECLHKFSTRDYIMEP
 SIFNTLKRYFQAGGSPENVIQLLSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLK
 SLLIKHFDPRKADSIETEEGETPAWLEQMIANTTWRDLFYKLAEAHPCDCLMLNFTVKLIS
 DAGYQGEITSVSTACQQLEVFSTRVLRSLATILDGGEENLEKNLPEFAKMOVCHGEHTYLF
 AQAMMSVLAQEEQGGSAVRRIAQEVQRFAQEKGHASQITLALGTAASYPRACQALGAML
 SKGALNPADITVLFKMFSTMDPPPVELIRVPAFLDLFMQSLFKPGARINQDHKKHYIHIL
 AYAASVETWKKNKRVSKDELKSTSKAVETVHNLCNENKGASELVAELSTLYQCIRF
 PVVAMGVLKWVDWTVSEPRYFQLQTDHTPVHLALLDEISTCHQLLHPQVLQLLVKLFETE
 HSQLDVMEQLELKKTLDRMVHLLSRGYVLPVVSYIRKCLEKLDTDISLIRYFVTEVLDV
 IAPPYTSDFVQLFLPILENDSTAGTIKTEGEHDPVTEFIAHCKSNFIMVN*

Fig. 86

SEQ ID NO: 86

MAMLRVQPEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLKEPALNEANLSNLKAP
LDIPVPDPVKEKEKEERKKQOEKEDKDEKKKGEDEDKGPPCGPVNCNEKIVVLLQRLKPE
IKDVIEQLNLVTTWLQLQIPRIEDGNNFGVAVQEKVFELMTSLHTKLEGFHTQISKYFSE
RGDAVTKAAKQPHVGDYRQLVHELDEAEYRDIRLMVMEIRNAYVRRQGQGRGGQRQLSQA
THSLTLQARG*

Fig. 87

SEQ ID NO: 87

MAMLRVQPEAQAKVDVFRDLCTKTENLLGSYFPKKISELDAFLKEPALNEANLSNLKAP
LDIPVPDPVKEKEKEERKKQQEKEDKDEKKKGEDEDKGPPCGPVNCNEKIVVLLQRLKPE
IKDVIEQLNLVTTWLQLQIPRIEDGNNFGVAVQEKVFELMTSLHTKLEGFHTQISKYFSE
RGDAVTKAARKQPHVGDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKNFEKLKKP
RGETKGMIY*

Fig. 88

SEQ ID NO: 88

MELRARGWLLCAAAALVACARGDPASKSRSCGEVRQIYGAKGFSLSVDPQAEISGEHLR
 ICPQGYTCCTSEMEENLANRSHAELETALRDSSRVLQAMLATQLRSFDDHFQHLNDSE
 TLQATFFGAFGELYTONARAFRDLYSELRLYYRGANLHLEETLAEFWARLLERLEFKQLHP
 QLLLDDYLDCLGKQAEALRPFGEAPRELRLRATRAFVAARSFVQGLGVASDVVRKVAQV
 PLGPECSRAVMKLVYCAHCLGVFGARPCPDYCRNVKLGCLANQADLDAEWRNLLDSMVL
 TDKFWGTSGVESVIGSVHTWLAEAINALQDNRDTLTAKVIQCGNPKVNPQGPPEEKRR
 RGKLAPRERPPSGTLEKLVSEAKAQLRDVQDFWISLPGTLCSEKMASTASDDRCWNGMA
 RGRYLPEVMGDGLANQINNPEVEVDITKPDMTIRQQIMQLKIMTNRLRSAYNGNDVDFQD
 ASDDGS GSGSGDGCLDDLC SRKVS RKSSSSRTPLTHALPGLSEQEGQKTSAA SCPQPPTF
 LLPLLLFLALTVARPRWR*

Fig. 89

SEQ ID NO: 89

MASCASIDIEDATQHLDILKLD RPAGGPSAESPRPSSAYNGDLNGLLVDPFLCSGDSTS
 ANKTGLRTMPF PINLQEKQVICLSGDDSSSTCIGILAKEVEIVASSDSSISSKARGSNKVKI
 QPVAKYDWEQKYYYGNLIAVSNSFLAYAIRAANNSSAMVRVISVSTSER TLLKGFTGSVA
 DLAF AHLNSPQLACLDEAGNLFVWRLALVNGKIQEEILVHIRQPEG TPLNHFRRIIWCPF
 IPEESEDCC EESSPTVALLHEDRAEVWDLMLRSSHSTWPFVDVSQIKQGFIVVKGHSTCL
 SEGALSPDGTVLATASHDGYVKFWQIYIEGQDEPRCLHEWKPHDGRPLSCLLFCDNHKKQ
 DPDVPFWRFLITGADQNRELKMWCTVSWTCLQTIRFSPDIFSSSVSVPPSLKVC LDLSAEY
 LILSDVQRKVLYVMELLQNQE EGHACFSSISEFLLTHPVLSFGIQVVSRCRLRHTEVLPA
 EEENDSLGADGTHGAGAMESAAGVLIKLFVHTKALQDVQIRFQPQLNPDVVAPLPHTHTA
 HEDFTTFGESRPELGSEGLGSAAHGSQPD LRRIVELPAPADFLSLSSE TKPKLMTPD AFMT
 PSASLQQITASPSSSSSSGSSSSSSSSSSSLTAVSAMSSTSAVDPSLTRPPEELT LSPKLQ
 LDGSLTMSSSGSLQASPRGLLPGLLPAPADKLT PKGPGQVPTATSALSLELQEVEPLGLP
 QASPSRTRSPDVISSASTALSQDIPEIASEALSRGFGSSAPEGLEPDSMASAASALHLLS
 PRPRPGPELGPQLGLDGGPGDGRHNTPSLLEAALTQEASTPDSQVWPTAPDITRETCST
 LAESPRNGLQEKHKSLAFHRPPYHLLQQRDSQDASAEQSDHDDEVASLASASGGFGTKVP
 APRLEPAKDWKTGSPRTSPKLKRKSKKDDGDAAMGSRLTEHQVAEPPEDWPALIWQQQRE
 LAELRHSQEELLQRLCTQLEGLQSTVTGHVERALETRHEQEQRRLERALEGQQRGGQLQ
 EQLTQQLSQALSSAVAGRLERSIRDEIKKTVPPCVSRSL EPMAGQLSNSVATKLTAVEGS
 MKENISKLLKSKNLTD AIAAAAADTLQGPMQAAYREAFQSVVLP AF EKSCQAMFQQINDS
 FRLGTQEYLLQQLESHMKS RKAREQEAREPVLAQLRGLVSTLQSATEQMPPWPAVFVLRCS
 TSCMWLWAACRSPF*

