(19) OFICINA ESPAÑOLA DE
PATENTES Y MARCAS

ESPAÑA

(11) Número de publicación: **2 360 746**

(15) Folleto corregido: T3

Texto afectado: Descripción

(48) Fecha de publicación de la corrección: 13.02.2012

(51) Int. Cl.:

C12N 15/62 (2006.01)

C07K 14/22 (2006.01)

C07K 19/00 (2006.01)

(12) TRADUCCIÓN DE PATENTE EUROPEA CORREGIDA T9

(96) Número de solicitud europea: **08075111 .8**

(96) Fecha de presentación : **28.02.2001**

(97) Número de publicación de la solicitud: **1947187**

(97) Fecha de publicación de la solicitud: **23.07.2008**

---

(54) Título: **Expresión híbrida de proteínas e *Neisseriales*.**

---

(30) Prioridad: **28.02.2000 GB 0004695**
13.11.2000 GB 0027675

(45) Fecha de publicación de la mención BOPI:
08.06.2011

(45) Fecha de la publicación del folleto de la patente:
08.06.2011

(73) Titular/es:
NOVARTIS VACCINES AND DIAGNOSTICS S.R.L.
Via Fiorentina 1
53100 Siena, SI, IT

(72) Inventor/es: **Arico, Maria Beatrice;**
Comanducci, Maurizio;
Galeotti, Cesira;
Masignani, Vega;
Giuliani, Marzia Monica y
Pizza, Mariagrazia

(74) Agente: **Carpintero López, Mario**

Aviso: En el plazo de nueve meses a contar desde la fecha de publicación en el Boletín europeo de patentes, de la mención de concesión de la patente europea, cualquier persona podrá oponerse ante la Oficina Europea de Patentes a la patente concedida. La oposición deberá formularse por escrito y estar motivada; sólo se considerará como formulada una vez que se haya realizado el pago de la tasa de oposición (art. 99.1 del Convenio sobre concesión de Patentes Europeas).

DESCRIPCIÓN

Expresión híbrida de proteínas neisseriales

Campo técnico

La presente invención pertenece al campo de la expresión de proteínas. En particular, se refiere a la expresión heteróloga de proteínas de *Neisseria* (por ejemplo, *N. gonorrhoeae* o, preferiblemente, *N. meningitidis*).

Técnica antecedente

Las solicitudes de patente internacional WO99/24578, WO99/35544, WO99/57280 y WO00/22430 divulgan proteínas de *Neisseria meningitidis* y *Neisseria gonorrhoeae*. Estas proteínas se describen, de forma típica, expresadas en *E. coli* (es decir, una expresión heteróloga) como fusiones con GST N-terminales o como fusiones con marcador de His C-terminales, aunque también se describen otros sistemas de expresión, incluyendo la expresión en *Neisseria* nativa.

Guillen et al., Biotecnología aplicada, 1996, vol. 13, nº 4, págs. 271-275 divulga una proteína de fusión de la proteína P.1.15 de *Neisseria* con la proteína P64-K de *Neisseria*, y su expresión en E. coli.

Un objeto de la presente invención es proporcionar estrategias alternativas y mejoradas para la expresión heteróloga de estas proteínas. Estas estrategias afectan, de modo típico, al nivel de expresión, la facilidad de purificación, la localización celular de la expresión y/o las propiedades inmunológicas de la proteína expresada.

Divulgación de la invención

Según la invención, se expresan dos proteínas de la invención como una única proteína híbrida. Se prefiere no utilizar un compañero de fusión que no provenga de *Neisseria* (por ejemplo, GST o poli-His).

Esto ofrece dos ventajas. En primer lugar, una proteína que puede ser inestable, o que se expresa poco por sí sola, puede mejorarse añadiendo un compañero de hibridación adecuado que solucione el problema. En segundo lugar, se simplifica la fabricación comercial, ya que sólo es necesario emplear una expresión y purificación para producir dos proteínas útiles por separado.

Así, la invención proporciona un procedimiento para la expresión heteróloga simultánea de dos proteínas de la invención, en el que dichas dos o más proteínas de la invención están fusionadas (es decir, se traducen como una sóla cadena polipeptídica).

El procedimiento incluirá de forma típica las etapas de obtener un primer ácido nucleico que codifique una primera proteína de la invención; obtener un segundo ácido nucleico que codifique una segunda proteína de la invención; ligar el primer y el segundo ácido nucleico. El ácido nucleico resultante puede insertarse en un vector de expresión, o puede ser ya parte de un vector de expresión.

La proteína híbrida puede representarse con la fórmula NH_2-A-B-COOH. A comprende la proteína 287 y B comprende la proteína 961.

287 es su forma ΔG-287 con deleciones de poliglicina (ΔG).

La proteína híbrida de la invención es ΔG287-961.

287 se usa en el extremo N-terminal como una forma ΔG de 287, como el extremo N-terminal de un híbrido con 961.

287 es preferentemente de la cepa 1996 o de la cepa 394/98. Pueden usarse las formas de dominios de 961.

Las alineaciones de formas polimórficas de ORF46, 287, 919 y 953 se divulgan en el documento WO00/66741. Cualquiera de estos polimorfos puede usarse de acuerdo con la presente invención.

Preferentemente, las proteínas constituyentes (A y B) e una proteína híbrida de acuerdo con la invención vendrán de la misma cepa.

Las proteínas fusionadas en el híbrido están unidas directamente.

Las proteínas fusionadas pueden carecer de los péptidos conductores nativos, o pueden incluir la secuencia peptídica conductora del compañero de fusión N-terminal

Huésped

Se prefiere utilizar un huésped heterólogo. El huésped heterólogo puede ser procariota o eucariota. Preferiblemente es *E. coli*, pero otros huéspedes adecuados incluyen *Bacillus subtilis, Vibrio cholerae, Salmonella typhi, Salmonella typhimurium, Neisseria meningitidis, Neisseria gonorrhoeae, Neisseria lactamica, Neisseria cinerea, Mycobacteria* (por ejemplo, *M. tuberculosis*), levaduras, etc.

Secuencias

La invención también proporciona una proteína que comprende las secuencias de la secuencia SEQ ID NO 8.

El grado de "identidad de secuencia" es preferiblemente mayor que 70%. Esto incluye mutantes y variantes alélicas [por ejemplo, véase el documento WO00/66741]. La identidad se determina preferiblemente mediante el algoritmo de búsqueda de homología de Smith-Waterman, ejecutado en el programa MPSRCH (Oxford Molecular), empleando una búsqueda de huecos afines con los parámetros *penalización de hueco abierto = 12* y *penalización de extensión de hueco = 1*.

Las proteínas de la invención preferidas se encuentran en el serogrupo B de *N. meningitidis*.

Las proteínas de la invención preferidas son las del serogrupo B de la cepa 2996 o de la cepa 394/98 (una cepa de Nueva Zelanda) . A menos que se indique lo contrario, las proteínas mencionadas en la presente proceden de la cepa 2996 de *N. meningitidis*. Sin embargo, se apreciará que la invención no está limitada, en general, por la cepa. Puede considerarse que las referencias a una proteína concreta (por ejemplo, “287”, “919”, etc.) incluyen esa proteína de cualquier cepa.

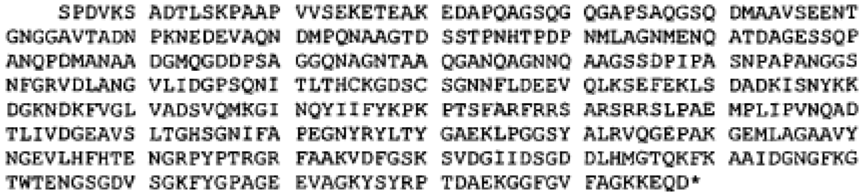
Breve descripción de los dibujos

Las figuras 1 y 2 muestran las proteínas híbridas de acuerdo con la invención.

Modos de realizar la invención

Ejemplo 1 - Híbridos de ΔG287

Se descubrió que la deleción de la secuencia $(Gly)_6$ en 287 tiene un profundo efecto sobre la expresión proteica. La proteína que carece de los aminoácidos N-terminales hasta GGGGGG se denomina "ΔG287". En la cepa MC58, su secuencia básica (el péptido conductor está subrayado) es:

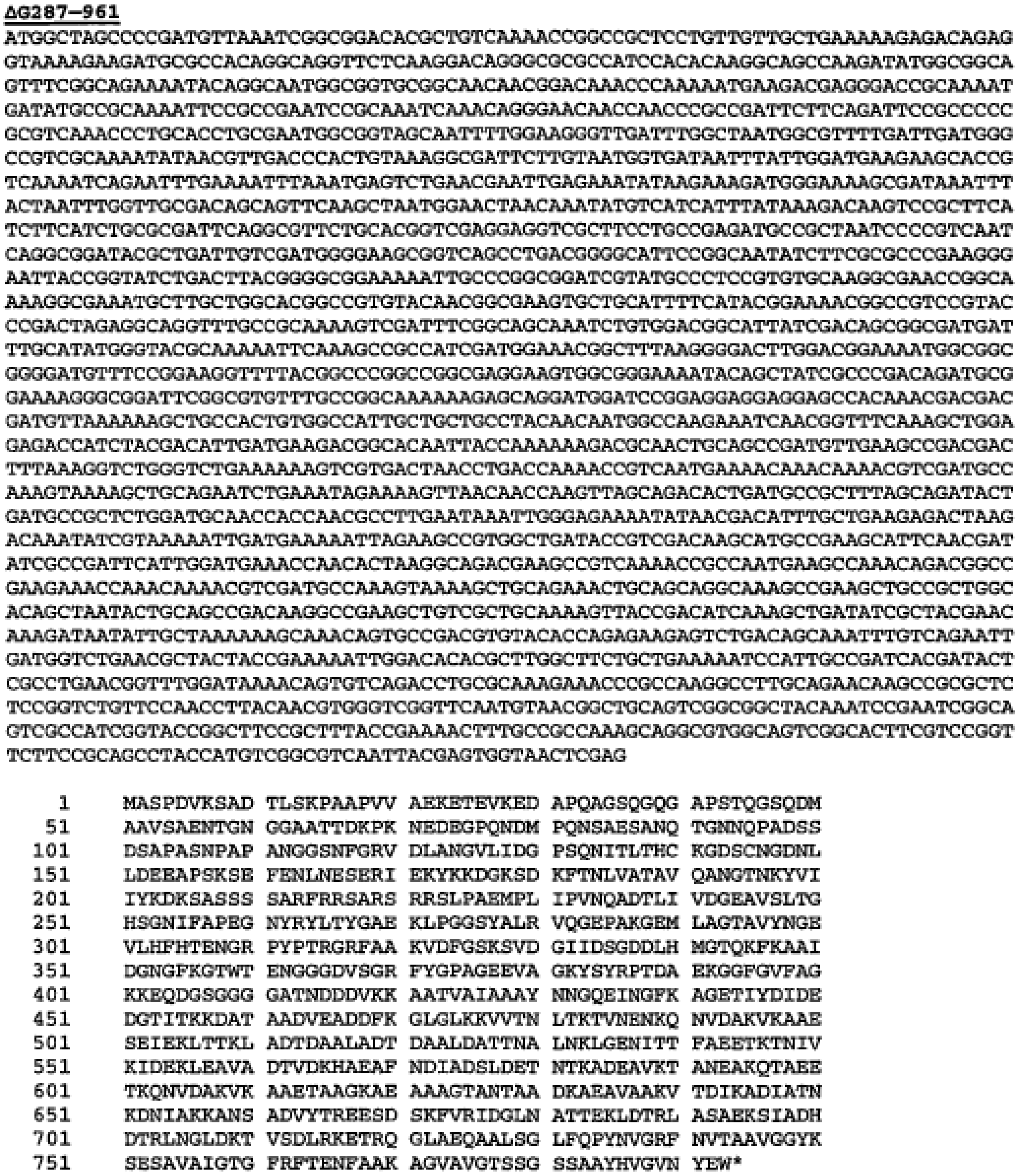


```
     SPDVKS ADTLSKPAAP VVSEKETEAK EDAPQAGSQG QGAPSAQGSQ DMAAVSEENT
GNGGAVTADN PKNEDEVAQN DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP
ANQPDMANAA DGMQGDDPSA GGQNAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
NFGRVDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS DADKISNYKK
DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRRS ARSRRSLPAE MPLIPVNQAD
TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY
NGEVLHFHTE NGRPYPTRGR FAAKVDFGSK SVDGIIDSGD DLHMGTQKFK AAIDGNGFKG
TWTENGSGDV SGKFYGPAGE EVAGKYSYRP TDAEKGGFGV FAGKKEQD*
```

La ΔG287, con o sin un marcador de His ("ΔG287-His" y "ΔG287K", respectivamente) se expresa a niveles muy buenos, comparada con "287-His" o "$287^{\text{sin marcar}}$".

Basándose en los datos de variabilidad genética, se expresaron variantes de Δ-G287-His en *E. coli* de una serie de cepas MenB, en particular de las cepas 2996, MC58, 1000 y BZ232. Los resultados también fueron buenos; cada uno de ellos produjo altas valoraciones con ELISA y también unas valoraciones bactericidas séricas >8192. La ΔG287K, expresada a partir de pET-24b, produjo excelentes valoraciones en el ensayo ELISA y bactericida sérico.

La ΔG287 se fusionó directamente dentro de marco cadena arriba de 919 (las secuencias que aparecen a continuación):



ΔG287–961

```
ATGGCTAGCCCCGATGTTAAATCGGCGGACACGCTGTCAAAACCGGCCGCTCCTGTTGTTGCTGAAAAAGAGACAGAG
GTAAAAGAAGATGCGCCACAGGCAGGTTCTCAAGGACAGGGCGCGCCATCCACACAAGGCAGCCAAGATATGGCGGCA
GTTTCGGCAGAAAATACAGGCAATGGCGGTGCGGCAACAACGGACAAACCCAAAAATGAAGACGAGGGACCGCAAAAT
GATATGCCGCAAAATTCCGCCGAATCCGCAAATCAAACAGGGAACAACCAACCCGCCGATTCTTCAGATTCCGCCCCC
GCGTCAAACCCTGCACCTGCGAATGGCGGTAGCAATTTTGGAAGGGTTGATTTGGCTAATGGCGTTTTGATTGATGGG
CCGTCGCAAAATATAACGTTGACCCACTGTAAAGGCGATTCTTGTAATGGTGATAATTTATTGGATGAAGAAGCACCG
TCAAAATCAGAATTTGAAAATTTAAATGAGTCTGAACGAATTGAGAAATATAAGAAAGATGGGAAAAGCGATAAATTT
ACTAATTTGGTTGCGACAGCAGTTCAAGCTAATGGAACTAACAAATATGTCATCATTTATAAAGACAAGTCCGCTTCA
TCTTCATCTGCGCGATTCAGGCGTTCTGCACGGTCGAGGAGGTCGCTTCCTGCCGAGATGCCGCTAATCCCCGTCAAT
CAGGCGGATACGCTGATTGTCGATGGGGAAGCGGTCAGCCTGACGGGGCATTCCGGCAATATCTTCGCGCCCGAAGGG
AATTACCGGTATCTGACTTACGGGGCGGAAAAATTGCCCGGCGGATCGTATGCCCTCCGTGTGCAAGGCGAACCGGCA
AAAGGCGAAATGCTTGCTGGCACGGCCGTGTACAACGGCGAAGTGCTGCATTTTCATACGGAAAACGGCCGTCCGTAC
CCGACTAGAGGCAGGTTTGCCGCAAAAGTCGATTTCGGCAGCAAATCTGTGGACGGCATTATCGACAGCGGCGATGAT
TTGCATATGGGTACGCAAAAATTCAAAGCCGCCATCGATGGAAACGGCTTTAAGGGGACTTGGACGGAAAATGGCGGC
GGGGATGTTTCCGGAAGGTTTTACGGCCCGGCCGGCGAGGAAGTGGCGGGAAAATACAGCTATCGCCCGACAGATGCG
GAAAAGGGCGGATTCGGCGTGTTTGCCGGCAAAAAAGAGCAGGATGGATCCGGAGGAGGAGGAGCCACAAACGACGAC
GATGTTAAAAAAGCTGCCACTGTGGCCATTGCTGCTGCCTACAACAATGGCCAAGAAATCAACGGTTTCAAAGCTGGA
GAGACCATCTACGACATTGATGAAGACGGCACAATTACCAAAAAAGACGCAACTGCAGCCGATGTTGAAGCCGACGAC
TTTAAAGGTCTGGGTCTGAAAAAAGTCGTGACTAACCTGACCAAAACCGTCAATGAAAACAAACAAAACGTCGATGCC
AAAGTAAAAGCTGCAGAATCTGAAATAGAAAAGTTAACAACCAAGTTAGCAGACACTGATGCCGCTTTAGCAGATACT
GATGCCGCTCTGGATGCAACCACCAACGCCTTGAATAAATTGGGAGAAAATATAACGACATTTGCTGAAGAGACTAAG
ACAAATATCGTAAAAATTGATGAAAAATTAGAAGCCGTGGCTGATACCGTCGACAAGCATGCCGAAGCATTCAACGAT
ATCGCCGATTCATTGGATGAAACCAACACTAAGGCAGACGAAGCCGTCAAAACCGCCAATGAAGCCAAACAGACGGCC
GAAGAAACCAAACAAAACGTCGATGCCAAAGTAAAAGCTGCAGAAACTGCAGCAGGCAAAGCCGAAGCTGCCGCTGGC
ACAGCTAATACTGCAGCCGACAAGGCCGAAGCTGTCGCTGCAAAAGTTACCGACATCAAAGCTGATATCGCTACGAAC
AAAGATAATATTGCTAAAAAAGCAAACAGTGCCGACGTGTACACCAGAGAAGAGTCTGACAGCAAATTTGTCAGAATT
GATGGTCTGAACGCTACTACCGAAAAATTGGACACACGCTTGGCTTCTGCTGAAAAATCCATTGCCGATCACGATACT
CGCCTGAACGGTTTGGATAAAACAGTGTCAGACCTGCGCAAAGAAACCCGCCAAGGCCTTGCAGAACAAGCCGCGCTC
TCCGGTCTGTTCCAACCTTACAACGTGGGTCGGTTCAATGTAACGGCTGCAGTCGGCGGCTACAAATCCGAATCGGCA
GTCGCCATCGGTACCGGCTTCCGCTTTACCGAAAACTTTGCCGCCAAAGCAGGCGTGGCAGTCGGCACTTCGTCCGGT
TCTTCCGCAGCCTACCATGTCGGCGTCAATTACGAGTGGTAACTCGAG
```

```
  1     MASPDVKSAD TLSKPAAPVV AEKETEVKED APQAGSQGQG APSTQGSQDM
 51     AAVSAENTGN GGAATTDKPK NEDEGPQNDM PQNSAESANQ TGNNQPADSS
101     DSAPASNPAP ANGGSNFGRV DLANGVLIDG PSQNITLTHC KGDSCNGDNL
151     LDEEAPSKSE FENLNESERI EKYKKDGKSD KFTNLVATAV QANGTNKYVI
201     IYKDKSASSS SARFRRSARS RRSLPAEMPL IPVNQADTLI VDGEAVSLTG
251     HSGNIFAPEG NYRYLTYGAE KLPGGSYALR VQGEPAKGEM LAGTAVYNGE
301     VLHFHTENGR PYPTRGRFAA KVDFGSKSVD GIIDSGDDLH MGTQKFKAAI
351     DGNGFKGTWT ENGGGDVSGR FYGPAGEEVA GKYSYRPTDA EKGGFGVFAG
401     KKEQDGSGGG GATNDDDVKK AATVAIAAAY NNGQEINGFK AGETIYDIDE
451     DGTITKKDAT AADVEADDFK GLGLKKVVTN LTKTVNENKQ NVDAKVKAAE
501     SEIEKLTTKL ADTDAALADT DAALDATTNA LNKLGENITT FAEETKTNIV
551     KIDEKLEAVA DTVDKHAEAF NDIADSLDET NTKADEAVKT ANEAKQTAEE
601     TKQNVDAKVK AAETAAGKAE AAAGTANTAA DKAEAVAAKV TDIKADIATN
651     KDNIAKKANS ADVYTREESD SKFVRIDGLN ATTEKLDTRL ASAEKSIADH
701     DTRLNGLDKT VSDLRKETRQ GLAEQAALSG LFQPYNVGRF NVTAAVGGYK
751     SESAVAIGTG FRFTENFAAK AGVAVGTSSG SSAAYHVGVN YEW*
```