Fig. 90

SEQ ID NO: 90

MASCASIDIEDATQHRLDILKLDRPAGGPSAESPRPSSAYNGDLNGLLVDPDPLCSGDSTS
 ANKTGLRTMPPINLQEKQVICLSGDDSSSTCIGILAKEVEIVASSDSSISSKARGSNKVKI
 QPVAKYDWEQKYYYGNLIAVSNSFLAYAIRAANNGSAMVRVISVSTSERILLKGFTGSVA
 DLAF AHLNSPQLACLDEAGNLFVWRLALVNGKIQEEILVHIRQPEGTPLNHFRRIIWCPF
 IPEESEDCCCESSPTVALLHEDRAEVWDLDMLRSSHSTWPDVVSQIKQGEIVVKGHSTCL
 SEGALSPDGTVLATASHDGYVKFWQIYIEGQDEPRCLHEWKPHDGRPLSCLLFCDNHKKQ
 DFDVPFWRFLITGADQNRELKMWCTVSWTCLQTIREFSPDIFSSVSVPPLKVCCLDLAEY
 LILSDVQRKVLVYMELLQNQEEGHACFSSISEFLTHPVLSTFGIQVVSRCRLRHTEVLP
 EEENDSLGADGTHGAGAMESAAGVLIKLCVHTKALQDVQIRFQPLNPDVVAPLPHTHTA
 HEDFTFGESRPELGSEGLGSAAHGSQPDLRRIVELPAPADFLSLSSSETKPKLMTPDAMT
 PSASLQQITASPPSSSSSGSSSSSSSSSSSSSLTAVSAMSSSTSAVDPSLTRPPEELTSPKLQ
 LDGSLTMSSSGSLQASPRGLLPGLLPAPADKLT PKGPGQVPTATSALSLELQVEEPLGLP
 QASPSRTRSPDVISSASTALSQDIPEIASEALS RGFSSSAPEGLEPDMSMASAASALHLLS
 PRPRPGPELGPQLGLDGGPGDGRHNTPSLLEAALTQEASTPDSQVWPTAPDITRETCST
 LAESPRNGLQEKHKSLAFHRFPYHLLQQRDSQDASAEQSDHDDEVASLASASGGFGTKVP
 APRLPKDWKTKGSPRTSPKLKRKSKKDDGDAAMGSRLTEHQVAEPPEDWPALIWOQQRE
 LAELRHSQEELLQRLCTQLEGLQSTVTGHVERALETRHEQEQRRLERALEGQQRGGQLQ
 EQLTQQLSQALSSAVAGRLERSIRDEIKKTVPVPCVSRSLPEMAGQLNSVATKLTAVEGS
 MKENISKLLKSKNLTDATARAADTLQGPMAAYREAFQSVVLPFAFEKSCQAMFQQINDS
 FRLGTQEYLQQLESHMKSARKAREQEAREPVLALRGLVSTLQSATEQMAATVAGSVRAEV
 QHQLHVAVGSLQESILAQVQRIVKGEVSVALKEQQAATSSIMQAMRSAAGTPVPSAHL
 CQAQQAHLQLLQGHNLNQAQQALTAADLNLVLYVCETVDPAQVFGQPPCPLSQPVLLS
 LIQQLASDLGTRTDLKLSYLEEAVMHLHDSDPITRDHMGSVMAQVRQKLFQFLQAEPHNS
 LGKAARRLSLMLHGLVTPSLP*

Fig. 91

SEQ ID NO: 91

MRRSEVLAEESIVCLQKALNHLREIWELIGIPEDQRLQRTQTEVVKKHIKELLDMMIAEEES
LKERLIKSISVCQKELNTLCSELHVEPFQEEGETTILQLEKDLRTQVELMRKQKKERKQE
LKLQEQDQELCEILCMPHYDIDSASVPSLEELNQFRQHVTTLRETKASRREEFVSIKRQ
IILCMEALDHTPDTSFERDVVCEDEDAFCLSLENIATLQKLLRQLEMQKSQNEAVCEGLR
TQIRELWDRLOIPEEEREAVATIMSGSKAKVRKALQLEVDRLLEELKMQNMKKVIEAIRVE
LVQYWDQCFYSQEQRQAFAPFCAEDYTESLLQLHDAEIVRLKNYYEVHKELFEGVQKWEE
TWRLFLEFERKASDPNRFTNRGGNLLKEEKQRAKLQKMLPKLEEELKARIELWEQEHSKA
FMVNGQKFMEYVAEQWEMHRLEKERAKQERQLKNKKQTETEMLYGSAPRTPSKRRGLAPN
TPGKARKLNTTMSNATANSSIRPIFGGTVYHSPVSRLPSPGSKPVAASTCSGKKTPTG
RHGANKENLELNGSILSGGYPGSAPLQRNFSINSVASTYSEFAKDPSSLSDSSSTVGLQREL
SKASKSDATSGILNSTNIQS*