	ELISA	**Bactericida**
ΔG287-961-His	108627	65536

Se prepararon las mismas proteínas híbridas utilizando la cepa 394/98 de Nueva Zelanda en lugar de 2996:

ΔG287NZ-961

```
ATGGCTAGCCCCGATGTCAAGTCGGCGGACACGCTGTCAAAACCTGCCGCCCCTGTTGTTTCTGAAAAAGAGACAGAG
GCAAAGGAAGATGCGCCACAGGCAGGTTCTCAAGGACAGGGCGCGCCATCCGCACAAGGCGGTCAAGATATGGCGGCG
GTTTCGGAAGAAAATACAGGCAATGGCGGTGCGGCAGCAACGGACAAACCCAAAAATGAAGACGAGGGGGCGCAAAAT
GATATGCCGCAAAATGCCGCCGATACAGATAGTTTGACACCGAATCACACCCCGGCTTCGAATATGCCGGCCGGAAAT
ATGGAAAACCAAGCACCGGATGCCGGGGAATCGGAGCAGCCGGCAAACCAACCGGATATGGCAAATACGGCGGACGGA
ATGCAGGGTGACGATCCGTCGGCAGGCGGGGAAAATGCCGGCAATACGGCTGCCCAAGGTACAAATCAAGCCGAAAAC
AATCAAACCGCCGGTTCTCAAAATCCTGCCTCTTCAACCAATCCTAGCGCCACGAATAGCGGTGGTGATTTTGGAAGG
ACGAACGTGGGCAATTCTGTTGTGATTGACGGGCCGTCGCAAAATATAACGTTGACCCACTGTAAAGGCGATTCTTGT
AGTGGCAATAATTTCTTGGATGAAGAAGTACAGCTAAAATCAGAATTTGAAAAATTAAGTGATGCAGACAAAATAAGT
AATTACAAGAAAGATGGGAAGAATGACGGGAAGAATGATAAATTTGTCGGTTTGGTTGCCGATAGTGTGCAGATGAAG
GGAATCAATCAATATATTATCTTTTATAAACCTAAACCCACTTCATTTGCGCGATTTAGGCGTTCTGCACGGTCGAGG
CGGTCGCTTCCGGCCGAGATGCCGCTGATTCCCGTCAATCAGGCGGATACGCTGATTGTCGATGGGGAAGCGGTCAGC
CTGACGGGGCATTCCGGCAATATCTTCGCGCCCGAAGGGAATTACCGGTATCTGACTTACGGGGCGGAAAAATTGCCC
GGCGGATCGTATGCCCTCCGTGTTCAAGGCGAACCTTCAAAAGGCGAAATGCTCGCGGGCACGGCAGTGTACAACGGC
GAAGTGCTGCATTTTCATACGGAAAACGGCCGTCCGTCCCCGTCCAGAGGCAGGTTTGCCGCAAAAGTCGATTTCGGC
AGCAAATCTGTGGACGGCATTATCGACAGCGGCGATGGTTTGCATATGGGTACGCAAAAATTCAAAGCCGCCATCGAT
GGAAACGGCTTTAAGGGGACTTGGACGGAAAATGGCGGCGGGGATGTTTCCGGAAAGTTTTACGGCCCGGCCGGCGAG
GAAGTGGCGGGAAAATACAGCTATCGCCCAACAGATGCGGAAAAGGGCGGATTCGGCGTGTTTGCCGGCAAAAAAGAG
CAGGATGGATCCGGAGGAGGAGGAGCCACAAACGACGACGATGTTAAAAAAGCTGCCACTGTGGCCATTGCTGCTGCC
TACAACAATGGCCAAGAAATCAACGGTTTCAAAGCTGGAGAGACCATCTACGACATTGATGAAGACGGCACAATTACC
AAAAAAGACGCAACTGCAGCCGATGTTGAAGCCGACGACTTTAAAGGTCTGGGTCTGAAAAAAGTCGTGACTAACCTG
ACCAAAACCGTCAATGAAAACAAACAAAACGTCGATGCCAAAGTAAAAGCTGCAGAATCTGAAATAGAAAAGTTAACA
ACCAAGTTAGCAGACACTGATGCCGCTTTAGCAGATACTGATGCCGCTCTGGATGCAACCACCAACGCCTTGAATAAA
TTGGGAGAAAATATAACGACATTTGCTGAAGAGACTAAGACAAATATCGTAAAAATTGATGAAAAATTAGAAGCCGTG
GCTGATACCGTCGACAAGCATGCCGAAGCATTCAACGATATCGCCGATTCATTGGATGAAACCAACACTAAGGCAGAC
GAAGCCGTCAAAACCGCCAATGAAGCCAAACAGACGGCCGAAGAAACCAAACAAAACGTCGATGCCAAAGTAAAAGCT
GCAGAAACTGCAGCAGGCAAAGCCGAAGCTGCCGCTGGCACAGCTAATACTGCAGCCGACAAGGCCGAAGCTGTCGCT
GCAAAAGTTACCGACATCAAAGCTGATATCGCTACGAACAAAGATAATATTGCTAAAAAAGCAAACAGTGCCGACGTG
TACACCAGAGAAGAGTCTGACAGCAAATTTGTCAGAATTGATGGTCTGAACGCTACTACCGAAAAATTGGACACACGC
TTGGCTTCTGCTGAAAAATCCATTGCCGATCACGATACTCGCCTGAACGGTTTGGATAAAACAGTGTCAGACCTGCGC
AAAGAAACCCGCCAAGGCCTTGCAGAACAAGCCGCGCTCTCCGGTCTGTTCCAACCTTACAACGTGGGTCGGTTCAAT
GTAACGGCTGCAGTCGGCGGCTACAAATCCGAATCGGCAGTCGCCATCGGTACCGGCTTCCGCTTTACCGAAAACTTT
GCCGCCAAAGCAGGCGTGGCAGTCGGCACTTCGTCCGGTTCTTCCGCAGCCTACCATGTCGGCGTCAATTACGAGTGG
TAAAAGCTT
```

```
  1   MASPDVKSAD TLSKPAAPVV SEKETEAKED APQAGSQGQG APSAQGGQDM
 51   AAVSEENTGN GGAAATDKPK NEDEGAQNDM PQNAADTDSL TPNHTPASNM
101   PAGNMENQAP DAGESEQPAN QPDMANTADG MQGDDPSAGG ENAGNTAAQG
151   TNQAENNQTA GSQNPASSTN PSATNSGGDF GRTNVGNSVV IDGPSQNITL
201   THCKGDSCSG NNFLDEEVQL KSEFEKLSDA DKISNYKKDG KNDGKNDKFV
251   GLVADSVQMK GINQYIIFYK PKPTSFARFR RSARSRRSLP AEMPLIPVNQ
301   ADTLIVDGEA VSLTGHSGNI FAPEGNYRYL TYGAEKLPGG SYALRVQGEP
351   SKGEMLAGTA VYNGEVLHFH TENGRPSPSR GRFAAKVDFG SKSVDGIIDS
401   GDGLHMGTQK FKAAIDGNGF KGTWTENGGG DVSGKFYGPA GEEVAGKYSY
451   RPTDAEKGGF GVFAGKKEQD GSGGGGATND DDVKKAATVA IAAAYNNGQE
501   INGFKAGETI YDIDEDGTIT KKDATAADVE ADDFKGLGLK KVVTNLTKTV
551   NENKQNVDAK VKAAESEIEK LTTKLADTDA ALADTDAALD ATTNALNKLG
601   ENITTFAEET KTNIVKIDEK LEAVADTVDK HAEAFNDIAD SLDETNTKAD
651   EAVKTANEAK QTAEETKQNV DAKVKAAETA AGKAEAAAGT ANTAADKAEA
701   VAAKVTDIKA DIATNKDNIA KKANSADVYT REESDSKFVR IDGLNATTEK
751   LDTRLASAEK SIADHDTRLN GLDKTVSDLR KETRQGLAEQ AALSGLFQPY
801   NVGRFNVTAA VGGYKSESAV AIGTGFRFTE NFAAKAGVAV GTSSGSSAAY
851   HVGVNYEW*
```

Ejemplo 2 - Híbridos de 287

La expresión de 287, de longitud completa con un marcador de His C-terminal, o sin su péptido conductor pero con un marcador de His C-terminal, produce unos niveles de expresión bastante bajos. Se logró una mejor expresión empleando una fusión con GST N-terminal. Cuando se fusiona con la proteína 961 (la secuencia NH_2-ΔG287-961-COOH mostrada anteriormente), la proteína resultante es insoluble y debe desnaturalizarse y renaturalizarse para la purificación. Después de la renaturalización, se descubrió que aproximadamente 50% de la proteína permanecía insoluble. Las proteínas soluble e insoluble se compararon, y se obtuvieron unas valoraciones bactericidas mucho mejores con la proteína soluble (FCA como adyuvante):

	2996	**BZ232**	**MC58**	**NGH38**	**F6124**	**BZ133**
Soluble	65536	128	4096	>2048	>2048	4096
Insoluble	8192	<4	<4	16	n.d.	n.d.

Sin embargo, las valoraciones con la forma insoluble mejoraron utilizando un adyuvante de alumbre:

Insoluble	32768	128	4096	>2048	>2048	2048

También se usó 961c en las proteínas híbridas (véase anteriormente). Puesto que 961 y sus variantes de dominio dirigen una expresión eficaz, son idealmente adecuados como porción N-terminal de una proteína híbrida.

Detalles experimentales

Estrategia de clonación y diseño de oligonucleótidos

Los genes que codifican los antígenos de interés se amplificaron mediante PCR, utilizando oligonucleótidos diseñados basándose en la secuencia genómica de *N. meningitidis* B MC58. Siempre se utiliza ADN genómico de la cepa 2996 como molde en las reacciones de PCR, a menos que se indique lo contrario, y los fragmentos amplificados se clonaron en el vector de expresión pET21b+ (Novagen) para expresar la proteína como producto marcado con His C-terminal, o en pET-24b+ (Novagen) para expresar la proteína en forma "no marcada" (por ejemplo, ΔG287K).

Cuando una proteína se expresa sin un compañero de fusión y con su propio péptido conductor (si está presente), se realiza una amplificación del marco de lectura abierto (codones desde ATG hasta FIN).

Cuando una proteína se expresa en forma "no marcada", el péptido conductor se omite diseñando el cebador de amplificación del 5'-terminal cadena abajo de la secuencia conductora predicha.

La temperatura de fusión de los cebadores utilizados en la PCR depende del número y tipo de nucleótidos hibridantes en el cebador completo, y se determinó empleando las fórmulas:

$$T_{m1} = 4(G+C) + 2(A+T) \qquad \text{(sin la cola)}$$

$$T_{m2} = 64{,}9 + 0{,}41\ (GC\%) - 600/N \qquad \text{(cebador completo)}$$

Las temperaturas de fusión de los oligonucleótidos seleccionados eran normalmente de 65-70ºC para el oligonucleótido completo, y de 50-60ºC para la región de hibridación sola.

Se sintetizaron oligonucleótidos utilizando un sintetizador de ADN/ARN Perkin Elmer 394, se eluyeron de las columnas en 2,0 ml de NH_4OH, y se desprotegieron mediante 5 horas de incubación a 56ºC. Los oligonucleótidos se precipitaron mediante la adición de acetato de Na 0,3 M y 2 volúmenes de etanol. Las muestras se centrifugaron y los sedimentos se resuspendieron en agua.

		Secuencias	Sitio de restricción
fu (961)-741(MC58)-His	Fwd	CGCGGATCC -GGAGGGGGTGGTGTCG	BamHI
	Rev	CCCGCTCGAG-TTGCTTGGCGGCAAGGG	XhoI
fu (961.)-983-His	Fwd	CGCGGATCC - GGCGGAGGCGGCACTT	BamHI
	Rev	CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
fu (961)-Orf16.1-His	Fwd	CGCGGATCCGGTGGTGGTGGT-TCAGATTTGGCAAACGATTC	BamHI
	Rev	CCCGCTCGAG-CGTATCATATTTCACGTGC	XhoI
fu (961 c-L)-741(MC58)	Fwd	CGCGGATCC -GGAGGGGGTGGTGTCG	BamHI
	Rev	CCCGCTCGAG-TTATTGCTTGGCGGCAAG	XhoI
fu (961c-L)-983	Fwd	CGCGGATCC - GGCGGAGGCGGCACTT	BamHI
	Rev	CCCGCTCGAG-TCAGAACCGGTAGCCTAC	XhoI
fu (961c-L)-Orf46.1	Fwd	CGCGGATCCGGTGGTGGTGGT-TCAGATTTGGCAAACGATTC	BamHI
	Rev	CCCGCTCGAG-TTACGTATCATATTTCACGTGC	XhoI
fu-(ΔG287)-919-His	Fwd	CGCGGATCCGGTGGTGGTGGT-CAAAGCAAGAGCATCCAAACC.	BamHI
	Rev	CCCAAGCTT-TTCGGGCGGTATTCGGGCTTC	HindIII
fu-(ΔG287)-953–Hισ	Fwd	CGCGGATCCGGTGGTGGTGGT-GCCACCTACAAAGTGGAC	BamHI
	Rev	GCCCAAGCTT-TTGTTTGGCTGCCTCGAT	HindIII
fu-(ΔG287)-961–Hισ	Fwd	CGCGGATCCGGTGGTGGTGGT-ACAAGCGACGACG	BamHI
	Rev	GCCCAAGCTT-CCACTCGTAATTGACGCC	HindIII
fu-(ΔG287)-Opφ46.1–Hισ	Fwd	CGCGGATCCGGTGGTGGTGGT-TCAGATTTGGCAAACGATTC	BamHI
	Rev	CCCAAGCTT-CGTATCATATTTCACGTGC	HindIII
fu-(ΔG287-919)-Opφ46.1–Hισ	Fwd	CCCAAGCTTGGTGGTGGTGGTGGT-TCAGATTTGGCAAACGATTC	HindIII
	Rev	CCCGCTCGAG-CGTATCATATTTCACGTGC	XhoI
fu-(ΔP787-Opφ46.1)–919–Hισ	Fwd	CCCAAGCITGGTGGTGGTGGTGGT-CAAAGCAAGAGCATCCAAACC	HindIII
		Rev CCCGCTCGAG-CGGGCGGTATTCGGGCTT	XhoI

(continuación)

		Secuencias	Sitio de restricción
fu ΔG287(394.98)-	Fwd	CGCGGATCCGCTAGC-CCCGATGTTAAATCGGC	Nhel
	Rev	CGGGGATCC-ATCCTGCTCTTTTTGCCGG	BamHI
fu Orf1-(Orf46.1)-His	Fwd	CGCGGATCCGCCTAGC-GGACACACTTATTTCGGCATC	Nhel
	Rev	CGCGGATCC-CCAGCGGTAGCGTAATTTGAT	
fu (Orf1)-Orf46.1-His	Fwd	CGCGGATCCGGTGGTGGTGGT-TCAGATTTGGCAAACGATTC	BamHI
	Rev	CCCAAGCTT-CGTATCATATTTCACGTGC	HindIII
fu (919)-Orf46.1-His	Fwd1	GCGGCGTCGACGGTGGCGGAGGCACTGGATCCTCAG	Sall
	Fwd2	GGAGGCACTGGATCCTCAGATTTGGAAACGATTC	
	Rev	CCCGCTCGAG-CGTATCATATTTCACGTGC	Xhol
Fu (orf46)-287-His	Fwd	CGGGATCCGGGGCGGCGGTGGCG	BamHI
	Rev	CCCAAGCTTATCCTGCTCTTTTTTGCCGGC	HindIII
Fu(orf46).919-His	Fwd	**CGCGGATCCGGTGGTGGTGGTCAAAGCAAGAGCATCCA AACC**	BamHI
	Rev	CCCAAGCGGGCGGTATTCGGGCTTC.	HindIII
Fu (orf46-919)-287-His	Fwd	CCCCAAGCTTGGGGGCGGCGGTGGCG	HindIII
	Rev	CCCGCTCGAGATCCTGCTCTTTTTTGCCGGC	Xhol
Fu (ort46-287)-919-His	Fwd	**CCCAAGCTTGGTGGTGGTGGTGGTCAAAGCAAGAGCAT CCAAACC**	HindIII
	Rev	CCCCGCTCGAGCGGGCGGTATTCGGGCTT	Xhol
(**ΔG741**)-961ε–Hισ	Fwd1	GGAGGCACTGGATCCGCAGCCACAAACGACGACGA	Xhol
	Fwd2	GCGGCCTCGAG-GGTGGCGGAGGCACTGGATCCGCAG	
	Rev	CCCGCTCGAG-ACCCAGCTTGTAAGGTTG	Xhol
(**ΔG741**)-961–Hισ	Fwd1	GGAGGCACTGGATCCGCAGCCACAAACGACGACGA	Xhol
	Fwd2	GCGGCCTCGAG-GGTGGCGGAGGCACTGGATCCGCAG	
	Rev	CCCGCTCGAG-CCACTCGTAATTGACGCC	Xhol

(continuación)

		Secuencias	Sitio de restricción
(ΔG741)-983.Hισ	Fwd	**GCGGCCTCGAG-GGATCCGGCGGAGGCGGCACTTCTGCG.**	XhoI
	Rev	CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
(ΔG741)-opϕ46.1–Hισ	Fwd1 Fwd2	GGAGGCACTGGATCCTCAGATTTGGCAAACGATTC GCGGCGTCGACGGTGGCGGAGGCACTGGATCCTCAGA	SalI
	Rev	CCCGCTCGAG-CGTATCATATTTCACGTGC	XhoI
(ΔG983)-741(MX58) -Hισ	Fwd	GCGGCCTCGAG-GGATCCGGAGGGGGTGGTGTCGCC	XhoI
	Rev	CCCGCTCGAG-TTGCTTGGCGGCAAG	XhoI
(ΔG983)-961χ–Hισ	Fwd1 Fwd2	GGAGGCACTGGATCCGCAGCCACAAACGACGACGA GCGGCCTCGAG-GGTGGCGGAGGCACTGGATCCGCAG	XhoI
	Rev	CCCGCTCGAG-ACCCAGCTTGTAAGGTTG	XhoI
(ΔG983)-961–Hισ	Fwd1 Fwd2	GGAGGCACTGGATCCGCAGCCACAAACGACGACGA GCGGCCTCGAG-GGTGGCGGAGGCACTGGATCCGCAG.	XhoI
	Rev	CCCGCTCGAG-CCACTCGTAATTGACGCC	XhoI
(ΔG983)- Opϕ46.1- Fwd1 His	 Fwd2	GGAGGCACTGGATCCTCAGATTTGGCAAACGATTC GCGGCGTCGACGGTGGCGGAGGCACTGGATCCTCAGA	SalI
	Rev	CCCGCTCGAG-CGTATCATATTTCACGTGC	XhoI

*Este cebador se uso como cebador inverso para todas las fusiones C-terminales de 287 a la cola de His.
Cebadores forward usados en combinación con el primer inverso de 287-His. Las reacciones de NB-AII PCR usan la cepa 2996 a no ser que se indique lo contrario. Por ejemplo, cepa MC58.

En todos los constructos que comienzan con un ATG no seguido por un sitio *Nhe*I exclusivo, el codón ATG es parte del sitio *Nhe*I utilizado para la clonación. Los constructos fabricados utilizando *Nhe*I como sitio de clonación en el extremo 5' (por ejemplo, los que contienen 287 en el N-terminal) tienen dos codones más (GCT AGC) fusionados a la secuencia codificadora del antígeno.

Preparación de moldes de ADN cromosómico

Las cepas 2996, MC58, 394.98, 1000 y BZ232 (y otras) de *N. meningitidis* se cultivaron hasta la fase exponencial en 100 ml de medio GC, se recogieron mediante centrifugación, y se resuspendieron en 5 ml de tampón (sacarosa al 20% p/v, Tris-HCl 50 mM, EDTA 50 mM, pH 8). Después de 10 min de incubación en hielo, las bacterias se lisaron añadiendo 10 ml de disolución de lisis (NaCl 50 mM, Na-Sarkosyl al 1%, proteinasa K 50 µg/ml), y la suspensión se incubó a 37ºC durante 2 horas. Se realizaron dos extracciones con fenol (equilibrado a pH 8) y una extracción con $CHCl_3$/alcohol isoamílico (24:1). El ADN se precipitó mediante la adición de acetato de sodio 0,3 M y 2 volúmenes de etanol, y se recogió mediante centrifugación. El sedimento se lavó una vez con etanol al 70% (v/v) y se redisolvió en 4,0 ml de tampón TE (Tris-HCl 10 mM, EDTA 1 mM, pH 8,0). Se midió la concentración de ADN mediante una lectura de DO_{260}.

Amplificación mediante PCR

El protocolo de PCR convencional fue el siguiente: se utilizó como molde 200 ng de ADN genómico procedente de las cepas 2996, MC581000 o BZ232, o 10 ng de preparación de ADN de plásmido de clones recombinantes, en presencia de 40 µM de cada uno de los cebadores oligonucleotídicos, disolución de dNTP 400-800 µM, 1x tampón de PCR (que incluye $MgCl_2$ 1,5 mM), 2,5 unidades de *TaqI* ADN polimerasa (utilizando Perkin-Elmer AmpliTaQ, molde largo Boehringer Mannheim Expand™).

Después de una incubación preliminar de 3 minutos de la mezcla completa a 95ºC, cada muestra se sometió a una amplificación en dos etapas: los primeros 5 ciclos se realizaron utilizando la temperatura de hibridación que excluye la cola de enzimas de restricción del cebador (T_{m1}). Después siguieron 30 ciclos según la temperatura de hibridación calculada para los oligonucleótidos de longitud completa (T_{m2}). Los tiempos de alargamiento, realizado a 68ºC o 72ºC, varían según la longitud del Orf (marco de lectura abierto) que se va a amplificar. En el caso de Orf1, el tiempo de alargamiento, comenzando a partir de 3 minutos, aumentó en 15 segundos cada ciclo. Los ciclos se completaron con una etapa de extensión de 10 minutos a 72ºC.

El ADN amplificado se cargó directamente sobre un gel de agarosa al 1%. El fragmento de ADN que corresponde a la banda del tamaño correcto se purificó del gel utilizando el kit de extracción de gel de Qiagen, siguiendo el protocolo del fabricante.

Digestión de los fragmentos de PCR y de los vectores de clonación

El ADN purificado que corresponde al fragmento amplificado se digirió con las enzimas de restricción apropiadas para clonarlo en pET-21b+, pET22b+ o pET-24b+. Los fragmentos digeridos se purificaron utilizando el kit de purificación de PCR QIAquick (siguiendo las instrucciones del fabricante) y se eluyeron con H_2O, o con Tris 10 mM, pH 8,5. Los vectores plásmidos se digirieron con las enzimas de restricción apropiadas, se cargaron sobre un gel de agarosa al 1,0%, y la banda correspondiente al vector digerido se purificó utilizando el kit de extracción de gel QIAquick de Qiagen.

Clonación

Los fragmentos que correspondían a cada gen, previamente digeridos y purificados, se acoplaron a pET-21b+, pET22b+ o pET-24b+. Se empleó una proporción molar de fragmento/vector 3:1 con ADN ligasa de T4 en el tampón de acoplamiento suministrado por el fabricante.

El plásmido recombinante se transformó en *E. coli* DH5 o HB101 competente mediante la incubación de la disolución de reacción de ligasa y bacterias durante 40 minutos en hielo, y después a 37ºC durante 3 minutos. A esto le siguió la adición de 800 µl de caldo de cultivo LB y una incubación a 37ºC durante 20 minutos. Las células se centrifugaron a velocidad máxima en una microcentífuga Eppendorf, se resuspendieron en aproximadamente 200 µl del sobrenadante, y se colocaron en placas con agar con ampicilina y LB (100 mg/ml).

La selección de los clones recombinantes se realizó cultivando colonias, seleccionadas aleatoriamente, durante la noche a 37ºC en 4,0 ml de caldo de cultivo LB + ampicilina 100 µg/ml. Las células se sedimentaron y el ADN del plásmido se extrajo utilizando el kit de minipreparaciones de centrifugación QIAprep de Qiagen, siguiendo las instrucciones del fabricante. Se digirió aproximadamente 1 µg de cada minipreparación individual con las enzimas de restricción apropiadas, y el digerido se cargó sobre un gel de agarosa al 1-1,5% (dependiendo del tamaño esperado del inserto), en paralelo con el marcador de peso molecular (1 kb de DNA Ladder, GIBCO). Los clones positivos se seleccionaron basándose en el tamaño del inserto.

Expresión

Después de clonar cada gen en el vector de expresión, los plásmidos recombinantes se transformaron en cepas de *E. coli* adecuadas para la expresión de la proteína recombinante. Se empleó 1 µl de cada constructo para transformar *E. coli* BL21-DE3 como se describió anteriormente. Se inocularon colonias recombinantes individuales en 2 ml de LB + ampicilina (100 µg/ml), se incubaron a 37ºC durante la noche, después se diluyeron 1:30 en 20 ml de LB + ampicilina (100 µg/ml) en matraces de 100 ml, para producir una DO_{600} entre 0,1 y 0,2. Los matraces se incubaron a 30ºC o a 37ºC en un agitador de baño de agua giratorio hasta que la DO_{600} indicó un crecimiento exponencial adecuado para la inducción de la expresión (0,4-0,8 DO). La expresión de las proteínas se indujo mediante la adición de IPTG 1,0 mM. Después de 3 horas de incubación a 30ºC o a 37ºC, se midió la DO_{600} y se estudió la expresión. Se centrifugaron 1,0 ml de cada muestra en una microcentrífuga, el sedimento se resuspendió en PBS y se analizó mediante SDS-PAGE y tinción con azul de Coomassie.

Purificación de proteínas marcadas con His

Se clonaron diversas formas de 287 a partir de las cepas 2996 y MC58. Se construyeron con una fusión de un marcador de His C-terminal e incluían una forma madura (aa 18-427), constructos con deleciones (Δ1, Δ2, Δ3 y Δ4), y clones compuestos de dominios B o C. Para cada clon purificado como una fusión con His, se realizó una siembra en estría de una única colonia y se cultivó durante la noche a 37ºC sobre una placa de agar con LB/ampicilina (100 µg/ml). Una colonia aislada de esta placa se inoculó en 20 ml de medio líquido de LB/ampicilina (100 µg/ml) y se cultivó durante la noche a 37ºC con agitación. El cultivo de la noche se diluyó 1:30 en 1,0 l de medio líquido de LB/ampicilina (100 µg/ml) y se dejó que creciese a la temperatura óptima (30ºC o 37ºC) hata que la DO_{550} alcanzó un valor de 0,6-0,8. La expresión de la proteína recombinante se indujo mediante la adición de IPTG (concentración final 1,0 mM) y el cultivo se incubó durante 3 horas más. Las bacterias se recolectaron mediante centrifugación a 8000 g durante 15 min a 4ºC. El sedimento bacteriano se resuspendió en 7,5 ml de (i) tampón A frío (NaCl 300 mM, tampón fosfato 50 mM, imidazol 10 mM, pH 8,0) para proteínas solubles, o (ii) tampón B (Tris-HCl 10 mM, tampón fosfato 100 mM, pH 8,8 y, opcionalmente, urea 8 M) para proteínas insolubles. Las proteínas purificadas en forma soluble incluían 287-His, Δ1, Δ2, Δ3 y Δ4287-His, Δ4287MC58-His, 287c-His y 287c-MC58-His. La proteína 287bMC58-His era insoluble y se purificó en consecuencia. Las células se rompieron mediante sonicación sobre hielo cuatro veces durante 30 seg a 40 W utilizando un sonicador 450 Branson, y se centrifugaron a 13000 x g durante 30 min a 4ºC. Para las proteínas insolubles, los sedimentos se resuspendieron en 2,0 ml de tampón C (clorhidrato de guanidina 6 M, tampón fosfato 100 mM, Tris-HCl 10 mM, pH 7,5), y se trataron con 10 pases con un homogeneizador Dounce. El homogeneizado se centrífugo a 13000 g durante 30 min y se guardó el sobrenadante.

Los sobrenadantes de las preparaciones soluble e insoluble se mezclaron con 150 µl de resina Ni^{2+} (previamente equilibrada con tampón A o tampón B, según sea apropiado) y se incubaron a temperatura ambiente con una agitación suave durante 30 min. La resina era Chelating Sepharose Fast Flow (Pharmacia), preparada según las instrucciones del fabricante. La preparación discontinua se centrífugo a 700 g durante 5 min a 4ºC y se rechazó el sobrenadante. La resina se lavó dos veces (de forma discontinua) con 10 ml de tampón A o B durante 10 min, se resuspendió en 1,0 ml de tampón A o B, y se cargó en una columna desechable. La resina continuó lavándose con (i) tampón A a 4ºC, o (ii) tampón B a temperatura ambiente, hasta que la DO_{280} de la corriente alcanzó un valor de 0,02-0,01. La resina se volvió a lavar con (i) tampón C frío (NaCl 300 mM, tampón fosfato 50 mM, imidazol 20 mM, pH 8,0), o (ii) tampón D (Tris-HCl 10 mM, tampón fosfato 100 mM, pH 6,3 y, opcionalmente, urea 8 M) hasta que la DO_{280} de la corriente alcanzó un valor de 0,02-0,01. La proteína de fusión-His se eluyó mediante la adición de 700 µl de (i) tampón de elución A frío (NaCl 300 mM, tampón fosfato 50 mM, imidazol 250 mM, pH 8,0), o (ii) tampón de elución B (Tris-HCl 10 mM, tampón fosfato 100 mM, pH 4,5 y, opcionalmente, urea 8 M), y las fracciones se recogieron hasta que la DO_{280} indicó que se había obtenido toda la proteína recombinante. Se analizaron partes alícuotas de 20 µl de cada fracción de elución mediante SDS-PAGE. Se estimaron las concentraciones de proteínas utilizando el ensayo de Bradford.

Renaturalización de las proteínas de fusión-His desnaturalizadas

Se requiere una desnaturalización para solubilizar 287bMC8, por tanto se empleó una etapa de renaturalización antes de la inmunización. Se añadió glicerol a las fracciones desnaturalizadas obtenidas anteriormente para producir una concentración final de 10% v/v. Las proteínas se diluyeron hasta 200 µg/ml utilizando tampón de diálisis I (glicerol al 10% v/v, arginina 0,5 M, tampón fosfato 50 mM, glutatión reducido 5,0 mM, glutatión oxidado 0,5 mM, urea 2,0 M, pH 8,8), y se dializaron contra el mismo tampón durante 12-14 horas a 4ºC. Se realizó otra diálisis con tampón II (glicerol al 10% v/v, arginina 0,5 M, tampón fosfato 50 mM, glutatión reducido 5,0 mM, glutatión oxidado 0,5 mM, pH 8,8) durante 12-14 horas a 4ºC. Se estimó la concentración de proteína utilizando la fórmula:

Proteína (mg/ml) = $(1,55 \times DO_{280}) - (0,76 \times DO_{260})$

Immunización

Se inmunizaron ratontes Balb/C con antígenos en los días 0, 21 y 35, y se analizaron los sueros el día 49.

Análisis de los sueros - ELISA

Las cepas MenB M7 acapsuladas y las capsuladas se cultivaron en placas de agar de chocolate y se incubaron durante la noche a 37ºC con CO_2 al 5%. Las colonias bacterianas se recogieron de las placas de agar utilizando un hisopo Dracon estéril y se inocularon en caldo de cultivo Mueller-Hinton (Difco) que contenía glucosa al 0,25%. El crecimiento bacteriano se controló cada 30 minutos siguiendo la DO_{620}. Se dejaron crecer las bacterias hasta que la DO alcanzó un valor de 0,4-0,5. El cultivo se centrífugo durante 10 minutos a 4000 rpm. El sobrenadante se eliminó y las bacterias se lavaron dos veces con PBS, se resuspendieron en PBS que contenía formaldehído al 0,025%, y se incubaron durante 1 hora a 37ºC, y después durante la noche a 4ºC con agitación. Se añadieron 100 µl de células bacterianas a cada pocillo de una placa Greiner de 96 pocillos y se incubaron durante la noche a 4ºC. Los pocillos entonces se lavaron tres veces con tampón de lavado PBT (Tween-20 al 0,1% en PBS). Se añadieron 200 µl de tampón de saturación (polivinilpirrolidona 10 al 2,7% en agua) a cada pocillo y las placas se incubaron durante 2 horas a 37ºC. Los pocillos se lavaron tres veces con PBT. Se añadieron 200 µl de los sueros diluidos (tampón de dilución: BSA al 1%, Tween-20 al 0,1%, NaN_3 al 0,1% en PBS) a cada pocillo, y las placas se incubaron durante 2 horas a 37ºC. Los pocillos se lavaron tres veces con PBT. Se añadieron 100 µl a cada pocillo de suero antirratón de conejo conjugado con HRP (Dako) diluido 1:2000 en tampón de dilución, y las placas se incubaron durante 90 minutos a 37ºC. Los pocillos se lavaron tres veces con tampón PBT. Se añadieron 100 µl de tampón sustrato para HRP (25 ml de tampón citrato, pH 5, 10 mg de O-fenildiamina, y 10 µl de H_2O_2) a cada pocillo, y las placas se dejaron a temperatura ambiente durante 20 minutos. Se añadieron 100 µl de H_2SO_4 al 12,5% a cada pocillo y se siguió la DO_{490}. Las valoraciones de ELISA se calcularon de manera arbitraria como la dilución de los sueros que produce un valor de DO_{490} de 0,4 por encima del nivel de los sueros preinmunológicos. El ELISA se consideró positivo cuando la dilución de los sueros con una DO_{490} de 0,4 era mayor que 1:400.