Fig. 92

SEQ ID NO: 92

TRLRPVARFEILRGSTARGAATRSDIAGVCGWLLLSGPCGVGLDLDLSRLLGASAMRRSEV
 LAEESIVCLQKALNHLREIWELIGIPEDQRLQRTQEVVKKHIKELLDMMIAEEESLKERLI
 KSISVCQKELNTLCSELHVEPFOEEGETTILQLEKDLRTQVELMRKQKKERKQELKLLQE
 QDQELCEILCMPHYDIDSASVPSLEELNQFRQHVTTLRETKASRREEFVSIKRQIILCME
 ALDHTPDTSFERDVVCEDEDAFCLSLNIATLQKLLRQLEMQKSQNEAVCEGLRTQIREL
 WDRLOIPEEEREAVATIMSGSKAKVRKALQLEVDRLLEELKMQNMKKVIEAIRVELVQYWD
 QCFYSQEQRQAFAPFCAEDYTESLLQLHDAEIVRLKNYYEVHKELFEGVQKWEETWRLFL
 EFERKASDPNRFNRRGGNLLKEEKQRAKLQKMLPKLEEELKARIELWEQEHSKAFMVNGQ
 KFMEYVAEQWEMHRLEKERAKQERQLKNKKQTETEMLYGSAPRTPSKRRGLAPNTPGKAR
 KLNTTMSNATANSIRPIFGGTVYHSPVSRLPSPSGSKPVAASTCSGKKTPTGRHGANK
 ENLELNGSILSGGYPGSAPLQRNFSINSVASTYSEFAKDPSSLSDSSTVGLQRELSKASKS
 DATSGILNSTNIQS*

Fig. 93

SEQ ID NO: 93

TRLRPVARFEILRGSTARGAATRSDIAGVCGWLLLSGPCGVGLDLDLSRLLGASAMRRSEV
 LAEESIVCLQKALNHLREIWELIGIPEDQRLQRTTEVVKKHIKELLDMMIAEEESLKERLI
 KSISVCQKELNTLCSELHVEPFQEEGETTILQLEKDLRTQVELMRKQKKERKQELKLLQE
 QDQELCEILCMPHYDIDSASVPSLEELNQFRQHVTTLRETKASRREEFVSIKRQIILCME
 ALDHTPDTSFERDVVCEDEDAFCLSLENIATLQKLLRQLEMQKSQNEAVCEGLRTQIREL
 WDRLQIPEEEREAVATIMSGSKAKVRKALQLEVDRLLEELKMQNMKKVIEAIRVELVQYWD
 QCFYSQEQRQAFAPFCAEDYTESLLQLHDAEIVRLKNYYEVHKELFEGVQKWEETWRLFL
 EFERKASDPNRFNTRGGNLLKEEKQRAKLQKMLPKLEEELKARIELWEQEHSKAFMVNGQ
 KFMFYVAEQWEMHRLEKERAKQERQLKNKKQTETEMLYGSAPRTPSKRRGLAPNTPGKAR
 KLN'TTMSNATANS SIRPIFGGTVYHSPVSRLPSPSGSKPVAASTCSGKKTPTTGRHGANK
 ENLELNGSILSGGYPGSAPLQRNFSINSVASTYSEFARELSKASKSDATSGILNSTNIQS
 *

Fig. 94

SEQ ID NO: 94

MTTQLGPALVLGVALCLGCGQPLPQVPERPFSVLWNVPSAHCEARFGVHLPLNALGIIAN
 RGQHFHGNMTIFYKNQLGLYPYFGPRGTAHNGGIPQALPLDRHLALAAYQIHHSLRPGF
 AGPAVLDWEEWCPLWAGNWGRRRAYQAASAWAQQVFFDLDFQEQLYKAYTGFEQAARAL
 MEDTLRVAQALRPHGLWGFYHYFACGNGWHSMASTNYTGRCHAATLARNTQLHWLWAASSA
 LFPSTYLPRLPPAHHQAFVRRHLEEAFRVALVGHRHPLPVLAYVRLTHRRSGRFLSQDD
 LVQSIGVSAALGAAGVVLWGDLSLSSEEECWHLHDYLVDTLGPYVINVTRAAMACSHQR
 CHGHGRCARRDPGQMEAFHLWPDGSLGDWKSFSCHCYWGWAGPTCQEPRPGPKAV*

Fig. 95

SEQ ID NO: 95

MTTQLGPALVLGVALCLGCGQPLPQVPERPFSVLWNVPSAHCEARFGVHLPLNALGIITAN
 RGQHFHGQNMITYKNQLGLYPYFGPRGTAHNGGIPQALPLDRHLALAAYQIHHSRLRPGF
 AGPAVLDWEEWCPLWAGNWRRRAYQAASWAWAQQVFPDLDPQEQLYKAYTGFEQAARAL
 MEDTLRVAQALRPHGLWGFYHYPACGNGWHSNASNYTGRCHAATLARNTQLHWLWAASSA
 LFPSIYLPRLPPAHHQAFVRHRLEEAFRVALVGHRHPLPVLAYVRLTHRRSGRFLSQDD
 LVQSIGVSAALGAAGVVLWGDLSLSSSEEECWHLHDYLVDTLGPYVINVTRAAMACSHQR
 CHGHGRCARRDPGQMEAFHLWPDGSLGDWKSFSCHCYGWAGPTCQEPGLGLKKQYKARA
 PATASSFPCCHFSSPGTTLSHSCSIQFTVNPPKHTPRFPWNP*

Fig. 96

SEQ ID NO: 96

MTTQLGPALVLGVALCLGCGQPLPQVPERPFSVLWNVPSAHCEARFGVHLPLNALGTIAN
RGQHFHGNMTIFYKNQLGLYPYFGPRGTAHNGGIPQALPLDRHLALAAYQIHHSLRPGF
AGPAVLDWEEWCPLWAGNWGRRRAYQAASWAWAQQVFPDLDPQEQLYKAYTGFEQAARAL
MEDTLRVAQALRPHGLWGFYHYPACGNGWHSNASNYTGRCHAATLARNTQLHWLWAASSA
LFPSIYLPRLPPAHHQAFVRHRLEEAFRVALVGHRHPLPVLAYVRLTHRRSGRFLSQEE
CWLHDYLDVDTLGPYVINVTAAACSHQRCHGHGRCARRDPGQMEAFHLWPDGSLGDW
KSFSCHCYWGWAGPTCQEP RP GPKEAV*

Fig. 97

SEQ ID NO: 97

MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAEMGKGSFKYAWVL
 DKLKAERERGITIDISLWKFETSKYYVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGV
 GEFEAGISKNGQTREHALLAYTLGVKQLIVGVNKMDSPEPPYSQKRYEEIVKEVSTYIKK
 IGYNPDTVAFVPISGWNGDNMLEPSANMPWFKGWKVTTRKDNASGTTLEALDCILPPTTR
 PTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTFAPVNVTTTEVKSVEMHHEALS
 EALPGDNVGFVKVKNVSVKDVRNGNVAGDSKNDPPMEAAGFTAQVIILNHFGQISAGYAPV
 LDCHMAHIACKFAELKEIDRRSGKKLEDGPKFLKSGDAIVDMVPGKPMCVESFSDYPP
 LGRFAVRDMRQTVAVGVKAVDKKAAGAGKVTKSAQKAQKAK*

Fig. 98

SEQ ID NO: 98

MALKAEGAALDCFEVTLKCEEGEDEEEAMVVAVIPRPEPMLRVTQQEKTPPPRPSPLEAG
SDGCEEPKQQVSWEQEFVLGSSPGGSGRALCMVCGAEIRAPSADTARSHILEQHPHTLDL
SPSEKSNILEAWSEGVALLDVRAEQSPSPNSDSGQDAHPDPDANPDAARMPAEIVVLLD
SEDNPSLFPKRSRPRGLRPLELPAVPATEPGNKKPRGQRWKEPPGEEPVRKKRGRPMTKNL
DPDPEPPSPDSPTETFAAPAEVRHFTDGSFPAGFVLQLFSHTQLRGPDSKDSPKDREVAE
GGLPRAESPPAPPPGLRGTLDLQVIRVRMEEPPAVSLLQDWSRHPQGTRKRVGAGDTSOW
PTVLSESSTTVAGKPEKGNGV*

Fig. 99

SEQ ID NO: 99

MSTHRSRLLTAAPLSMEQRRPWPRALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSN
 RDWTFNHLTVHQGTGAVYVGAINRVYKLTGNLTIQVAHKTGPEEDNKSCYPPLIVQPCSE
 VLTLTNNVNKLLIIDYSENRLACGSLYQGVCCKLLRLDDLFI LVEPSHKKEHYLSSVNKT
 GTMYGVIVRSEGEDGKLFIGTAVDGKQDYFFTLSSRKLPRDPRESSAMLDYELHSDFVSSL
 IKIPSDTLALVSHFDIFYIYGFASSGGFVYFLTVQPETPEGVAINSAAGDLFYTSRIVRLCK
 DDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSLAAQAFNITSQDDVLFALFSKGQKQ
 YHHPDDSAALCAFPPIRAINLQIKERLQSCYQGEGLNLLNWLKGKDVQCTKAPVPIDDNFC
 GLDINQPLGGSTPVEGLTYTTSRDRMTSVASYVYNGYSVVVFGTKSGKLLKIRADGPPH
 GGVQYEMVSVLKDGSPILRDMAFSIDQRYLYVMSEKQVTRVPVESCEQYTTTCGECLSSGD
 PHCGWCALHNMCSRDKCQQAWEPNRFASISQCVSLAVHFPSSISVSEHSRLLSLVVSDA
 PDLASAGIACAFGNLTEVEGQVSGSQVICISPGPKDVPVIPLDQDWFGLELQLRSKETGKI
 FVSTEFKFYNCSAHQLCLSCVNSAFRCHWKYRNLC THDPTTCSFQEGRINISED CPQLV
 PTEEILIPVGEVKPITLKARNLPQPQSGQRGYECVLNIQGAHRVPALRFNSSSVQCQNS
 SYQYDGMDISNLAVDFAVVWNGNFIIDNPQDLKVHLYKCAAQRESCGLCLKADRKFECGW
 CSGERRCTLHQHCTSPSSPWLWSSHNVKCSNPQITEILTVSGPPEGGTRVTIHGVNLGL
 DFSEIAHHVQVAGVPCTPLPGEYIIAEQIVCEMHALVGTTSGPVRLCIGECKPEFMTKS
 HQQYTFVNPSVLSLNPGRGPESSGTMVTITGHYLGAGSSVAVYLGNOTCEFYGRSMSEIV
 CVSPSSNGLGPVPVSVSVDRHVDSNLQFEYIDDPVQRIEPEWSIASGHTPLTITGFN
 LDVIQEPRIRVKFNGKESVNVCKVNTTTLTCLAPSLTIDYRPGLDTERPDEFGFVFN
 VQSLLIYNDTKFIYYPNPTFELLSPTGVLDQKPGSPIILKGKNLCPASGGAKLNYTVLI
 GETPCAVTVSETQLLCEPPNLTGQHKVMVHVGGMVFSFGSVSVISDLSLLTPAIVSIAAG
 GSLLLIIVIIIVLIAYKRKSRENDLTLKRLQMQMDNLESRALECKEAFELQTDINELTS
 DLDRSGIPYLDYRTYAMRVLPFGIEDHPVLRLELVQNGQGHVEKALKLFAQLINNKVFL
 LTFIRTLQLRSFMSRDRGNVASLIMTGLQGRLEYATDVLKQLLSDLDKNLENKNHPKL
 LLRRTESVAEKMLTNWFAFLHKLKECAGEPLFMYCAIKQMEKGPIDAITGEARYSL
 SEDKLIRQQIEYKTLILNCVNPDNENSPEIPVKVLNCDTITQVKEKILDAVYKNVPYSQR
 PRAVDMDLEWRQGRIARVVLQDEDITTKIEGDWKRLNTLMHYQVSDRSVVALVPKQTSSY
 NIPASASISRTSISRYDSSFRYTGPSDSLRSRAPMITPDLESGVKVWHLVKNHHDGQKE
 GDRGSKMVSEIYLTRLLATKGT LQKFVDDL FETLFSTVHRGSALPLAIKYMFDLDEQAD
 RSHIHDTDVRHTWKSNCPLRFWVNVKPNQFVFDIHKGSITDACLSVVAQT FMDSCSTS
 EHR LGKDSPSNKLKYAKDIPSYKSWVERYADI AKLPAISDQDMNAYLAEQSRLHAVEFN
 MLSALNEIYSYVSKYSEELIGALEQDEQARRQRLAYKVEQLINAMSIES*