Análisis de los sueros - Ensayo de unión de bacterias con barrido FACS

La cepa MenB M7 acapsulada se cultivó en placas de agar de chocolate y se incubó durante la noche a 37ºC con CO_2 al 5%. Las colonias bacterianas se recogieron de las placas de agar utilizando un hisopo Dracon estéril y se inocularon en 4 tubos que contenían cada uno 8 ml de caldo de cultivo Mueller-Hinton (Difco) que contenía glucosa al 0,25%. El crecimiento bacteriano se controló cada 30 minutos siguiendo la DO_{620}. Se dejaron crecer las bacterias hasta que la DO alcanzó un valor de 0,35-0,5. El cultivo se centrífugo durante 10 minutos a 4000 rpm. El sobrenadante se eliminó y el sedimento se resuspendió en tampón de bloqueo (BSA al 1% en PBS, NaN_3 al 0,1% en PBS) y se centrífugo durante 5 minutos a 4000 rpm. Las células se resuspendieron en tampón de bloqueo para alcanzar una DO_{620} de 0,05. Se añadieron 100 µl de células bacterianas a cada pocillo de una placa Costar de 96 pocillos. Se añadieron 100 µl de los sueros diluidos (1:100, 1:200, 1:400) (en tampón de bloqueo) a cada pocillo, y las placas se incubaron durante 2 horas a 4ºC. Las células se centrifugaron durante 5 minutos a 4000 rpm, el sobrenadante se aspiró y las células se lavaron mediante la adición de 200 µl/pocillo de tampón de bloqueo en cada pocillo. Se añadieron 100 µl de $F(ab)_2$ de cabra antirratón conjugado con R-ficoeritrina, diluido 1:100, a cada pocillo, y las placas se incubaron durante 1 hora a 4ºC. Las células se sedimentaron mediante centrifugación a 4000 rpm durante 5 minutos, y se lavaron mediante la adición de 200 µl/pocillo de tampón de bloqueo. El sobrenadante se aspiró y las células se resuspendieron en 200 µl/pocillo de PBS, formaldehído al 0,25%. Las muestras se trasladaron a tubos FACScan y se leyeron. Los ajustes del FACScan (potencia del láser 15 mW) fueron: FL2 activo; umbral de FSC-H: 92; voltaje de FSC PMT: E 01; SSC PMT: 474; ganancias de amp. 61; FL-2 PMT: 586; valores de compensación: 0.

Análisis de los sueros - Ensayo bactericida

Se cultivó la cepa 2996 de *N. meningitidis* durante la noche a 37ºC sobre placas de agar de chocolate (a partir de una cepa congelada) con CO_2 al 5%. Las colonias se recogieron y se utilizaron para inocular 7 ml de caldo de cultivo Mueller-Hinton que contenía glucosa al 0,25% hasta alcanzar una DO_{620} de 0,05-0,08. El cultivo se incubó durante aproximadamente 1,5 horas a 37ºC con agitación hasta que la DO_{620} alcanzó un valor de 0,23-0,24. Las bacterias se diluyeron en tampón fosfato 50 mM, pH 7,2, que contenía $MgCl_2$ 10 mM, $CaCl_2$ 10 mM, y BSA al 0,5% (p/v) (tampón de ensayo) con una dilución de trabajo de 10^5 CFU/ml. El volumen total de la mezcla de reacción final era de 50 µl, con 25 µl de dilución en dos veces en serie del suero de ensayo, 12,5 µl de bacterias en la dilución de trabajo, y 12,5 µl de complemento de cría de conejo (concentración final 25%).

Los controles incluían bacterias incubadas con suero de complemento, sueros inmunológicos incubados con bacterias y con complemento inactivado mediante calentamiento a 56ºC durante 30 minutos. Inmediatamente después de la adición del complemento de cría de conejo, 10 µl de los controles se cultivaron en placas de agar Mueller-Hinton utilizando el procedimiento de plano inclinado (tiempo 0). La placa de 96 pocillos se incubó durante 1 hora a 37ºC con rotación. Se colocaron 7 µl de cada muestra sobre placas de agar Mueller-Hinton como gotas, mientras que 10 µl de los controles se cultivaron en placas de agar Mueller-Hinton utilizando el procedimiento de plano inclinado (tiempo 1). Las placas de agar se incubaron durante 18 horas a 37ºC y se contaron las colonias correspondientes al tiempo 0 y tiempo 1.

Análisis de los sueros - Análisis de la transferencia Western

Proteínas purificadas (500 ng/carril), vesículas de membrana externa (5 µg) y extractos de células totales (25 µg) procedentes de la cepa 2996 MenB se cargaron sobre un gel de SDS al 12%-poliacrilamida y se transfirieron a una membrana de nitrocelulosa. La transferencia se realizó durante 2 horas a 150 mA a 4ºC, utilizando tampón de transferencia (base Tris al 0,3%, glicina al 1,44%, etanol al 20% (v/v)). La membrana se saturó mediante una incubación durante la noche a 4ºC en tampón de saturación (leche desnatada al 10%, Triton X100 al 0,1% en PBS). La membrana se lavó dos veces con tampón de lavado (leche desnatada al 3%, Triton X100 al 0,1% en PBS) y se incubó durante 2 horas a 37ºC con sueros de ratón diluidos 1:200 en tampón de lavado. La membrana se lavó dos veces y se incubó durante 90 minutos con una dilución 1:2000 de anti-Ig de ratón marcada con peroxidasa de rábano. La membrana se lavó dos veces con Triton X100 al 0,1% en PBS y se reveló con el kit de sustrato Opti-4CN (Bio-Rad). La reacción se detuvo añadiendo agua.

Las VME (vesículas de membrana externa) se prepararon como sigue: la cepa 2996 de *N. meningitidis* se cultivó durante la noche a 37ºC con CO_2 al 5% en 5 placas GC, se recolectó con un asa de siembra y se resuspendió en 10 ml de Tris-HCl 20 mM, pH 7,5, EDTA 2 mM. La inactivación con calor se realizó a 56ºC durante 45 minutos y las bacterias se rompieron mediante sonicación durante 5 min en hielo (50% del ciclo de servicio, 50% de salida, micropunta de 3 mm de sonicador Branson). Las células sin romper se retiraron mediante centrifugaciópn a 5000 g durante 10 minutos, el sobrenadante que contenía la fracción de la envuelta celular total se recuperó y se volvió a centrifugar durante la noche a 50000 g a una temperatura de 4ºC. El sedimento que contenía las membranas se resuspendió en Sarkosyl al 2%, Tris-HCl 20 mM, pH 7,5, EDTA 2 mM, y se incubó a temperatura ambiente durante 20 minutos para solubilizar las membranas internas. La suspensión se centrífugo a 1000 g durante 10 minutos para retirar los agregados, y el sobrenadante se volvió a centrifugar a 50000 g durante 3 horas. El sedimento, que contenía las membranas externas, se lavó en PBS y se resuspendió en el mismo tampón. La concentración de proteínas se midió mediante el ensayo de proteínas D.C. Bio-Rad (procedimiento de Lowry modificado), utilizando BSA como patrón.

Los extractos de células totales se prepararon como sigue: la cepa 2996 de *N. meningitidis* se cultivó durante la noche en una placa GC, se recolectó con un asa de siembra y se resuspendió en 1 ml de Tris-HCl 20 mM. La inactivación con calor se realizó a 56ºC durante 30 minutos.

Listado de secuencias

<110> Novartis Vaccines and Diagnostics SRL

<120> Expresión híbrida de proteínas e *Neisseriales*

<130> P048826EP

<150> EP-01914098.7

<151> 28 de febrero de 2001

<150> PCT/IB01/00420

<151> 28 de febrero 2001

<150> GB 0004695.3

<151> 28 de febrero 200

<150> GB0027875.8

<151> 13 de noviembre 2000

<160> 121

<170> SeqWin99, versión 1.02

<210> 1

<211> 608

<212> PRT

<213> *Neisseria meningitidis*

<400> 1

```
Leu Gly Ile Ser Arg Lys Ile Ser Leu Ile Leu Ser Ile Leu Ala Val
1               5                   10                  15

Cys Leu Pro Met His Ala His Ala Ser Asp Leu Ala Asn Asp Ser Phe
            20                  25                  30

Ile Arg Gln Val Leu Asp Arg Gln His Phe Glu Pro Asp Gly Lys Tyr
        35                  40                  45

His Leu Phe Gly Ser Arg Gly Glu Leu Ala Glu Arg Ser Gly His Ile
    50                  55                  60

Gly Leu Gly Lys Ile Gln Ser His Gln Leu Gly Asn Leu Met Ile Gln
65                  70                  75                  80

Gln Ala Ala Ile Lys Gly Asn Ile Gly Tyr Ile Val Arg Phe Ser Asp
                85                  90                  95

His Gly His Glu Val His Ser Pro Phe Asp Asn His Ala Ser His Ser
            100                 105                 110

Asp Ser Asp Glu Ala Gly Ser Pro Val Asp Gly Phe Ser Leu Tyr Arg
        115                 120                 125

Ile His Trp Asp Gly Tyr Glu His His Pro Ala Asp Gly Tyr Asp Gly
    130                 135                 140

Pro Gln Gly Gly Gly Tyr Pro Ala Pro Lys Gly Ala Arg Asp Ile Tyr
145                 150                 155                 160

Ser Tyr Asp Ile Lys Gly Val Ala Gln Asn Ile Arg Leu Asn Leu Thr
```

```
                165                 170                 175

Asp Asn Arg Ser Thr Gly Gln Arg Leu Ala Asp Arg Phe His Asn Ala
            180                 185                 190

Gly Ser Met Leu Thr Gln Gly Val Gly Asp Gly Phe Lys Arg Ala Thr
        195                 200                 205

Arg Tyr Ser Pro Glu Leu Asp Arg Ser Gly Asn Ala Ala Glu Ala Phe
    210                 215                 220

Asn Gly Thr Ala Asp Ile Val Lys Asn Ile Ile Gly Ala Ala Gly Glu
225                 230                 235                 240

Ile Val Gly Ala Gly Asp Ala Val Gln Gly Ile Ser Glu Gly Ser Asn
                245                 250                 255

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

Ala Arg Ile Asn Asp Leu Ala Asp Met Ala Gln Leu Lys Asp Tyr Ala
        275                 280                 285

Ala Ala Ala Ile Arg Asp Trp Ala Val Gln Asn Pro Asn Ala Ala Gln
    290                 295                 300

Gly Ile Glu Ala Val Ser Asn Ile Phe Met Ala Ala Ile Pro Ile Lys
305                 310                 315                 320

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

His Pro Ile Lys Arg Ser Gln Met Gly Ala Ile Ala Leu Pro Lys Gly
            340                 345                 350

Lys Ser Ala Val Ser Asp Asn Phe Ala Asp Ala Ala Tyr Ala Lys Tyr
        355                 360                 365

Pro Ser Pro Tyr His Ser Arg Asn Ile Arg Ser Asn Leu Glu Gln Arg
    370                 375                 380

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

Lys Asn Val Lys Leu Ala Asp Gln Arg His Pro Lys Thr Gly Val Pro
                405                 410                 415

Phe Asp Gly Lys Gly Phe Pro Asn Phe Glu Lys His Val Lys Tyr Asp
            420                 425                 430

Thr Lys Leu Asp Ile Gln Glu Leu Ser Gly Gly Gly Ile Pro Lys Ala
        435                 440                 445

Lys Pro Val Ser Asp Ala Lys Pro Arg Trp Glu Val Asp Arg Lys Leu
    450                 455                 460

Asn Lys Leu Thr Thr Arg Glu Gln Val Glu Lys Asn Val Gln Glu Ile
465                 470                 475                 480

Arg Asn Gly Asn Lys Asn Ser Asn Phe Ser Gln His Ala Gln Leu Glu
                485                 490                 495
```

```
Arg Glu Ile Asn Lys Leu Lys Ser Ala Asp Glu Ile Asn Phe Ala Asp
            500                 505                 510

Gly Met Gly Lys Phe Thr Asp Ser Met Asn Asp Lys Ala Phe Ser Arg
        515                 520                 525

Leu Val Lys Ser Val Lys Glu Asn Gly Phe Thr Asn Pro Val Val Glu
    530                 535                 540

Tyr Val Glu Ile Asn Gly Lys Ala Tyr Ile Val Arg Gly Asn Asn Arg
545                 550                 555                 560

Val Phe Ala Ala Glu Tyr Leu Gly Arg Ile His Glu Leu Lys Phe Lys
                565                 570                 575

Lys Val Asp Phe Pro Val Pro Asn Thr Ser Trp Lys Asn Pro Thr Asp
            580                 585                 590

Val Leu Asn Glu Ser Gly Asn Val Lys Arg Pro Arg Tyr Arg Ser Lys
        595                 600                 605
```

<210> 2

<211> 464

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG287

<400> 2

```
Ser Pro Asp Val Lys Ser Ala Asp Thr Leu Ser Lys Pro Ala Ala Pro
1               5                   10                  15

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

Gly Ser Gln Gly Gln Gly Ala Pro Ser Ala Gln Gly Ser Gln Asp Met
        35                  40                  45

Ala Ala Val Ser Glu Glu Asn Thr Gly Asn Gly Gly Ala Val Thr Ala
    50                  55                  60

Asp Asn Pro Lys Asn Glu Asp Glu Val Ala Gln Asn Asp Met Pro Gln
65                  70                  75                  80

Asn Ala Ala Gly Thr Asp Ser Ser Thr Pro Asn His Thr Pro Asp Pro
                85                  90                  95

Asn Met Leu Ala Gly Asn Met Glu Asn Gln Ala Thr Asp Ala Gly Glu
            100                 105                 110

Ser Ser Gln Pro Ala Asn Gln Pro Asp Met Ala Asn Ala Ala Asp Gly
        115                 120                 125

Met Gln Gly Asp Asp Pro Ser Ala Gly Gly Gln Asn Ala Gly Asn Thr
    130                 135                 140

Ala Ala Gln Gly Ala Asn Gln Ala Gly Asn Asn Gln Ala Ala Gly Ser
145                 150                 155                 160
```

```
Ser Asp Pro Ile Pro Ala Ser Asn Pro Ala Pro Ala Asn Gly Gly Ser
                165                 170                 175

Asn Phe Gly Arg Val Asp Leu Ala Asn Gly Val Leu Ile Asp Gly Pro
            180                 185                 190

Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser Cys Ser Gly
        195                 200                 205

Asn Asn Phe Leu Asp Glu Glu Val Gln Leu Lys Ser Glu Phe Glu Lys
    210                 215                 220

Leu Ser Asp Ala Asp Lys Ile Ser Asn Tyr Lys Lys Asp Gly Lys Asn
225                 230                 235                 240

Asp Lys Phe Val Gly Leu Val Ala Asp Ser Val Gln Met Lys Gly Ile
                245                 250                 255

Asn Gln Tyr Ile Ile Phe Tyr Lys Pro Lys Pro Thr Ser Phe Ala Arg
            260                 265                 270

Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser Leu Pro Ala Glu Met Pro
        275                 280                 285

Leu Ile Pro Val Asn Gln Ala Asp Thr Leu Ile Val Asp Gly Glu Ala
    290                 295                 300

Val Ser Leu Thr Gly His Ser Gly Asn Ile Phe Ala Pro Glu Gly Asn
305                 310                 315                 320

Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys Leu Pro Gly Gly Ser Tyr
                325                 330                 335

Ala Leu Arg Val Gln Gly Glu Pro Ala Lys Gly Glu Met Leu Ala Gly
            340                 345                 350

Ala Ala Val Tyr Asn Gly Glu Val Leu His Phe His Thr Glu Asn Gly
        355                 360                 365

Arg Pro Tyr Pro Thr Arg Gly Arg Phe Ala Ala Lys Val Asp Phe Gly
    370                 375                 380

Ser Lys Ser Val Asp Gly Ile Ile Asp Ser Gly Asp Asp Leu His Met
385                 390                 395                 400

Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp Gly Asn Gly Phe Lys Gly
                405                 410                 415

Thr Trp Thr Glu Asn Gly Ser Gly Asp Val Ser Gly Lys Phe Tyr Gly
            420                 425                 430

Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr Ser Tyr Arg Pro Thr Asp
        435                 440                 445

Ala Glu Lys Gly Gly Phe Gly Val Phe Ala Gly Lys Lys Glu Gln Asp
    450                 455                 460
```

<210> 3

<211> 2505

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG287-919

<400> 3

```
atggctagcc ccgatgttaa atcggcggac acgctgtcaa aaccggccgc tcctgttgtt    60
gctgaaaaag agacagaggt aaaagaagat gcgccacagg caggttctca aggacagggc   120
gcgccatcca cacaaggcag ccaagatatg gcggcagttt cggcagaaaa tacaggcaat   180
ggcggtgcgg caacaacgga caaacccaaa aatgaagacg agggaccgca aaatgatatg   240
ccgcaaaatt ccgccgaatc cgcaaatcaa acagggaaca accaacccgc cgattcttca   300
gattccgccc ccgcgtcaaa ccctgcacct gcgaatggcg gtagcaattt tggaagggtt   360
gatttggcta atggcgtttt gattgatggg ccgtcgcaaa atataacgtt gacccactgt   420
aaaggcgatt cttgtaatgg tgataattta ttggatgaag aagcaccgtc aaaatcagaa   480
tttgaaaatt taaatgagtc tgaacgaatt gagaaatata agaaagatgg gaaaagcgat   540
aaatttacta atttggttgc gacagcagtt caagctaatg gaactaacaa atatgtcatc   600
atttataaag acaagtccgc ttcatcttca tctgcgcgat tcaggcgttc tgcacggtcg   660
aggaggtcgc ttcctgccga gatgccgcta atccccgtca atcaggcgga tacgctgatt   720
gtcgatgggg aagcggtcag cctgacgggg cattccggca atatcttcgc gcccgaaggg   780
aattaccggt atctgactta cggggcggaa aaattgcccg gcggatcgta tgccctccgt   840
gtgcaaggcg aaccggcaaa aggcgaaatg cttgctggca cggccgtgta caacggcgaa   900
gtgctgcatt ttcatacgga aaacggccgt ccgtacccga ctagaggcag gtttgccgca   960
aaagtcgatt tcggcagcaa atctgtggac ggcattatcg acagcggcga tgatttgcat  1020
atgggtacgc aaaaattcaa agccgccatc gatggaaacg gctttaaggg gacttggacg  1080
gaaaatggcg gcggggatgt ttccggaagg ttttacggcc cggccggcga ggaagtggcg  1140
ggaaaataca gctatcgccc gacagatgcg gaaaagggcg gattcggcgt gtttgccggc  1200
aaaaaagagc aggatggatc cggaggagga ggatgccaaa gcaagagcat ccaaaccttt  1260
ccgcaacccg acacatccgt catcaacggc ccggaccggc cggtcggcat ccccgacccc  1320
gccggaacga cggtcggcgg cggcggggcc gtctataccg ttgtaccgca cctgtccctg  1380
ccccactggg cggcgcagga tttcgccaaa agcctgcaat ccttccgcct cggctgcgcc  1440
aatttgaaaa accgccaagg ctggcaggat gtgtgcgccc aagcctttca aacccccgtc  1500
cattcctttc aggcaaaaca gtttttgaa cgctatttca cgccgtggca ggttgcaggc  1560
aacggaagcc ttgccggtac ggttaccggc tattacgagc cggtgctgaa gggcgacgac  1620
aggcggacgg cacaagcccg cttcccgatt tacggtattc ccgacgattt tatctccgtc  1680
cccctgcctg ccggtttgcg gagcggaaaa gcccttgtcc gcatcaggca gacgggaaaa  1740
aacagcggca caatcgacaa taccggcggc acacataccg ccgacctctc ccgattcccc  1800
atcaccgcgc gcacaacggc aatcaaaggc aggtttgaag gaagccgctt cctcccctac  1860
cacacgcgca accaaatcaa cggcggcgcg cttgacggca aagccccgat actcggttac  1920
gccgaagacc ccgtcgaact ttttttatg cacatccaag gctcgggccg tctgaaaacc  1980
ccgtccggca aatacatccg catcggctat gccgacaaaa acgaacatcc ctacgtttcc  2040
atcggacgct atatggcgga caaaggctac ctcaagctcg ggcagacctc gatgcagggc  2100
atcaaagcct atatgcggca aaatccgcaa cgcctcgccg aagttttggg tcaaaacccc  2160
agctatatct tttccgcga gcttgccgga agcagcaatg acggtcccgt cggcgcactg  2220
ggcacgccgt tgatggggga atatgccggc gcagtcgacc ggcactacat taccttgggc  2280
gcgcccttat ttgtcgccac cgcccatccg gttacccgca aagccctcaa ccgcctgatt  2340
atggcgcagg ataccggcag cgcgattaaa ggcgcggtgc gcgtggatta tttttgggga  2400
tacggcgacg aagccggcga acttgccggc aaacagaaaa ccacgggtta cgtctggcag  2460
ctcctaccca acggtatgaa gcccgaatac cgcccgtaac tcgag                   2505
```