Fig. 100

SEQ ID NO: 100

MEQRRPWPRALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSENROWTFNHLTVHQGTG
 AVYVGAINRVYKLTGNLTIQVAHKTGPEEDNKSCYPPLIVQPCSEVLTLTNNVNKLLIID
 YSENRLACGSLYQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDG
 KLFITAVDVGKQDYFPTLSSRKLPRDPRESSAMLDYELHSDVSSLIKIPSDTLALVSHFD
 IFYIYGFASSGGFVYFLTVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGC
 TRAGVEYRLLQAAYLAKPGDSLAAQAFNITSQDDVLFAlFSKGQKQYHHPPDDSA LCAFPPI
 RAINLQIKERLQSCYQGEENLELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVE
 GLTLYTTSRDRMTSVASYVYNGYSVVVFVGTKSGKLLKIRADGPPHGGVQYEMVSVLKDGS
 PILRDMAFSIDQRYLYVMSEKQVTRVPVESCEQYTTCEGLSSGDPHCGWALHNMCSRR
 DKCQQAWEPNRFAASISQCVSLAVHPSSISVSEHSRLSLVSDAPDLSAGIACAFGNLT
 EVEGQVSGSQVICISPGPKDVPVIPLDQDWFGLQLRSKETGKIFVSTEFKFNCSAHQ
 LCLSCVNSAFRCHWKYRNLCTHDPTTCSFQEGRINISEDQPLVPTTEEILIPVGEVKPI
 TLKARNLPQPQSGQRGYECVLNIQGAHRVPALRFNSSSVQCNSSYQYDGMDISNLAVD
 FAVVWNGNFIIDNPQDLKVHLYKCAAQRESCGLCLKADRKFECGWCSGERRCTLHQHCTS
 PSSPWLWSSHNVKCSNPQITEILT VSGPPEGGTRVTIHGVNLGLDFSEIAHHVQVAGVP
 CTPLPGEYIIAEQIVCEMHALVGTTSGPVRLCIGECKPEFMTKSHQYTFVNPSVLSLN
 PIRGPESGGTMVTITGHYLGAGSSVAVYLGNTCEFYGRSMSEIVCVSPSSNGLGPVPV
 SVSVDRAHVDSNLQFEYIDDPVQRIEPEWSIASGHTPLTITGFNL DVIQEPRI RVKFNG
 KESVNVCKVNTTTLTCLAPSLT TDYRPGLDTVERPDEFGEFVFN NVQSLLIYNDTKFIYY
 PNPTFELLSP TGVL DQKPGSPIILKGKNLCPASGGAKLNYTVLIGETPCAVTVSETQLL
 CEPFNL TGQHKVMVHVGGMVFS PGSVSVISDSILTLPAIVSTAAGGSLLLIITVIVLIA Y
 KRKSRENDLT LKRLQM QMDNLES RVALECKEAFELQTDINELTSD LDRSGIPYLDYRTY
 AMRVLFPGIEDHPVLRELEVQNGQOHVEKALKLFAQLINNKVFLLT FIRTLELQRSFSM
 RDRGNVASLIMTGLQGRLEYATDVLKQLLSD LIDKNLENKNHPKLLLRRTESVAEKMLTN
 WFAFL LHKFLKECAGEPLFMYCAIKQQMEKGPIDAITGEARYSLSEDK LIRQQIEYKTL
 ILNCVNP DNENSPEIPVKVLNCDTITQVKEKILDAVYKNVPYSQRPRAVDMDLEWRQGRI
 ARVVLQDE DITTKIEGDWKRLNTLMHYQVSDRSVVALVPKQTSSYNI PASASISRTSISR
 YDSSFRYTGSPDSLRSRAPMITPDLESGVKVWHLVKNHDHGDQKEGDRGSKMVSEIYLTR
 LLATKGTLQKFVDDL FETLFSTVHRGSALPLAIKYMFDLDEQADRHSIHDTDVRHTWKS
 NCLPLRFWVNVIKNPQFVFDIHKGSITDACL SVVAQT FMDSCSTSEHRLGKDSPSNKLLY
 AKDIPSYKSWVERYYADIAKLPAISDQDMNAYLAEQSRLH AVEFNMLSALNEIYSYVSKY
 SEELIGALEQDEQARRQRLAYKVEQLINAMSIES*

Fig. 101

SEQ ID NO: 101

MPPPSDIVKVAIEWPGANAQLLEIDQKRPLASIIKEVCDGWSLPNPEYYTLRYADGPQLY
 ITEQTRSDIKNGTILQLAISPSRAARQLMERTQSSNMETRLDAMKELAKLSADVTFATEF
 INMDGIIIVLTRLVESGTKLLSHYSEMLAFTLTAFLELMDHGIVSWDMVSITFIKQIAGYV
 SQPMVDVSILQRSLAILESMVLNSQSLYQKIAEEITVGQLISHLQVSNQEIQTYAIALIN
 ALFLKAPEDKRQDMANAFQAQHLRSIILNHVIRGNRPKTEMAHOLYVLOVLTFFNLLEER
 MMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTEKRAKAMYTKDYKMLGFTNHINP
 AMDFTQTTPGMLALDNMLYLAKVHQDTYIRIVLENSREDKHECPFGRSAIELTKMLCEI
 LQVGELPNEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFNKVMQVVREQ
 ITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSERMSQDDFQSPPIVELREKIQPEILEL
 IKQORLNRLCEGSSFRKIGNRRRQERFWYCRALNHNKVLHYGDLDDNPQGEVTFESLQEK
 IPVADIKAIVTGKDCPHMKEKSALKQNKVELELAFSILYDPDETLENIAPNKYEYCIWID
 GLSALLGKDMSELTKSDLDTLSEMEMKLRLLDLENIQIPEAPPPPIKPESSYDFVYHYG
 *