<210> 4

<211> 832

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG287-919

<400> 4

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

```
Ala Pro Val Val Ala Glu Lys Glu Thr Glu Val Lys Glu Asp Ala Pro
            20                  25                  30

Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Thr Gln Gly Ser Gln
        35                  40                  45

Asp Met Ala Ala Val Ser Ala Glu Asn Thr Gly Asn Gly Gly Ala Ala
    50                  55                  60

Thr Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Pro Gln Asn Asp Met
65                  70                  75                  80

Pro Gln Asn Ser Ala Glu Ser Ala Asn Gln Thr Gly Asn Asn Gln Pro
                85                  90                  95

Ala Asp Ser Ser Asp Ser Ala Pro Ala Ser Asn Pro Ala Pro Ala Asn
            100                 105                 110

Gly Gly Ser Asn Phe Gly Arg Val Asp Leu Ala Asn Gly Val Leu Ile
        115                 120                 125

Asp Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser
    130                 135                 140

Cys Asn Gly Asp Asn Leu Leu Asp Glu Glu Ala Pro Ser Lys Ser Glu
145                 150                 155                 160

Phe Glu Asn Leu Asn Glu Ser Glu Arg Ile Glu Lys Tyr Lys Lys Asp
                165                 170                 175

Gly Lys Ser Asp Lys Phe Thr Asn Leu Val Ala Thr Ala Val Gln Ala
            180                 185                 190

Asn Gly Thr Asn Lys Tyr Val Ile Ile Tyr Lys Asp Lys Ser Ala Ser
        195                 200                 205

Ser Ser Ser Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser Leu
    210                 215                 220

Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu Ile
225                 230                 235                 240

Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile Phe
                245                 250                 255

Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys Leu
            260                 265                 270

Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro Ala Lys Gly
        275                 280                 285

Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His Phe
    290                 295                 300

His Thr Glu Asn Gly Arg Pro Tyr Pro Thr Arg Gly Arg Phe Ala Ala
305                 310                 315                 320

Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile Asp Ser Gly
                325                 330                 335
```

```
Asp Asp Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp Gly
            340                 345                 350

Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val Ser
        355                 360                 365

Gly Arg Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr Ser
    370                 375                 380

Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala Gly
385                 390                 395                 400

Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Cys Gln Ser Lys Ser
                405                 410                 415

Ile Gln Thr Phe Pro Gln Pro Asp Thr Ser Val Ile Asn Gly Pro Asp
            420                 425                 430

Arg Pro Val Gly Ile Pro Asp Pro Ala Gly Thr Thr Val Gly Gly Gly
        435                 440                 445

Gly Ala Val Tyr Thr Val Val Pro His Leu Ser Leu Pro His Trp Ala
    450                 455                 460

Ala Gln Asp Phe Ala Lys Ser Leu Gln Ser Phe Arg Leu Gly Cys Ala
465                 470                 475                 480

Asn Leu Lys Asn Arg Gln Gly Trp Gln Asp Val Cys Ala Gln Ala Phe
                485                 490                 495

Gln Thr Pro Val His Ser Phe Gln Ala Lys Gln Phe Phe Glu Arg Tyr
            500                 505                 510

Phe Thr Pro Trp Gln Val Ala Gly Asn Gly Ser Leu Ala Gly Thr Val
        515                 520                 525

Thr Gly Tyr Tyr Glu Pro Val Leu Lys Gly Asp Asp Arg Arg Thr Ala
    530                 535                 540

Gln Ala Arg Phe Pro Ile Tyr Gly Ile Pro Asp Asp Phe Ile Ser Val
545                 550                 555                 560

Pro Leu Pro Ala Gly Leu Arg Ser Gly Lys Ala Leu Val Arg Ile Arg
                565                 570                 575

Gln Thr Gly Lys Asn Ser Gly Thr Ile Asp Asn Thr Gly Gly Thr His
            580                 585                 590

Thr Ala Asp Leu Ser Arg Phe Pro Ile Thr Ala Arg Thr Thr Ala Ile
        595                 600                 605

Lys Gly Arg Phe Glu Gly Ser Arg Phe Leu Pro Tyr His Thr Arg Asn
    610                 615                 620

Gln Ile Asn Gly Gly Ala Leu Asp Gly Lys Ala Pro Ile Leu Gly Tyr
625                 630                 635                 640

Ala Glu Asp Pro Val Glu Leu Phe Phe Met His Ile Gln Gly Ser Gly
                645                 650                 655

Arg Leu Lys Thr Pro Ser Gly Lys Tyr Ile Arg Ile Gly Tyr Ala Asp
```

```
            660                 665                 670

Lys Asn Glu His Pro Tyr Val Ser Ile Gly Arg Tyr Met Ala Asp Lys
        675                 680                 685

Gly Tyr Leu Lys Leu Gly Gln Thr Ser Met Gln Gly Ile Lys Ala Tyr
    690                 695                 700

Met Arg Gln Asn Pro Gln Arg Leu Ala Glu Val Leu Gly Gln Asn Pro
705                 710                 715                 720

Ser Tyr Ile Phe Phe Arg Glu Leu Ala Gly Ser Ser Asn Asp Gly Pro
                725                 730                 735

Val Gly Ala Leu Gly Thr Pro Leu Met Gly Glu Tyr Ala Gly Ala Val
            740                 745                 750

Asp Arg His Tyr Ile Thr Leu Gly Ala Pro Leu Phe Val Ala Thr Ala
        755                 760                 765

His Pro Val Thr Arg Lys Ala Leu Asn Arg Leu Ile Met Ala Gln Asp
    770                 775                 780

Thr Gly Ser Ala Ile Lys Gly Ala Val Arg Val Asp Tyr Phe Trp Gly
785                 790                 795                 800

Tyr Gly Asp Glu Ala Gly Glu Leu Ala Gly Lys Gln Lys Thr Thr Gly
                805                 810                 815

Tyr Val Trp Gln Leu Leu Pro Asn Gly Met Lys Pro Glu Tyr Arg Pro
            820                 825                 830
```

<210> 5

<211> 1746

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG287-953

<400> 5

```
atggctagcc ccgatgttaa atcggcggac acgctgtcaa aaccggccgc tcctgttgtt   60
gctgaaaaag agacagaggt aaaagaagat gcgccacagg caggttctca aggacagggc  120
gcgccatcca cacaaggcag ccaagatatg gcggcagttt cggcagaaaa tacaggcaat  180
ggcggtgcgg caacaacgga caaacccaaa aatgaagacg agggaccgca aaatgatatg  240
ccgcaaaatt ccgccgaatc cgcaaatcaa acagggaaca accaacccgc cgattcttca  300
gattccgccc ccgcgtcaaa ccctgcacct gcgaatggcg gtagcaattt tggaagggtt  360
gatttggcta atggcgtttt gattgatggg ccgtcgcaaa atataacgtt gacccactgt  420
aaaggcgatt cttgtaatgg tgataattta ttggatgaag aagcaccgtc aaaatcagaa  480
tttgaaaatt taaatgagtc tgaacgaatt gagaaatata agaaagatgg gaaaagcgat  540
aaatttacta atttggttgc gacagcagtt caagctaatg gaactaacaa atatgtcatc  600
atttataaag acaagtccgc ttcatcttca tctgcgcgat tcaggcgttc tgcacggtcg  660
aggaggtcgc ttcctgccga gatgccgcta atccccgtca atcaggcgga tacgctgatt  720
gtcgatgggg aagcggtcag cctgacgggg cattccggca atatcttcgc gcccgaaggg  780
aattaccggt atctgactta cggggcggaa aaattgcccg gcggatcgta tgccctccgt  840
gtgcaaggcg aaccggcaaa aggcgaaatg cttgctggca cggccgtgta caacggcgaa  900
gtgctgcatt ttcatacgga aaacggccgt ccgtacccga ctagaggcag gtttgccgca  960
aaagtcgatt tcggcagcaa atctgtggac ggcattatcg acagcggcga tgatttgcat 1020
atgggtacgc aaaaattcaa agccgccatc gatggaaacg gctttaaggg gacttggacg 1080
gaaaatggcg gcggggatgt ttccggaagg ttttacggcc cggccggcga ggaagtggcg 1140

ggaaaataca gctatcgccc gacagatgcg gaaaagggcg gattcggcgt gtttgccggc 1200
aaaaaagagc aggatggatc cggaggagga ggagccacct acaaagtgga cgaatatcac 1260
gccaacgccc gtttcgccat cgaccatttc aacaccagca ccaacgtcgg cggtttttac 1320
ggtctgaccg gttccgtcga gttcgaccaa gcaaaacgcg acggtaaaat cgacatcacc 1380
atccccgttg ccaacctgca aagcggttcg caacacttta ccgaccacct gaaatcagcc 1440
gacatcttcg atgccgccca atatccggac atccgctttg tttccaccaa attcaacttc 1500
aacggcaaaa aactggtttc cgttgacggc aacctgacca tgcacggcaa aaccgccccc 1560
gtcaaactca aagccgaaaa attcaactgc taccaaagcc cgatggcgaa aaccgaagtt 1620
tgcggcggcg acttcagcac caccatcgac cgcaccaaat ggggcgtgga ctacctcgtt 1680
aacgttggta tgaccaaaag cgtccgcatc gacatccaaa tcgaggcagc caaacaataa 1740
ctcgag                                                            1746
```

<210> 6

<211> 579

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG287-953

<400> 6

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

Ala Pro Val Val Ala Glu Lys Glu Thr Glu Val Lys Glu Asp Ala Pro
            20                  25                  30

Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Thr Gln Gly Ser Gln
        35                  40                  45

Asp Met Ala Ala Val Ser Ala Glu Asn Thr Gly Asn Gly Gly Ala Ala
    50                  55                  60

Thr Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Pro Gln Asn Asp Met
65                  70                  75                  80

Pro Gln Asn Ser Ala Glu Ser Ala Asn Gln Thr Gly Asn Asn Gln Pro
                85                  90                  95

Ala Asp Ser Ser Asp Ser Ala Pro Ala Ser Asn Pro Ala Pro Ala Asn
            100                 105                 110

Gly Gly Ser Asn Phe Gly Arg Val Asp Leu Ala Asn Gly Val Leu Ile
        115                 120                 125

Asp Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser
    130                 135                 140

Cys Asn Gly Asp Asn Leu Leu Asp Glu Glu Ala Pro Ser Lys Ser Glu
145                 150                 155                 160

Phe Glu Asn Leu Asn Glu Ser Glu Arg Ile Glu Lys Tyr Lys Lys Asp
                165                 170                 175

Gly Lys Ser Asp Lys Phe Thr Asn Leu Val Ala Thr Ala Val Gln Ala
            180                 185                 190

Asn Gly Thr Asn Lys Tyr Val Ile Ile Tyr Lys Asp Lys Ser Ala Ser
        195                 200                 205

Ser Ser Ser Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser Leu
```

```
    210                 215                 220

Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu Ile
225                 230                 235                 240

Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile Phe
                245                 250                 255

Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys Leu
            260                 265                 270

Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro Ala Lys Gly
        275                 280                 285

Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His Phe
    290                 295                 300

His Thr Glu Asn Gly Arg Pro Tyr Pro Thr Arg Gly Arg Phe Ala Ala
305                 310                 315                 320

Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile Asp Ser Gly
                325                 330                 335

Asp Asp Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp Gly
            340                 345                 350

Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val Ser
        355                 360                 365

Gly Arg Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr Ser
    370                 375                 380

Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala Gly
385                 390                 395                 400

Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Ala Thr Tyr Lys Val
                405                 410                 415

Asp Glu Tyr His Ala Asn Ala Arg Phe Ala Ile Asp His Phe Asn Thr
            420                 425                 430

Ser Thr Asn Val Gly Gly Phe Tyr Gly Leu Thr Gly Ser Val Glu Phe
        435                 440                 445

Asp Gln Ala Lys Arg Asp Gly Lys Ile Asp Ile Thr Ile Pro Val Ala
    450                 455                 460

Asn Leu Gln Ser Gly Ser Gln His Phe Thr Asp His Leu Lys Ser Ala
465                 470                 475                 480

Asp Ile Phe Asp Ala Ala Gln Tyr Pro Asp Ile Arg Phe Val Ser Thr
                485                 490                 495

Lys Phe Asn Phe Asn Gly Lys Lys Leu Val Ser Val Asp Gly Asn Leu
            500                 505                 510

Thr Met His Gly Lys Thr Ala Pro Val Lys Leu Lys Ala Glu Lys Phe
        515                 520                 525

Asn Cys Tyr Gln Ser Pro Met Ala Lys Thr Glu Val Cys Gly Gly Asp
    530                 535                 540
```

```
Phe Ser Thr Thr Ile Asp Arg Thr Lys Trp Gly Val Asp Tyr Leu Val
545                 550                 555                 560

Asn Val Gly Met Thr Lys Ser Val Arg Ile Asp Ile Gln Ile Glu Ala
                565                 570                 575

Ala Lys Gln
```

<210> 7

<211> 2388

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG287-961

<400> 7

```
atggctagcc ccgatgttaa atcggcggac acgctgtcaa aaccggccgc tcctgttgtt   60
gctgaaaaag agacagaggt aaaagaagat gcgccacagg caggttctca aggacagggc  120
gcgccatcca cacaaggcag ccaagatatg gcggcagttt cggcagaaaa tacaggcaat  180
ggcggtgcgg caacaacgga caaacccaaa aatgaagacg agggaccgca aaatgatatg  240
ccgcaaaatt ccgccgaatc cgcaaatcaa acagggaaca accaacccgc cgattcttca  300
gattccgccc ccgcgtcaaa ccctgcacct gcgaatggcg gtagcaattt tggaagggtt  360
gatttggcta atggcgtttt gattgatggg ccgtcgcaaa atataacgtt gacccactgt  420
aaaggcgatt cttgtaatgg tgataattta ttggatgaag aagcaccgtc aaaatcagaa  480
tttgaaaatt taaatgagtc tgaacgaatt gagaaatata agaaagatgg gaaaagcgat  540
aaatttacta atttggttgc gacagcagtt caagctaatg gaactaacaa atatgtcatc  600
atttataaag acaagtccgc ttcatcttca tctgcgcgat tcaggcgttc tgcacggtcg  660
aggaggtcgc ttcctgccga gatgccgcta atccccgtca atcaggcgga tacgctgatt  720
gtcgatgggg aagcggtcag cctgacgggg cattccggca atatcttcgc gcccgaaggg  780
aattaccggt atctgactta cggggcggaa aaattgcccg gcggatcgta tgccctccgt  840
gtgcaaggcg aaccggcaaa aggcgaaatg cttgctggca cggccgtgta caacggcgaa  900
gtgctgcatt ttcatacgga aaacggccgt ccgtacccga ctagaggcag gtttgccgca  960
aaagtcgatt tcggcagcaa atctgtggac ggcattatcg acagcggcga tgatttgcat 1020
atgggtacgc aaaaattcaa agccgccatc gatggaaacg gctttaaggg gacttggacg 1080
gaaaatggcg gcggggatgt ttccggaagg ttttacggcc cggccggcga ggaagtggcg 1140
ggaaaataca gctatcgccc gacagatgcg gaaaagggcg gattcggcgt gtttgccggc 1200
aaaaaagagc aggatggatc cggaggagga ggagccacaa acgacgacga tgttaaaaaa 1260
gctgccactg tggccattgc tgctgcctac aacaatggcc aagaaatcaa cggtttcaaa 1320
gctggagaga ccatctacga cattgatgaa gacggcacaa ttaccaaaaa agacgcaact 1380
gcagccgatg ttgaagccga cgactttaaa ggtctgggtc tgaaaaaagt cgtgactaac 1440
ctgaccaaaa ccgtcaatga aaacaaacaa aacgtcgatg ccaaagtaaa agctgcagaa 1500
tctgaaatag aaaagttaac aaccaagtta gcagacactg atgccgcttt agcagatact 1560
gatgccgctc tggatgcaac caccaacgcc ttgaataaat tgggagaaaa tataacgaca 1620
tttgctgaag agactaagac aaatatcgta aaaattgatg aaaaattaga agccgtggct 1680
gataccgtcg acaagcatgc cgaagcattc aacgatatcg ccgattcatt ggatgaaacc 1740
aacactaagg cagacgaagc cgtcaaaacc gccaatgaag ccaaacagac ggccgaagaa 1800
accaaacaaa acgtcgatgc caaagtaaaa gctgcagaaa ctgcagcagg caaagccgaa 1860
gctgccgctg gcacagctaa tactgcagcc gacaaggccg aagctgtcgc tgcaaaagtt 1920
accgacatca aagctgatat cgctacgaac aaagataata ttgctaaaaa agcaaacagt 1980
gccgacgtgt acaccagaga agagtctgac agcaaatttg tcagaattga tggtctgaac 2040
gctactaccg aaaaattgga cacacgcttg gcttctgctg aaaaatccat tgccgatcac 2100
gatactcgcc tgaacggttt ggataaaaca gtgtcagacc tgcgcaaaga aacccgccaa 2160
ggccttgcag aacaagccgc gctctccggt ctgttccaac cttacaacgt gggtcggttc 2220
aatgtaacgg ctgcagtcgg cggctacaaa tccgaatcgg cagtcgccat cggtaccggc 2280
ttccgcttta ccgaaaactt tgccgccaaa gcaggcgtgg cagtcggcac ttcgtccggt 2340
tcttccgcag cctaccatgt cggcgtcaat tacgagtggt aactcgag             2388
```

<210> 8

<211> 793

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG287-961

<400> 8

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

Ala Pro Val Val Ala Glu Lys Glu Thr Glu Val Lys Glu Asp Ala Pro
            20                  25                  30

Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Thr Gln Gly Ser Gln
        35                  40                  45

Asp Met Ala Ala Val Ser Ala Glu Asn Thr Gly Asn Gly Gly Ala Ala
    50                  55                  60

Thr Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Pro Gln Asn Asp Met
65                  70                  75                  80

Pro Gln Asn Ser Ala Glu Ser Ala Asn Gln Thr Gly Asn Asn Gln Pro
                85                  90                  95

Ala Asp Ser Ser Asp Ser Ala Pro Ala Ser Asn Pro Ala Pro Ala Asn
            100                 105                 110

Gly Gly Ser Asn Phe Gly Arg Val Asp Leu Ala Asn Gly Val Leu Ile
        115                 120                 125

Asp Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser
    130                 135                 140

Cys Asn Gly Asp Asn Leu Leu Asp Glu Glu Ala Pro Ser Lys Ser Glu
145                 150                 155                 160

Phe Glu Asn Leu Asn Glu Ser Glu Arg Ile Glu Lys Tyr Lys Lys Asp
                165                 170                 175

Gly Lys Ser Asp Lys Phe Thr Asn Leu Val Ala Thr Ala Val Gln Ala
            180                 185                 190

Asn Gly Thr Asn Lys Tyr Val Ile Ile Tyr Lys Asp Lys Ser Ala Ser
        195                 200                 205

Ser Ser Ser Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser Leu
    210                 215                 220

Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu Ile
225                 230                 235                 240

Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile Phe
                245                 250                 255

Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys Leu
            260                 265                 270

Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro Ala Lys Gly
        275                 280                 285
```

```
Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His Phe
    290                 295                 300

His Thr Glu Asn Gly Arg Pro Tyr Pro Thr Arg Gly Arg Phe Ala Ala
305                 310                 315                 320

Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile Asp Ser Gly
                325                 330                 335

Asp Asp Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp Gly
            340                 345                 350

Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val Ser
        355                 360                 365

Gly Arg Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr Ser
    370                 375                 380

Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala Gly
385                 390                 395                 400

Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Ala Thr Asn Asp Asp
                405                 410                 415

Asp Val Lys Lys Ala Ala Thr Val Ala Ile Ala Ala Ala Tyr Asn Asn
            420                 425                 430

Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly Glu Thr Ile Tyr Asp Ile
        435                 440                 445

Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp Ala Thr Ala Ala Asp Val
    450                 455                 460

Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu Lys Lys Val Val Thr Asn
465                 470                 475                 480

Leu Thr Lys Thr Val Asn Glu Asn Lys Gln Asn Val Asp Ala Lys Val
                485                 490                 495

Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu Thr Thr Lys Leu Ala Asp
            500                 505                 510

Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala Ala Leu Asp Ala Thr Thr
        515                 520                 525

Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile Thr Thr Phe Ala Glu Glu
    530                 535                 540

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

Asp Thr Val Asp Lys His Ala Glu Ala Phe Asn Asp Ile Ala Asp Ser
                565                 570                 575

Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu Ala Val Lys Thr Ala Asn
            580                 585                 590

Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys Gln Asn Val Asp Ala Lys
        595                 600                 605
```

```
Val Lys Ala Ala Glu Thr Ala Ala Gly Lys Ala Glu Ala Ala Ala Gly
    610                 615                 620

Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu Ala Val Ala Ala Lys Val
625                 630                 635                 640

Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn Lys Asp Asn Ile Ala Lys
                645                 650                 655

Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg Glu Glu Ser Asp Ser Lys
            660                 665                 670

Phe Val Arg Ile Asp Gly Leu Asn Ala Thr Thr Glu Lys Leu Asp Thr
        675                 680                 685

Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala Asp His Asp Thr Arg Leu
    690                 695                 700

Asn Gly Leu Asp Lys Thr Val Ser Asp Leu Arg Lys Glu Thr Arg Gln
705                 710                 715                 720

Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Asn
                725                 730                 735

Val Gly Arg Phe Asn Val Thr Ala Ala Val Gly Gly Tyr Lys Ser Glu
            740                 745                 750

Ser Ala Val Ala Ile Gly Thr Gly Phe Arg Phe Thr Glu Asn Phe Ala
        755                 760                 765

Ala Lys Ala Gly Val Ala Val Gly Thr Ser Ser Gly Ser Ser Ala Ala
    770                 775                 780

Tyr His Val Gly Val Asn Tyr Glu Trp
785                 790
```

<210> 9

<211> 2700

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG287NZ-919

<400> 9

```
atggctagcc ccgatgtcaa gtcggcggac acgctgtcaa aacctgccgc ccctgttgtt   60
tctgaaaaag agacagaggc aaaggaagat gcgccacagg caggttctca aggacagggc  120
gcgccatccg cacaaggcgg tcaagatatg gcggcggttt cggaagaaaa tacaggcaat  180
ggcggtgcgg cagcaacgga caaacccaaa aatgaagacg agggggcgca aaatgatatg  240
ccgcaaaatg ccgccgatac agatagtttg acaccgaatc acaccccggc ttcgaatatg  300
ccggccggaa atatggaaaa ccaagcaccg gatgccgggg aatcggagca gccggcaaac  360
caaccggata tggcaaatac ggcggacgga atgcagggtg acgatccgtc ggcaggcggg  420
gaaaatgccg gcaatacggc tgcccaaggt acaaatcaag ccgaaaacaa tcaaaccgcc  480
ggttctcaaa atcctgcctc ttcaaccaat cctagcgcca cgaatagcgg tggtgatttt  540
ggaaggacga acgtgggcaa ttctgttgtg attgacgggc cgtcgcaaaa tataacgttg  600
acccactgta aaggcgattc ttgtagtggc aataatttct tggatgaaga agtacagcta  660
aaatcagaat ttgaaaaatt aagtgatgca gacaaaataa gtaattacaa gaaagatggg  720
aagaatgacg ggaagaatga taaatttgtc ggtttggttg ccgatagtgt gcagatgaag  780
ggaatcaatc aatatattat cttttataaa cctaaaccca cttcatttgc gcgatttagg  840
cgttctgcac ggtcgaggcg gtcgcttccg gccgagatgc cgctgattcc cgtcaatcag  900
gcggatacgc tgattgtcga tggggaagcg gtcagcctga cggggcattc cggcaatatc  960

ttcgcgcccg aagggaatta ccggtatctg acttacgggg cggaaaaatt gcccggcgga  1020
tcgtatgccc tccgtgttca aggcgaacct tcaaaaggcg aaatgctcgc gggcacggca  1080
gtgtacaacg gcgaagtgct gcattttcat acggaaaacg gccgtccgtc cccgtccaga  1140
ggcaggtttg ccgcaaaagt cgatttcggc agcaaatctg tggacggcat tatcgacagc  1200
ggcgatggtt tgcatatggg tacgcaaaaa ttcaaagccg ccatcgatgg aaacggcttt  1260
aaggggactt ggacggaaaa tggcggcggg gatgtttccg gaaagtttta cggcccggcc  1320
ggcgaggaag tggcgggaaa atacagctat cgcccaacag atgcggaaaa gggcggattc  1380
ggcgtgtttg ccggcaaaaa agagcaggat ggatccggag gaggaggatg ccaaagcaag  1440
agcatccaaa cctttccgca acccgacaca tccgtcatca acggcccgga ccggccggtc  1500
ggcatccccg accccgccgg aacgacggtc ggcggcggcg gggccgtcta taccgttgta  1560
ccgcacctgt ccctgcccca ctgggcggcg caggatttcg ccaaaagcct gcaatccttc  1620
cgcctcggct gcgccaattt gaaaaaccgc caaggctggc aggatgtgtg cgcccaagcc  1680
tttcaaaccc ccgtccattc ctttcaggca aaacagtttt ttgaacgcta tttcacgccg  1740
tggcaggttg caggcaacgg aagccttgcc ggtacggtta ccggctatta cgagccggtg  1800
ctgaagggcg acgacaggcg gacggcacaa gcccgcttcc cgatttacgg tattcccgac  1860
gattttatct ccgtcccct gcctgccggt ttgcggagcg gaaaagccct tgtccgcatc  1920
aggcagacgg gaaaaaacag cggcacaatc gacaataccg gcggcacaca taccgccgac  1980
ctctcccgat tccccatcac cgcgcgcaca acggcaatca aaggcaggtt tgaaggaagc  2040
cgcttcctcc cctaccacac gcgcaaccaa atcaacggcg gcgcgcttga cggcaaagcc  2100
ccgatactcg gttacgccga agaccccgtc gaactttttt ttatgcacat ccaaggctcg  2160
ggccgtctga aaaccccgtc cggcaaatac atccgcatcg gctatgccga caaaaacgaa  2220
catccctacg tttccatcgg acgctatatg gcggacaaag gctacctcaa gctcgggcag  2280
acctcgatgc agggcatcaa agcctatatg cggcaaaatc cgcaacgcct cgccgaagtt  2340
ttgggtcaaa accccagcta tatctttttc cgcgagcttg ccggaagcag caatgacggt  2400
cccgtcggcg cactgggcac gccgttgatg gggggaatatg ccggcgcagt cgaccggcac  2460
tacattacct tgggcgcgcc cttatttgtc gccaccgccc atccggttac ccgcaaagcc  2520
ctcaaccgcc tgattatggc gcaggatacc ggcagcgcga ttaaaggcgc ggtgcgcgtg  2580
gattattttt ggggatacgg cgacgaagcc ggcgaacttg ccggcaaaca gaaaaccacg  2640
ggttacgtct ggcagctcct acccaacggt atgaagcccg aataccgccc gtaaaagctt  2700
```

<210> 10

<211> 897

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG287NZ-919

<400> 10

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

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

Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Ala Gln Gly Gly Gln
        35                  40                  45

Asp Met Ala Ala Val Ser Glu Glu Asn Thr Gly Asn Gly Gly Ala Ala
    50                  55                  60

Ala Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Ala Gln Asn Asp Met
65                  70                  75                  80

Pro Gln Asn Ala Ala Asp Thr Asp Ser Leu Thr Pro Asn His Thr Pro
                85                  90                  95

Ala Ser Asn Met Pro Ala Gly Asn Met Glu Asn Gln Ala Pro Asp Ala
            100                 105                 110

Gly Glu Ser Glu Gln Pro Ala Asn Gln Pro Asp Met Ala Asn Thr Ala
```

```
        115                 120                 125

Asp Gly Met Gln Gly Asp Asp Pro Ser Ala Gly Gly Glu Asn Ala Gly
    130                 135                 140

Asn Thr Ala Ala Gln Gly Thr Asn Gln Ala Glu Asn Asn Gln Thr Ala
145                 150                 155                 160

Gly Ser Gln Asn Pro Ala Ser Ser Thr Asn Pro Ser Ala Thr Asn Ser
                165                 170                 175

Gly Gly Asp Phe Gly Arg Thr Asn Val Gly Asn Ser Val Val Ile Asp
            180                 185                 190

Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser Cys
        195                 200                 205

Ser Gly Asn Asn Phe Leu Asp Glu Glu Val Gln Leu Lys Ser Glu Phe
    210                 215                 220

Glu Lys Leu Ser Asp Ala Asp Lys Ile Ser Asn Tyr Lys Lys Asp Gly
225                 230                 235                 240

Lys Asn Asp Gly Lys Asn Asp Lys Phe Val Gly Leu Val Ala Asp Ser
                245                 250                 255

Val Gln Met Lys Gly Ile Asn Gln Tyr Ile Ile Phe Tyr Lys Pro Lys
            260                 265                 270

Pro Thr Ser Phe Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser
        275                 280                 285

Leu Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu
    290                 295                 300

Ile Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile
305                 310                 315                 320

Phe Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys
                325                 330                 335

Leu Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro Ser Lys
            340                 345                 350

Gly Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His
        355                 360                 365

Phe His Thr Glu Asn Gly Arg Pro Ser Pro Ser Arg Gly Arg Phe Ala
    370                 375                 380

Ala Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile Asp Ser
385                 390                 395                 400

Gly Asp Gly Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp
                405                 410                 415

Gly Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val
            420                 425                 430

Ser Gly Lys Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr
        435                 440                 445
```

```
Ser Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala
    450                 455                 460

Gly Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Cys Gln Ser Lys
465                 470                 475                 480

Ser Ile Gln Thr Phe Pro Gln Pro Asp Thr Ser Val Ile Asn Gly Pro
                485                 490                 495

Asp Arg Pro Val Gly Ile Pro Asp Pro Ala Gly Thr Thr Val Gly Gly
            500                 505                 510

Gly Gly Ala Val Tyr Thr Val Val Pro His Leu Ser Leu Pro His Trp
        515                 520                 525

Ala Ala Gln Asp Phe Ala Lys Ser Leu Gln Ser Phe Arg Leu Gly Cys
    530                 535                 540

Ala Asn Leu Lys Asn Arg Gln Gly Trp Gln Asp Val Cys Ala Gln Ala
545                 550                 555                 560

Phe Gln Thr Pro Val His Ser Phe Gln Ala Lys Gln Phe Phe Glu Arg
                565                 570                 575

Tyr Phe Thr Pro Trp Gln Val Ala Gly Asn Gly Ser Leu Ala Gly Thr
            580                 585                 590

Val Thr Gly Tyr Tyr Glu Pro Val Leu Lys Gly Asp Asp Arg Arg Thr
        595                 600                 605

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

Val Pro Leu Pro Ala Gly Leu Arg Ser Gly Lys Ala Leu Val Arg Ile
625                 630                 635                 640

Arg Gln Thr Gly Lys Asn Ser Gly Thr Ile Asp Asn Thr Gly Gly Thr
                645                 650                 655

His Thr Ala Asp Leu Ser Arg Phe Pro Ile Thr Ala Arg Thr Thr Ala
            660                 665                 670

Ile Lys Gly Arg Phe Glu Gly Ser Arg Phe Leu Pro Tyr His Thr Arg
        675                 680                 685

Asn Gln Ile Asn Gly Gly Ala Leu Asp Gly Lys Ala Pro Ile Leu Gly
    690                 695                 700

Tyr Ala Glu Asp Pro Val Glu Leu Phe Phe Met His Ile Gln Gly Ser
705                 710                 715                 720

Gly Arg Leu Lys Thr Pro Ser Gly Lys Tyr Ile Arg Ile Gly Tyr Ala
                725                 730                 735

Asp Lys Asn Glu His Pro Tyr Val Ser Ile Gly Arg Tyr Met Ala Asp
            740                 745                 750

Lys Gly Tyr Leu Lys Leu Gly Gln Thr Ser Met Gln Gly Ile Lys Ala
        755                 760                 765
```

```
Tyr Met Arg Gln Asn Pro Gln Arg Leu Ala Glu Val Leu Gly Gln Asn
    770                 775                 780

Pro Ser Tyr Ile Phe Phe Arg Glu Leu Ala Gly Ser Ser Asn Asp Gly
785                 790                 795                 800

Pro Val Gly Ala Leu Gly Thr Pro Leu Met Gly Glu Tyr Ala Gly Ala
                805                 810                 815

Val Asp Arg His Tyr Ile Thr Leu Gly Ala Pro Leu Phe Val Ala Thr
            820                 825                 830

Ala His Pro Val Thr Arg Lys Ala Leu Asn Arg Leu Ile Met Ala Gln
        835                 840                 845

Asp Thr Gly Ser Ala Ile Lys Gly Ala Val Arg Val Asp Tyr Phe Trp
    850                 855                 860

Gly Tyr Gly Asp Glu Ala Gly Glu Leu Ala Gly Lys Gln Lys Thr Thr
865                 870                 875                 880

Gly Tyr Val Trp Gln Leu Leu Pro Asn Gly Met Lys Pro Glu Tyr Arg
                885                 890                 895

Pro
```

<210> 11

<211> 1941

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG287NZ-953

<400> 11