Fig. 102

SEQ ID NO: 102

MPPPSDIVKVAIEWPGANAQLLEIDQKRPLASIIKEVCDGWSLPNPEYYTLRYADGPQLY
 ITEQTRSDIKNGTILQLAISPSRAARQLMERTQSSNMETRLDAMKELAKLSADVTFATEF
 INMDGIIVLTRLVESGTKLLSHYSEMLAFTLTAFLELMDHGIVSWDMVSITFIKQIAGYV
 SQPMVDVSILQRSLAILESMVLNSQSLYQKIAEEITVGQLISHLQVSNQEIQTYAIALIN
 ALFLKAPEDKRQDMANAFQKHLRSIILNHVIRGNRPKITEMAHQLYVLQVLTFTNLEER
 MMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTEKRKAMYTKDYKMLGFTNHINP
 AMDFTQTTPGMLALDNMLYLAKVHQDTYIRIVLENSREDKHECPFGRSAIELTKMLCEI
 LQVGELPNEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFNKVMQVVREQ
 ITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSERMSQDDFQSPPIVELREKIQPEILEL
 IKQQRNLNRLCEGSSFRKIGNRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEK
 IPVADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLENFAPNKYEYCIWID
 GLSALLGKDMSSSELTKSOLDTLTLLSMEMKLRLLOLENIQIPEAPPPIPKEPSSYDFVYHYG
 *

Fig. 103**SEQ ID NO: 103**

MPPPSDIVKVAIEWPGANAQLLEIDQKRPLASIIKEVCDGWSLPNPEYYTLRYADGPQLY
 ITEQTRSDIKNGTILQLAISPSRAARQLMERTQSSNMETRLDAMKELAKLSADVTFATEF
 INMDGIIVLTRLVESGTKLLSHEMLAFTLTAFLELMDHGIVSWDMVSITFIKQIAGYVSQ
 PMVDVSILQRSLAILESMVLNSQSILYQKIAEEITVGQLISHLQVSNQEIQTYAIALINAL
 FLKAPEDKRQDMANAFQKHLRSIILNHVIRGNRPKITEMAHQLYVLQVLTFTNLEERMM
 TKMDPNDQAQRDII FELRRIAFDAESDPSNAPGSGTEKRKAMYTKDYKMLGFTNHINPAM
 DFTQTTPPGMLALDNMLYLAKVHQDTYIRIVLENSREDKHECPFGRSAIELTKMLCEILQ
 VGELPNEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFNKVMQVVREQIT
 RALPSKPNSLDQFKSKLRSLSYSEILRLRQSERMSQDDFQSPPIVELREKIQPEILELIK
 QQRLNRLCEGSSFRKIGNRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIP
 VADIKAIVTGKDCPHMKEKSALKQNKVLELAFSILYDPDETNLNFIAPNKYEYCIWIDGL
 SALLGKDMSSSELTKSOLDTLLSMEMKLRLLDLENIQIPEAPPPIPKPESSSYDFVYHYG*

Fig. 104

SEQ ID NO: 104

MERTQSSNMETRLDAMKELAKLSADVTFATEFINMDGIIIVLTRLVESGTKLLSHYSEMLA
 FTLTAFLELMDHGIVSWDMVSITFIKQIAGYVSQPMVDVSILQSLAILESMVLNSQSLY
 QKIAEEITVGQLISHLQVSNQEIQTYAIALINALFLKAPEDKRQDMANAFQAQKHLRSIIL
 NHVIRGNRPKITEMAHQLYVLQVLTFTNLEERMMTKMDPNDQAQORDIIFELRRIAFDAES
 DPSNAPGSGTEKRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKVHQDTY
 IRIVLENSREDKHECPFGRSAIELTKMLCEILQVGELPNEGRNDYHPMFFTHDRAFEEL
 FGICIQLLNKTWKEMRATAEDFNKVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEIL
 RLRQSERMSQDDFQSPPIVELREKIQPEILELIKQQRNLRLCEGSSFRKIGNRRRQERFW
 YCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPVADIKAIVTGKDCPHMKEKSALKQNK
 EVLELAFSILYDPDETLENFAPNKYEYCIWIDGLSALLGKDMSSSELTKSOLDTLLSMEMK
 LRLLDLENIQIPEAPPPPIKPESSSYDFVYHYG*

Fig. 105

SEQ ID NO: 105

MAALRALCGFRGVAAQVLRPGAGVRLPIQPSRGVRQWQPDVEWAQQFGGAVMYPSEKTAH
WKPPPWNVDVPPKDTIVKNITLNFGPQHAAHGVLRRLVMELSGEMVRKCDEPHIGLLHRGT
EKLIEYKTYLQALPYFDRLDYVSMMCNEQAYSLAVEKLLNIRPPPPRAQWIRVLFGEITRL
LNHIMAVTTHALDLGAMTPFFWLFEEREKMFIFYERVSGARMHAAYIRPGGVHQDLPLGL
MDDIYQFSKNFSLRLDELEELLTNNRIWRNRTIDIGVVTAEALNYGFSGVMLRGSGIQW
DLRKTQPYDVYDQVEFDVPVGSRGDCYDRYLCRVEEMRQSLRIIAQCLNKMPPGEIKVDD
AKVSPPKRAEMKTSMESLIHHFKLYTEGYQVPPGATYTAIEAPKGEFGVYLVSDGSSRPY
RCKIKAPGFAHLAGLDKMSKGHMLADVVAIIGTQDIVFGEVDR*

Fig. 106

SEQ ID NO: 106

MAALRALCGFRGVAAQVLRPGAGVRLPIQPSRGVRQWQPDVEWAQQFGGAVMYPSETAH
WKPPFWNDVDPPKDTIVKNITLNEGPHQHPAAHGVRLRLVMEISGEMVRKCDPHIGLLHRGT
EKLIEYKTYLQALPYFDRLDYVSMMCNEQAYSLAVEKLLNIRPPRAQWIRVLFGEITRL
LNHIMAVTTHALDLGAMTPFFWLFEEREKMFEEYERVSARMHAAYIRPGGVHQDLPLGL
MDDIYQFSKNFSLRLDELEELLTNNRIWRNRITDIGVVTAEALNYGFGVMLRGSGIQW
DLRKTQPYDVYDQVEFDVPVGSRGDCYDRYLCRVEEMRQSLRIIAQCLNKMPPEIKVDD
AKVSPPKRAEMKTSMESLIHFFKLYTEGYQVPPGATYTAIEAPKGEFGVYLVSDGSSRPY
RCKIKAPGFAHLAGLDKMSKGHMLADVVAIIIGTQDIVFGEVDR*

Fig. 107

SEQ ID NO: 107

MAGGPGGEPAAFGAQHFLYEVFPWVMCRFYKVMDALEPADWCQFGGWRRRAAGGREARGL
 LAPTPDAPRPAAALIVRDQTELRLCERSGORTASVLWPWINRNARVADLVHILTHLQLLR
 ARDIITAWHPPAPLPSPGTTAPRPSSIPAPAEAEAWSPRKLPSASTFLSPAFFPGSQTHS
 GPGLGLVPSPASLWPPPPSPAPSSSTKPGPESSVSLQGARFPFCWPLCEISRGTNHFSE
 ELKIGEGGGFCVYRAVMRNTVYAVKRLKENADLEWTAVKQSFLTEVEQLSRFRHPNIVDF
 AGYCAQNGFYCLVYGFLPNGSLEDRLHCQTQACPPLSWPQRLDILLGTARAIQFLHQDSP
 SLIHGDIKSSNVLLDERLTPKLGDFGLARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEE
 YIKTGRLAVDQDTFSFGVVVLETLAQRAVKTHGARTKYLKDLVEEEAEEAGVALRSTQS
 TLQAGLAADAWAAPIAMQIYKKHLGQLACCCLHRRAKRRPPMTQENSYVSSTGRAHSGAA
 PWQPLAAPSGASQAQAEQLQRGPNQPVESDES LGGLSAAALRSWHLTPSCPLDPAPLREAG
 CPQGD TAGESSWGS GPGSRPTAVEGLALGSSASSSSSEPPQIIINPARQKMQKLALYEDG
 ALDSLQLLSSSSLPGLGLEQDRQGPEESDEFQS*

Fig. 108

SEQ ID NO: 108

MAGGPGPGEPAAPGAQHFLYEVPWVMCRFYKVMDALEPADWCQFAALIVRDQTELRRLCE
 RSGQRTASVLWPWINRNARVADLVHILTHLQLLRARDIITAWHPPAPLPSPGTTAPRPSS
 IPAPAEAEAWSPRKLPSASTFLSPAFFPGSQTHSGPELGLVPSPASLWPPPPSPAPSSTK
 PGPSSSVSLQGARPPFCWPLCEISRGTNHFSEELKIGEGGFGCVYRAVMRNTVYAVKR
 LKENADLEWTAVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL
 HCQTQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERLTPKLGDFG
 LARFSRFAGSSPSQSSMVARTQTVRGFLAYLPEEYIKTGRLAVDQDTFSFGVVVLETLG
 QRAVKTHGARTKYLKDLVEEEAEEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLD
 RFGPCPELGLGLGQLACCCCLHRRARRPPMTQVYERLEKLQAVVAGVPGHSEAASCIPP
 SPQENSYVSSSTGRAHSGAAPWQPLAAPSGASAAEQLRGPNQPVESDES LGGLSAAALR
 SWHLTFSCPLDPAPLREAGCPQGD TAGESSWGSGPSRPTAVEGLALGSSASSSSEPPQI
 IINPARQKMQKLALYEDGALDSLQLLSSSSLPGLGLEQDRQGPEESDEFQS*

Fig. 109

SEQ ID NO: 109

MAGGPGPGEPAAPGAQHFLYEVPWPVMCRFYKVMDALEPADWCQFAALIVRDQTELRLCE
 RSGQRTASVLWPWINRNARVADLVHILTHLQLLRARDIITAWHPPAPLPSPGTTAPRPSS
 IPAPAEAEAWSFRKLPSSASTFLSPAFFPGSQTHSGPELGLVPSPASLWPPPPSPAPSSTK
 PGPESVSLLQGARPPFFCWPLCEISRGTNHFSEELKIGEGGFGCVYRAVMRNTVYAVKR
 LKENADLEWTAVKQSFLEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL
 HCQTQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERLTPKLGDFG
 LARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEEYIKTGRLAVD TD TFSFGVVVLETLAG
 QRAVKTHGARTKYLKDLVEEEAEEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDP
 RPGPCPPELGLGLGQLACCCLHRRAKRRPMTQENSYVSSTGRAHSGAAPWQPLAAPSGA
 SAQAAEQLRGPNQPVESDES LGGLSAALRSWHLTPSCPLDPAPLREAGCPQGD TAGESS
 WSGPGSRPTAVEGLALGSSASSSSSEPPQIIINPARQKMVQKLALYEDGALDSLQLLSSS
 SLPGLGLEQDRQGPEESDEFQS*

Fig. 110

SEQ ID NO: 110

MAGGPGGEPAAFGAQHFLYEVPPWVMCRFYKVMDALEPADWCQFAALIVRDQTELRRLCE
 RSGQRTASVLWPWINRNARVADLVHILTHLQLLRARDIITAWHPPAPLPSPGTTAPRPSS
 IPAPAEAEAWSPRKLPSSASTFLSPAFFPGSQTHSGPELGLVPSPASLWPPPPSPAPSSTK
 PGPESVSLLQGARPFFFCWPLCEISRGTNHFSEELKIGEGGFGCVYRAVMRNTVYAVKR
 LKENADLEWTAVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL
 HCQTQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERLTPKLGDFG
 LARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEEYIKTGRLAVD TDTFSFGVVVLETLAG
 QRAVKTHGARTKYL VYERLEKLQAVVAGVEGHSEAASCI PPSPQENS YVSSTGRAHSGAA
 PWQFLAAPSGASQAQAEQLQRGPNQPVESDES LGGLSAA LRSWHLTPSCPLDPAPLREAG
 CPQGD TAGESSWGSGPGSRPTAVEGLALGSSASSSSEPPQII INPARQKMVQKLALYEDG
 ALDSLQLLSSSSLPGLGLEQDRQGPEESDEFQS*