```
atggctagcc ccgatgtcaa gtcggcggac acgctgtcaa aacctgccgc ccctgttgtt   60
tctgaaaaag agacagaggc aaaggaagat gcgccacagg caggttctca aggacagggc  120
gcgccatccg cacaaggcgg tcaagatatg gcggcggttt cggaagaaaa tacaggcaat  180
ggcggtgcgg cagcaacgga caaacccaaa aatgaagacg agggggcgca aaatgatatg  240
ccgcaaaatg ccgccgatac agatagtttg acaccgaatc acaccccggc ttcgaatatg  300
ccggccggaa atatggaaaa ccaagcaccg gatgccgggg aatcggagca gccggcaaac  360
caaccggata tggcaaatac ggcggacgga atgcagggtg acgatccgtc ggcaggcggg  420
gaaaatgccg gcaatacggc tgcccaaggt acaaatcaag ccgaaaacaa tcaaaccgcc  480
ggttctcaaa atcctgcctc ttcaaccaat cctagcgcca cgaatagcgg tggtgatttt  540
ggaaggacga acgtgggcaa ttctgttgtg attgacgggc cgtcgcaaaa tataacgttg  600
acccactgta aaggcgattc ttgtagtggc aataatttct tggatgaaga agtacagcta  660
aaatcagaat ttgaaaaatt aagtgatgca gacaaaataa gtaattacaa gaaagatggg  720
aagaatgacg ggaagaatga taaatttgtc ggtttggttg ccgatagtgt gcagatgaag  780
ggaatcaatc aatatattat cttttataaa cctaaaccca cttcatttgc gcgatttagg  840
cgttctgcac ggtcgaggcg gtcgcttccg gccgagatgc cgctgattcc cgtcaatcag  900
gcggatacgc tgattgtcga tggggaagcg gtcagcctga cggggcattc cggcaatatc  960
ttcgcgcccg aagggaatta ccggtatctg acttacgggg cggaaaaatt gcccggcgga 1020
tcgtatgccc tccgtgttca aggcgaacct tcaaaaggcg aaatgctcgc gggcacggca 1080
gtgtacaacg gcgaagtgct gcattttcat acggaaaacg gccgtccgtc cccgtccaga 1140
ggcaggtttg ccgcaaaagt cgatttcggc agcaaatctg tggacggcat tatcgacagc 1200
ggcgatggtt tgcatatggg tacgcaaaaa ttcaaagccg ccatcgatgg aaacggcttt 1260
aaggggactt ggacggaaaa tggcggcggg gatgtttccg gaaagtttta cggcccggcc 1320
ggcgaggaag tggcgggaaa atacagctat cgcccaacag atgcggaaaa gggcggattc 1380
ggcgtgtttg ccggcaaaaa agagcaggat ggatccggag gaggaggagc cacctacaaa 1440
gtggacgaat atcacgccaa cgcccgtttc gccatcgacc atttcaacac cagcaccaac 1500

gtcggcggtt tttacggtct gaccggttcc gtcgagttcg accaagcaaa acgcgacggt 1560
aaaatcgaca tcaccatccc cgttgccaac ctgcaaagcg gttcgcaaca ctttaccgac 1620
cacctgaaat cagccgacat cttcgatgcc gcccaatatc cggacatccg ctttgtttcc 1680
accaaattca acttcaacgg caaaaaactg gtttccgttg acggcaacct gaccatgcac 1740
ggcaaaaccg cccccgtcaa actcaaagcc gaaaaattca actgctacca aagcccgatg 1800
gcgaaaaccg aagtttgcgg cggcgacttc agcaccacca tcgaccgcac caaatggggc 1860
gtggactacc tcgttaacgt tggtatgacc aaaagcgtcc gcatcgacat ccaaatcgag 1920
gcagccaaac aataaaagct t                                            1941
```

<210> 12

<211> 644

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG287NZ-953

<400> 12

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

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

Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Ala Gln Gly Gly Gln
        35                  40                  45

Asp Met Ala Ala Val Ser Glu Glu Asn Thr Gly Asn Gly Gly Ala Ala
    50                  55                  60

Ala Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Ala Gln Asn Asp Met
65                  70                  75                  80

Pro Gln Asn Ala Ala Asp Thr Asp Ser Leu Thr Pro Asn His Thr Pro
                85                  90                  95

Ala Ser Asn Met Pro Ala Gly Asn Met Glu Asn Gln Ala Pro Asp Ala
            100                 105                 110

Gly Glu Ser Glu Gln Pro Ala Asn Gln Pro Asp Met Ala Asn Thr Ala
        115                 120                 125

Asp Gly Met Gln Gly Asp Asp Pro Ser Ala Gly Gly Glu Asn Ala Gly
    130                 135                 140

Asn Thr Ala Ala Gln Gly Thr Asn Gln Ala Glu Asn Asn Gln Thr Ala
145                 150                 155                 160

Gly Ser Gln Asn Pro Ala Ser Ser Thr Asn Pro Ser Ala Thr Asn Ser
                165                 170                 175

Gly Gly Asp Phe Gly Arg Thr Asn Val Gly Asn Ser Val Val Ile Asp
            180                 185                 190

Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser Cys
        195                 200                 205

Ser Gly Asn Asn Phe Leu Asp Glu Glu Val Gln Leu Lys Ser Glu Phe
    210                 215                 220

Glu Lys Leu Ser Asp Ala Asp Lys Ile Ser Asn Tyr Lys Lys Asp Gly
```

```
225                 230                 235                 240

Lys Asn Asp Gly Lys Asn Asp Lys Phe Val Gly Leu Val Ala Asp Ser
                245                 250                 255

Val Gln Met Lys Gly Ile Asn Gln Tyr Ile Ile Phe Tyr Lys Pro Lys
            260                 265                 270

Pro Thr Ser Phe Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser
        275                 280                 285

Leu Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu
    290                 295                 300

Ile Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile
305                 310                 315                 320

Phe Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys
                325                 330                 335

Leu Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro Ser Lys
            340                 345                 350

Gly Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His
        355                 360                 365

Phe His Thr Glu Asn Gly Arg Pro Ser Pro Ser Arg Gly Arg Phe Ala
    370                 375                 380

Ala Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile Asp Ser
385                 390                 395                 400

Gly Asp Gly Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp
                405                 410                 415

Gly Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val
            420                 425                 430

Ser Gly Lys Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr
        435                 440                 445

Ser Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala
    450                 455                 460

Gly Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Ala Thr Tyr Lys
465                 470                 475                 480

Val Asp Glu Tyr His Ala Asn Ala Arg Phe Ala Ile Asp His Phe Asn
                485                 490                 495

Thr Ser Thr Asn Val Gly Gly Phe Tyr Gly Leu Thr Gly Ser Val Glu
            500                 505                 510

Phe Asp Gln Ala Lys Arg Asp Gly Lys Ile Asp Ile Thr Ile Pro Val
        515                 520                 525

Ala Asn Leu Gln Ser Gly Ser Gln His Phe Thr Asp His Leu Lys Ser
    530                 535                 540

Ala Asp Ile Phe Asp Ala Ala Gln Tyr Pro Asp Ile Arg Phe Val Ser
545                 550                 555                 560
```

```
Thr Lys Phe Asn Phe Asn Gly Lys Lys Leu Val Ser Val Asp Gly Asn
                565                 570                 575

Leu Thr Met His Gly Lys Thr Ala Pro Val Lys Leu Lys Ala Glu Lys
            580                 585                 590

Phe Asn Cys Tyr Gln Ser Pro Met Ala Lys Thr Glu Val Cys Gly Gly
        595                 600                 605

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

Val Asn Val Gly Met Thr Lys Ser Val Arg Ile Asp Ile Gln Ile Glu
625                 630                 635                 640

Ala Ala Lys Gln
```

<210> 13

<211> 2583

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG287NZ-961

<400> 13

```
atggctagcc ccgatgtcaa gtcggcggac acgctgtcaa aacctgccgc ccctgttgtt   60
tctgaaaaag agacagaggc aaaggaagat gcgccacagg caggttctca aggacagggc  120
gcgccatccg cacaaggcgg tcaagatatg gcggcggttt cggaagaaaa tacaggcaat  180
ggcggtgcgg cagcaacgga caaacccaaa aatgaagacg agggggcgca aaatgatatg  240
ccgcaaaatg ccgccgatac agatagtttg acaccgaatc acaccccggc ttcgaatatg  300
ccggccggaa atatggaaaa ccaagcaccg gatgccgggg aatcggagca gccggcaaac  360
caaccggata tggcaaatac ggcggacgga atgcagggtg acgatccgtc ggcaggcggg  420
gaaaatgccg gcaatacggc tgcccaaggt acaaatcaag ccgaaaacaa tcaaaccgcc  480
ggttctcaaa atcctgcctc ttcaaccaat cctagcgcca cgaatagcgg tggtgatttt  540
ggaaggacga acgtgggcaa ttctgttgtg attgacgggc cgtcgcaaaa tataacgttg  600
acccactgta aaggcgattc ttgtagtggc aataatttct tggatgaaga agtacagcta  660
aaatcagaat ttgaaaaatt aagtgatgca gacaaaataa gtaattacaa gaaagatggg  720
aagaatgacg ggaagaatga taaatttgtc ggtttggttg ccgatagtgt gcagatgaag  780
ggaatcaatc aatatattat cttttataaa cctaaaccca cttcatttgc gcgatttagg  840
cgttctgcac ggtcgaggcg gtcgcttccg gccgagatgc cgctgattcc cgtcaatcag  900
gcggatacgc tgattgtcga tggggaagcg gtcagcctga cggggcattc cggcaatatc  960
ttcgcgcccg aagggaatta ccggtatctg acttacgggg cggaaaaatt gcccggcgga 1020
tcgtatgccc tccgtgttca aggcgaacct tcaaaaggcg aaatgctcgc gggcacggca 1080
gtgtacaacg gcgaagtgct gcattttcat acggaaaacg gccgtccgtc cccgtccaga 1140
ggcaggtttg ccgcaaaagt cgatttcggc agcaaatctg tggacggcat tatcgacagc 1200
ggcgatggtt tgcatatggg tacgcaaaaa ttcaaagccg ccatcgatgg aaacggcttt 1260
aaggggactt ggacggaaaa tggcggcggg gatgtttccg gaaagtttta cggcccggcc 1320
ggcgaggaag tggcgggaaa atacagctat cgcccaacag atgcggaaaa gggcggattc 1380
ggcgtgtttg ccggcaaaaa agagcaggat ggatccggag gaggaggagc cacaaacgac 1440
gacgatgtta aaaaagctgc cactgtggcc attgctgctg cctacaacaa tggccaagaa 1500
atcaacggtt tcaaagctgg agagaccatc tacgacattg atgaagacgg cacaattacc 1560
aaaaaagacg caactgcagc cgatgttgaa gccgacgact ttaaaggtct gggtctgaaa 1620
aaagtcgtga ctaacctgac caaaaccgtc aatgaaaaca aacaaaacgt cgatgccaaa 1680
gtaaaagctg cagaatctga aatagaaaag ttaacaacca agttagcaga cactgatgcc 1740
gctttagcag atactgatgc cgctctggat gcaaccacca acgccttgaa taaattggga 1800
gaaaatataa cgacatttgc tgaagagact aagacaaata tcgtaaaaat tgatgaaaaa 1860
ttagaagccg tggctgatac cgtcgacaag catgccgaag cattcaacga tatcgccgat 1920
tcattggatg aaaccaacac taaggcagac gaagccgtca aaaccgccaa tgaagccaaa 1980

cagacggccg aagaaaccaa acaaaacgtc gatgccaaag taaaagctgc agaaactgca 2040
gcaggcaaag ccgaagctgc cgctggcaca gctaatactg cagccgacaa ggccgaagct 2100
gtcgctgcaa aagttaccga catcaaagct gatatcgcta cgaacaaaga taatattgct 2160
aaaaaagcaa acagtgccga cgtgtacacc agagaagagt ctgacagcaa atttgtcaga 2220
attgatggtc tgaacgctac taccgaaaaa ttggacacac gcttggcttc tgctgaaaaa 2280
tccattgccg atcacgatac tcgcctgaac ggtttggata aaacagtgtc agacctgcgc 2340
aaagaaaccc gccaaggcct tgcagaacaa gccgcgctct ccggtctgtt ccaaccttac 2400
aacgtgggtc ggttcaatgt aacggctgca gtcggcggct acaaatccga atcggcagtc 2460
gccatcggta ccggcttccg ctttaccgaa aactttgccg ccaaagcagg cgtggcagtc 2520
ggcacttcgt ccggttcttc cgcagcctac catgtcggcg tcaattacga gtggtaaaag 2580
ctt                                                               2583
```

<210> 14

<211> 858

5 <212> PRT

<213> Secuencia artificial

<220>

<223> deltaG287NZ-961

<400> 14

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

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

Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Ala Gln Gly Gly Gln
        35                  40                  45

Asp Met Ala Ala Val Ser Glu Glu Asn Thr Gly Asn Gly Gly Ala Ala
    50                  55                  60

Ala Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Ala Gln Asn Asp Met
65                  70                  75                  80

Pro Gln Asn Ala Ala Asp Thr Asp Ser Leu Thr Pro Asn His Thr Pro
                85                  90                  95

Ala Ser Asn Met Pro Ala Gly Asn Met Glu Asn Gln Ala Pro Asp Ala
            100                 105                 110

Gly Glu Ser Glu Gln Pro Ala Asn Gln Pro Asp Met Ala Asn Thr Ala
        115                 120                 125

Asp Gly Met Gln Gly Asp Asp Pro Ser Ala Gly Gly Glu Asn Ala Gly
    130                 135                 140

Asn Thr Ala Ala Gln Gly Thr Asn Gln Ala Glu Asn Asn Gln Thr Ala
145                 150                 155                 160

Gly Ser Gln Asn Pro Ala Ser Ser Thr Asn Pro Ser Ala Thr Asn Ser
                165                 170                 175

Gly Gly Asp Phe Gly Arg Thr Asn Val Gly Asn Ser Val Val Ile Asp
            180                 185                 190

Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser Cys
        195                 200                 205

Ser Gly Asn Asn Phe Leu Asp Glu Glu Val Gln Leu Lys Ser Glu Phe
```

```
    210                 215                 220

Glu Lys Leu Ser Asp Ala Asp Lys Ile Ser Asn Tyr Lys Lys Asp Gly
225                 230                 235                 240

Lys Asn Asp Gly Lys Asn Asp Lys Phe Val Gly Leu Val Ala Asp Ser
                245                 250                 255

Val Gln Met Lys Gly Ile Asn Gln Tyr Ile Ile Phe Tyr Lys Pro Lys
            260                 265                 270

Pro Thr Ser Phe Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser
        275                 280                 285

Leu Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu
    290                 295                 300

Ile Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile
305                 310                 315                 320

Phe Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala Glu Lys
                325                 330                 335

Leu Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro Ser Lys
            340                 345                 350

Gly Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His
        355                 360                 365

Phe His Thr Glu Asn Gly Arg Pro Ser Pro Ser Arg Gly Arg Phe Ala
    370                 375                 380

Ala Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile Asp Ser
385                 390                 395                 400

Gly Asp Gly Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp
                405                 410                 415

Gly Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val
            420                 425                 430

Ser Gly Lys Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr
        435                 440                 445

Ser Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala
    450                 455                 460

Gly Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Ala Thr Asn Asp
465                 470                 475                 480

Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile Ala Ala Ala Tyr Asn
                485                 490                 495

Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly Glu Thr Ile Tyr Asp
            500                 505                 510

Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp Ala Thr Ala Ala Asp
        515                 520                 525

Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu Lys Lys Val Val Thr
    530                 535                 540
```

```
Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln Asn Val Asp Ala Lys
545                 550                 555                 560

Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu Thr Thr Lys Leu Ala
                565                 570                 575

Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala Ala Leu Asp Ala Thr
            580                 585                 590

Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile Thr Thr Phe Ala Glu
        595                 600                 605

Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu Lys Leu Glu Ala Val
    610                 615                 620

Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe Asn Asp Ile Ala Asp
625                 630                 635                 640

Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu Ala Val Lys Thr Ala
                645                 650                 655

Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys Gln Asn Val Asp Ala
            660                 665                 670

Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys Ala Glu Ala Ala Ala
        675                 680                 685

Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu Ala Val Ala Ala Lys
    690                 695                 700

Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn Lys Asp Asn Ile Ala
705                 710                 715                 720

Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg Glu Glu Ser Asp Ser
                725                 730                 735

Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr Thr Glu Lys Leu Asp
            740                 745                 750

Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala Asp His Asp Thr Arg
        755                 760                 765

Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu Arg Lys Glu Thr Arg
    770                 775                 780

Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr
785                 790                 795                 800

Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val Gly Gly Tyr Lys Ser
                805                 810                 815

Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg Phe Thr Glu Asn Phe
            820                 825                 830

Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser Ser Gly Ser Ser Ala
        835                 840                 845

Ala Tyr His Val Gly Val Asn Tyr Glu Trp
    850                 855
```

<210> 15

<211> 1082

<212> PRT

<213> Secuencia artificial

<220>

<223> 983

<400> 15

```
Met Arg Thr Thr Pro Thr Phe Pro Thr Lys Thr Phe Lys Pro Thr Ala
1               5                   10                  15

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

Gly Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile
        35                  40                  45

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

Ala Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala
65                  70                  75                  80

Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala
                85                  90                  95

Pro Pro Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala
            100                 105                 110

Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr
        115                 120                 125

Gly Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly
    130                 135                 140

Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn
145                 150                 155                 160

Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu
                165                 170                 175

Asp Gly Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val
            180                 185                 190

Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile
        195                 200                 205

Gly His Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp
    210                 215                 220

Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met
225                 230                 235                 240

Asn Thr Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg
                245                 250                 255

Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn
            260                 265                 270

Ser Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile
```

```
        275                 280                 285

Ala Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly
    290                 295                 300

Gly Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr
305                 310                 315                 320

Gly Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe
                325                 330                 335

Ser Thr Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu
            340                 345                 350

Pro Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly
        355                 360                 365

Val Asp Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro
    370                 375                 380

Gly Thr Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala
385                 390                 395                 400

Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg
                405                 410                 415

Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val
            420                 425                 430

Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn
        435                 440                 445

Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala
    450                 455                 460

Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys
465                 470                 475                 480

Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp
                485                 490                 495

Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser
            500                 505                 510

Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His
        515                 520                 525

Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu
    530                 535                 540

Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly
545                 550                 555                 560

Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp
                565                 570                 575

Gly Ile Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr
            580                 585                 590

Val His Ile Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu Tyr
        595                 600                 605
```

```
Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly
    610                 615                 620

Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn
625                 630                 635                 640

Ser Thr Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln
                645                 650                 655

Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala
            660                 665                 670

Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu
        675                 680                 685

Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala
    690                 695                 700

Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly
705                 710                 715                 720

Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser
                725                 730                 735

Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met
            740                 745                 750

Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val
        755                 760                 765

Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala
    770                 775                 780

Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly
785                 790                 795                 800

Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly
                805                 810                 815

Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln
            820                 825                 830

Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile
        835                 840                 845

Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met
    850                 855                 860

Gly Arg Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser
865                 870                 875                 880

Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr
                885                 890                 895

Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg
            900                 905                 910

Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu
        915                 920                 925
```

```
Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr
    930                 935                 940

Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln
945                 950                 955                 960

Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser
                965                 970                 975

Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln
            980                 985                 990

Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg
        995                 1000                1005

Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala
    1010                1015                1020

Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg
1025                1030                1035                1040

Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn
                1045                1050                1055

Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His
            1060                1065                1070