Fig. 111

SEQ ID NO: 111

MAGGPGPGEPAAPGAQHFLYEVPWVMCRFYKVMDALEPADWCQFGGWRRRAAGGREARGL
 LAPTPDAPRPAAALIVRDQTELRRCERSGQRTASVLWFWINRNARVADLVHILTHLQLLR
 ARDIITAWHPPAPLPSPGTTAPRPSSIIPAPAEAEAWSPRKLPSSASTFLSPAFFGSQTHS
 GPGLGLVPSPASLWPPPPSPAPSSTKPGPESSVSLQGARPPFCWPLCEISRGTNHFSE
 ELKIGEGGFGCVYRAVMRNTVYAVKRLKENADLEWTAVKQSFLTEVEQLSRFRHPNIVDF
 AGYCAQNGFYCLVYGFLPNGSLEDRLHCQTQACPPLSWPQRLDILLGTARAIQFLHQDSP
 SLIHGDIKSSNVLLDERLTPKLGDFGLARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEE
 YIKTGRLAVDITDTFSFGVVVLETLAQRAVKTHGARTKYLKDLVEEEAEEAGVALRSTQS
 TLQAGLAADAWAAPIAMQIYKKHLDFRPGPCPPELGLGLGQLACCCLHRRAKRRPPMTQE
 NSYVSSTGRAHSGAAPWQFLAAPSGASQAQAEQLQRGPNQPVESDES LGGLSAALRSWHL
 TPSCPLDPAPLREAGCPQGD TAGESSWGSGPGSRPTAVEGLALGSSASSSSEPPQIINP
 ARQKMVQKLALYEDGALDSLQLLSSSSLPGLGLEQDRQGPEESDEFQS*

Fig. 112

SEQ ID NO: 112

MAAIPSSGSLVATHDYRRRLGSTSSNSSCSSTECPGAIPHPPGECRIAPFSRSSRSW
QHQPPTSLLSGLPKADPGHWWASFFFGKSTLPFMATVLESAEHSEPPQASSSMTACGLAR
DAPRKQPGGQSSTASAGPPS*

Fig. 113

SEQ ID NO: 113

**MAAIPSSGSLVATHDYRRRLGSTSSNSSCSSTECPGAIPHPGLPKADPGHWWASFFF
GKSTLPPPTL***

Fig. 114

SEQ ID NO: 114

MAAIPSSGSLVATHDYRRRLGSTSSNSSCSSTECPEALPHPPGLPKADPGHWWASEFF
GKSTLFFMATVLESAEHSEPPQASSSMTACGLARDAPRKQPGGQSSTASAGPPS*

Fig. 115

SEQ ID NO: 115

MEDGVYEPPDLTPEERMELNIRRRKQELLVEIQRLREELSEAMSEVEGLEANEKSKTLQ
RNRKMAMGRKKFNMDPKKGIQFLVENELLQNTPEEIARFLYKGEGLNKTAIGDYLGEREE
LNLAVLHAFVDLHEFTDLNLVQALRQFLWSFRLPGEAQKIDRMMEAFQRYCLCNPGVFQ
STDTCYVLSFAVIMLNTSLHNPVNRDKPGLERFVAMNRGINEGGDLPEELLRNLYDSIRN
EPFKIPEDDGNDLTHHTFFNPDRGWLLKLGRGRVKTWKRRWFILTDNCLYYFEYTTDKEP
RGIIPLENLSIREVDDPRKPNCFELYIPNNKGQLIKACKTEADGRVVEGNHVMYRISAPT
QEEKDEWIKSIQAAVSVDPFYEMLAARKKRISVKKKQEQP*

Fig. 116

SEQ ID NO: 116

MEDGVYEPPDLTPEERMELNIRRRKQELLVEIQRLREELSEAMSEVEGLEANEKSKTLQ
RNRKMAMGRKKFNMDPKKGIQFLVENELLQNTPEEIARFLYKGEGLNKTAIGDYLGEREE
LNLAVLHAFVDLHEFTDLNLVQALRQFLWSFRLPGEAQKIDRMMEAFQRYCLCNPGVFQ
STDTCYVLSFAVIMLNTSLHNPNVRDKPGLERFVAMNRGINEGGDLPEELLRNLYDSIRN
EPFKIPEDDGNDLTHHTFFNPDRGWLLKLGGRVKTKRRWFILTDNCLYYFEYTTDKPR
GIIPLENLSIREVDDPRKPNCFELYIPNNKGQLIKACKTEADGRVVEGNHVMYRISAPTQ
EEKDEWIKSIQAASVDPFYEMLAARKKRISVKKKQEQP*

Fig. 117

SEQ ID NO: 117

MVNPTVFFDIAVDGEPLGRVSFELFADKVPKTAENFRALSTGEKGFYKGS CFHRIIPGF
MCQGGDFTRHNGTGKSIYGEKFEDENFILKHTGPGILSMANAGPNTNGSQFFICTAKTE
WLDGKHVVFGKVKEGMNIVEAMERFGSRNGKTSKKIT IADCGQLE*

Fig. 118

SEQ ID NO: 118

TAESEASSEACAGPATRSPGWGDPGISHRDCCRRKAEWGTAESR*

Fig. 119

SEQ ID NO: 119

**EAELPDRGGAAVQVSSPKHCGLCWLLCSERLLLPGVRLPAQRLPGGSPPLPDPGLPTSLL
ASATGHPSGYSPGNSVSTSGQPQPHPWRHQEFQRPSG***

Fig. 120

SEQ ID NO: 120

LRGLAPPSPPVIVRRGPRGVAAQIPPASKLKHGGHPLQRLARGHPRLLPAPPGFHFQQQ
LLQQYRVPRGSHSPPPRSPQG*

Fig. 121

SEQ ID NO: 121

APWPSAPVPATRDRAPRPARGRRPDFTSQQAKAWRPSPPAARSWPPTTTTGAAWVLPAT
APAAVPSAPGKPFPTPQVSPRLTRVIGGPASFSGSPPSRSWPRCWSPQSTRNLPRPPAA*

Fig. 122

SEQ ID NO: 122

WTCSPHPTPTTRRSTTSRSASWSARCAST*