Ser Gly Arg Val Gly Val Gly Tyr Arg Phe
        1075                1080
```

<210> 16

<211> 1047

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG983

<400> 16

```
Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser Asn
1               5                   10                  15

Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly Ile
            20                  25                  30

Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg Asp
        35                  40                  45

Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro Pro
    50                  55                  60

Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys Asn
65                  70                  75                  80

Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg Gly
                85                  90                  95

Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile Ser
            100                 105                 110

Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn Tyr
```

```
        115                 120                 125

Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly Gly
    130                 135                 140

Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu Thr
145                 150                 155                 160

Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His Ile
                165                 170                 175

Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg Pro
            180                 185                 190

Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr Asn
        195                 200                 205

Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg Asn Ala Trp
    210                 215                 220

Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe Gly
225                 230                 235                 240

Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn Ser
                245                 250                 255

Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly Gly Asp Lys
            260                 265                 270

Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn Leu
        275                 280                 285

Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr Gly
    290                 295                 300

Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe Tyr
305                 310                 315                 320

Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp Arg
                325                 330                 335

Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr Glu
            340                 345                 350

Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp Cys
        355                 360                 365

Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn Pro
    370                 375                 380

Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly Thr
385                 390                 395                 400

Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn Leu
                405                 410                 415

Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly Val
            420                 425                 430

Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met Asn
        435                 440                 445
```

```
Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys Gly
    450                 455                 460

Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr Gly
465                 470                 475                 480

Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn Asn
                485                 490                 495

Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu Tyr
            500                 505                 510

Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu Ile
        515                 520                 525

Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile Val
    530                 535                 540

Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His Ile
545                 550                 555                 560

Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu Tyr Thr Arg Leu
                565                 570                 575

Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys Leu
            580                 585                 590

Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr Gly
        595                 600                 605

Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr Ser
    610                 615                 620

Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu Asp
625                 630                 635                 640

Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr Tyr
                645                 650                 655

Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His Ser
            660                 665                 670

Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn Leu
        675                 680                 685

Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr Pro
    690                 695                 700

Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly Ile
705                 710                 715                 720

Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His Ala
                725                 730                 735

Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr Val
            740                 745                 750

Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly Arg Arg Leu
        755                 760                 765
```

```
Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg Val
    770                 775                 780

Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly Val
785                 790                 795                 800

Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala Lys
                805                 810                 815

Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg Ser
            820                 825                 830

Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser Leu
        835                 840                 845

Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys Gly
    850                 855                 860

Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr Gly
865                 870                 875                 880

Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln Leu
                885                 890                 895

Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp Leu
            900                 905                 910

Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala Phe
        915                 920                 925

Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr Glu
    930                 935                 940

Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu Ser
945                 950                 955                 960

Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu Asn
                965                 970                 975

Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala Ala
            980                 985                 990

Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val Ala
        995                 1000                1005

Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu Ala
    1010                1015                1020

Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly Arg
1025                1030                1035                1040

Val Gly Val Gly Tyr Arg Phe
                1045
```

<210> 17

<211> 4425

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG983-ORF46.1

<400> 17

```
atgacttctg cgcccgactt caatgcaggc ggtaccggta tcggcagcaa cagcagagca   60
acaacagcga aatcagcagc agtatcttac gccggtatca agaacgaaat gtgcaaagac  120
agaagcatgc tctgtgccgg tcgggatgac gttgcggtta cagacaggga tgccaaaatc  180
aatgcccccc ccccgaatct gcataccgga gactttccaa acccaaatga cgcatacaag  240
aatttgatca acctcaaacc tgcaattgaa gcaggctata caggacgcgg ggtagaggta  300
ggtatcgtcg acacaggcga atccgtcggc agcatatcct ttcccgaact gtatggcaga  360
aaagaacacg gctataacga aaattacaaa aactatacgg cgtatatgcg gaaggaagcg  420
cctgaagacg gaggcggtaa agacattgaa gcttctttcg acgatgaggc cgttatagag  480
actgaagcaa agccgacgga tatccgccac gtaaaagaaa tcggacacat cgatttggtc  540
tcccatatta ttggcgggcg ttccgtggac ggcagacctg caggcggtat tgcgcccgat  600
gcgacgctac acataatgaa tacgaatgat gaaaccaaga acgaaatgat ggttgcagcc  660
atccgcaatg catgggtcaa gctgggcgaa cgtggcgtgc gcatcgtcaa taacagtttt  720
ggaacaacat cgagggcagg cactgccgac cttttccaaa tagccaattc ggaggagcag  780
taccgccaag cgttgctcga ctattccggc ggtgataaaa cagacgaggg tatccgcctg  840
atgcaacaga gcgattacgg caacctgtcc taccacatcc gtaataaaaa catgctttc   900
atcttttcga caggcaatga cgcacaagct cagcccaaca catatgccct attgccattt  960
tatgaaaaag acgctcaaaa aggcattatc acagtcgcag gcgtagaccg cagtggagaa 1020
aagttcaaac gggaaatgta tggagaaccg ggtacagaac cgcttgagta tggctccaac 1080
cattgcggaa ttactgccat gtggtgcctg tcggcaccct atgaagcaag cgtccgtttc 1140
acccgtacaa acccgattca aattgccgga acatcctttt ccgcacccat cgtaaccggc 1200
acggcggctc tgctgctgca gaaatacccg tggatgagca acgacaacct gcgtaccacg 1260
ttgctgacga cggctcagga catcggtgca gtcggcgtgg acagcaagtt cggctgggga 1320
ctgctggatg cgggtaaggc catgaacgga cccgcgtcct ttccgttcgg cgactttacc 1380
gccgatacga aaggtacatc cgatattgcc tactccttcc gtaacgacat ttcaggcacg 1440
ggcggcctga tcaaaaaagg cggcagccaa ctgcaactgc acggcaacaa cacctatacg 1500
ggcaaaacca ttatcgaagg cggttcgctg gtgttgtacg gcaacaacaa atcggatatg 1560
cgcgtcgaaa ccaaaggtgc gctgatttat aacggggcgg catccggcgg cagcctgaac 1620
agcgacggca ttgtctatct ggcagatacc gaccaatccg gcgcaaacga aaccgtacac 1680
atcaaaggca gtctgcagct ggacggcaaa ggtacgctgt acacacgttt gggcaaactg 1740
ctgaaagtgg acggtacggc gattatcggc ggcaagctgt acatgtcggc acgcggcaag 1800
ggggcaggct atctcaacag taccggacga cgtgttccct tcctgagtgc cgccaaaatc 1860
gggcaggatt attctttctt cacaaacatc gaaaccgacg gcggcctgct ggcttccctc 1920
gacagcgtcg aaaaaacagc gggcagtgaa ggcgacacgc tgtcctatta tgtccgtcgc 1980
ggcaatgcgg cacggactgc ttcggcagcg gcacattccg cgcccgccgg tctgaaacac 2040
gccgtagaac agggcggcag caatctggaa aacctgatgg tcgaactgga tgcctccgaa 2100
tcatccgcaa cacccgagac ggttgaaact gcggcagccg accgcacaga tatgccgggc 2160
atccgcccct acggcgcaac tttccgcgca gcggcagccg tacagcatgc gaatgccgcc 2220
gacggtgtac gcatcttcaa cagtctcgcc gctaccgtct atgccgacag taccgccgcc 2280
catgccgata tgcagggacg ccgcctgaaa gccgtatcgg acgggttgga ccacaacggc 2340
acgggtctgc gcgtcatcgc gcaaacccaa caggacggtg gaacgtggga acagggcggt 2400
gttgaaggca aaatgcgcgg cagtacccaa accgtcggca ttgccgcgaa aaccggcgaa 2460
aatacgacag cagccgccac actgggcatg ggacgcagca catggagcga aaacagtgca 2520
aatgcaaaaa ccgacagcat tagtctgttt gcaggcatac ggcacgatgc gggcgatatc 2580
ggctatctca aaggcctgtt ctcctacgga cgctacaaaa acagcatcag ccgcagcacc 2640
ggtgcggacg aacatgcgga aggcagcgtc aacggcacgc tgatgcagct gggcgcactg 2700
ggcggtgtca acgttccgtt tgccgcaacg ggagatttga cggtcgaagg cggtctgcgc 2760
tacgacctgc tcaaacagga tgcattcgcc gaaaaaggca gtgctttggg ctggagcggc 2820
aacagcctca ctgaaggcac gctggtcgga ctcgcgggtc tgaagctgtc gcaacccttg 2880
agcgataaag ccgtcctgtt tgcaacggcg ggcgtggaac gcgacctgaa cggacgcgac 2940
tacacggtaa cgggcggctt taccggcgcg actgcagcaa ccggcaagac gggggcacgc 3000
aatatgccgc acacccgtct ggttgccggc ctgggcgcgg atgtcgaatt cggcaacggc 3060
tggaacggct tggcacgtta cagctacgcc ggttccaaac agtacggcaa ccacagcgga 3120
cgagtcggcg taggctaccg gttcctcgac ggtggcggag gcactggatc ctcagatttg 3180
gcaaacgatt cttttatccg gcaggttctc gaccgtcagc atttcgaacc cgacgggaaa 3240
taccacctat tcggcagcag gggggaactt gccgagcgca gcggccatat cggattggga 3300
aaaatacaaa gccatcagtt gggcaacctg atgattcaac aggcggccat taaaggaaat 3360
atcggctaca ttgtccgctt ttccgatcac gggcacgaag tccattcccc cttcgacaac 3420
catgcctcac attccgattc tgatgaagcc ggtagtcccg ttgacggatt tagcctttac 3480
cgcatccatt gggacggata cgaacaccat cccgccgacg gctatgacgg gccacagggc 3540
```

```
ggcggctatc ccgctcccaa aggcgcgagg gatatataca gctacgacat aaaaggcgtt   3600
gcccaaaata tccgcctcaa cctgaccgac aaccgcagca ccggacaacg gcttgccgac   3660
cgtttccaca atgccggtag tatgctgacg caaggagtag gcgacggatt caaacgcgcc   3720
acccgataca gccccgagct ggacagatcg ggcaatgccg ccgaagcctt caacggcact   3780
gcagatatcg ttaaaaacat catcggcgcg gcaggagaaa ttgtcggcgc aggcgatgcc   3840
gtgcagggca taagcgaagg ctcaaacatt gctgtcatgc acggcttggg tctgctttcc   3900
accgaaaaca agatggcgcg catcaacgat ttggcagata tggcgcaact caaagactat   3960
gccgcagcag ccatccgcga ttgggcagtc caaaacccca atgccgcaca aggcatagaa   4020
gccgtcagca atatctttat ggcagccatc cccatcaaag ggattggagc tgttcgggga   4080
aaatacggct tgggcggcat cacggcacat cctatcaagc ggtcgcagat gggcgcgatc   4140
gcattgccga aagggaaatc cgccgtcagc gacaattttg ccgatgcggc atacgccaaa   4200
tacccgtccc cttaccattc ccgaaatatc cgttcaaact tggagcagcg ttacggcaaa   4260
gaaaacatca cctcctcaac cgtgccgccg tcaaacggca aaaatgtcaa actggcagac   4320
caacgccacc cgaagacagg cgtaccgttt gacggtaaag ggtttccgaa ttttgagaag   4380
cacgtgaaat atgatacgct cgagcaccac caccaccacc actga                   4425
```

<210> 18

<211> 1474

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG983-ORF46.1

<400> 18

```
Met Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser
1               5                   10                  15

Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly
            20                  25                  30

Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg
        35                  40                  45

Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro
    50                  55                  60

Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys
65                  70                  75                  80

Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg
                85                  90                  95

Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile
            100                 105                 110

Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn
        115                 120                 125

Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly
    130                 135                 140

Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu
145                 150                 155                 160

Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His
                165                 170                 175

Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg
            180                 185                 190
```

```
Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr
        195                 200                 205

Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg Asn Ala
    210                 215                 220

Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe
225                 230                 235                 240

Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn
                245                 250                 255

Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly Gly Asp
            260                 265                 270

Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn
        275                 280                 285

Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr
    290                 295                 300

Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe
305                 310                 315                 320

Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp
                325                 330                 335

Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr
            340                 345                 350

Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp
        355                 360                 365

Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn
    370                 375                 380

Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly
385                 390                 395                 400

Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn
                405                 410                 415

Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly
            420                 425                 430

Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met
        435                 440                 445

Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys
    450                 455                 460

Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr
465                 470                 475                 480

Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn
                485                 490                 495

Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu
            500                 505                 510

Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu
```

```
        515                 520                 525

Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile
    530                 535                 540

Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His
545                 550                 555                 560

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

Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys
            580                 585                 590

Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr
        595                 600                 605

Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr
    610                 615                 620

Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu
625                 630                 635                 640

Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr
                645                 650                 655

Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His
            660                 665                 670

Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn
        675                 680                 685

Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr
    690                 695                 700

Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly
705                 710                 715                 720

Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His
                725                 730                 735

Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr
            740                 745                 750

Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly Arg Arg
        755                 760                 765

Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg
    770                 775                 780

Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly
785                 790                 795                 800

Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala
                805                 810                 815

Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg
            820                 825                 830

Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser
        835                 840                 845
```

```
Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys
    850                 855                 860

Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr
865                 870                 875                 880

Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln
                885                 890                 895

Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp
            900                 905                 910

Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala
        915                 920                 925

Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr
    930                 935                 940

Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu
945                 950                 955                 960

Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu
                965                 970                 975

Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala
            980                 985                 990

Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val
        995                 1000                1005

Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu
    1010                1015                1020

Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly
1025                1030                1035                1040

Arg Val Gly Val Gly Tyr Arg Phe Leu Asp Gly Gly Gly Gly Thr Gly
                1045                1050                1055

Ser Ser Asp Leu Ala Asn Asp Ser Phe Ile Arg Gln Val Leu Asp Arg
            1060                1065                1070

Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe Gly Ser Arg Gly
        1075                1080                1085

Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly Lys Ile Gln Ser
    1090                1095                1100

His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala Ile Lys Gly Asn
1105                1110                1115                1120

Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His Glu Val His Ser
                1125                1130                1135

Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp Glu Ala Gly Ser
            1140                1145                1150

Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp Asp Gly Tyr Glu
        1155                1160                1165
```

```
His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly Gly Tyr Pro
    1170                1175                1180

Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile Lys Gly Val
1185                1190                1195                1200

Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser Thr Gly Gln
                1205                1210                1215

Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met Leu Thr Gln Gly
            1220                1225                1230

Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro Glu Leu Asp
        1235                1240                1245

Arg Ser Gly Asn Ala Ala Glu Ala Phe Asn Gly Thr Ala Asp Ile Val
    1250                1255                1260

Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly Ala Gly Asp Ala
1265                1270                1275                1280

Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val Met His Gly Leu
                1285                1290                1295

Gly Leu Leu Ser Thr Glu Asn Lys Met Ala Arg Ile Asn Asp Leu Ala
            1300                1305                1310

Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ala Ile Arg Asp Trp
        1315                1320                1325

Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala Val Ser Asn
    1330                1335                1340

Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala Val Arg Gly
1345                1350                1355                1360

Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile Lys Arg Ser Gln
                1365                1370                1375

Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala Val Ser Asp Asn
            1380                1385                1390

Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr His Ser Arg
        1395                1400                1405

Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu Asn Ile Thr
    1410                1415                1420

Ser Ser Thr Val Pro Pro Ser Asn Gly Lys Asn Val Lys Leu Ala Asp
1425                1430                1435                1440

Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly Lys Gly Phe Pro
                1445                1450                1455

Asn Phe Glu Lys His Val Lys Tyr Asp Thr Leu Glu His His His His
            1460                1465                1470

His His
```

<210> 19

<211> 3939

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG983-741

<400> 19

```
atgacttctg cgcccgactt caatgcaggc ggtaccggta tcggcagcaa cagcagagca   60
acaacagcga aatcagcagc agtatcttac gccggtatca agaacgaaat gtgcaaagac  120
agaagcatgc tctgtgccgg tcgggatgac gttgcggtta cagacaggga tgccaaaatc  180
aatgcccccc ccccgaatct gcataccgga gactttccaa acccaaatga cgcatacaag  240
aatttgatca acctcaaacc tgcaattgaa gcaggctata caggacgcgg ggtagaggta  300
ggtatcgtcg acacaggcga atccgtcggc agcatatcct ttcccgaact gtatggcaga  360
aaagaacacg gctataacga aaattacaaa aactatacgg cgtatatgcg gaaggaagcg  420
cctgaagacg gaggcggtaa agacattgaa gcttctttcg acgatgaggc cgttatagag  480
actgaagcaa agccgacgga tatccgccac gtaaaagaaa tcggacacat cgatttggtc  540
tcccatatta ttggcgggcg ttccgtggac ggcagacctg caggcggtat tgcgcccgat  600
gcgacgctac acataatgaa tacgaatgat gaaaccaaga acgaaatgat ggttgcagcc  660
atccgcaatg catgggtcaa gctgggcgaa cgtggcgtgc gcatcgtcaa taacagtttt  720
ggaacaacat cgagggcagg cactgccgac cttttccaaa tagccaattc ggaggagcag  780
taccgccaag cgttgctcga ctattccggc ggtgataaaa cagacgaggg tatccgcctg  840
atgcaacaga gcgattacgg caacctgtcc taccacatcc gtaataaaaa catgctttc  900
atcttttcga caggcaatga cgcacaagct cagcccaaca catatgccct attgccattt  960
tatgaaaaag acgctcaaaa aggcattatc acagtcgcag gcgtagaccg cagtggagaa 1020
aagttcaaac gggaaatgta tggagaaccg ggtacagaac cgcttgagta tggctccaac 1080
cattgcggaa ttactgccat gtggtgcctg tcggcaccct atgaagcaag cgtccgtttc 1140
acccgtacaa acccgattca aattgccgga acatcctttt ccgcacccat cgtaaccggc 1200
acggcggctc tgctgctgca gaaatacccg tggatgagca acgacaacct gcgtaccacg 1260
ttgctgacga cggctcagga catcggtgca gtcggcgtgg acagcaagtt cggctgggga 1320
ctgctggatg cgggtaaggc catgaacgga cccgcgtcct ttccgttcgg cgactttacc 1380
gccgatacga aaggtacatc cgatattgcc tactccttcc gtaacgacat ttcaggcacg 1440
ggcggcctga tcaaaaaagg cggcagccaa ctgcaactgc acggcaacaa cacctatacg 1500
ggcaaaacca ttatcgaagg cggttcgctg gtgttgtacg gcaacaacaa atcggatatg 1560
cgcgtcgaaa ccaaaggtgc gctgatttat aacggggcgg catccggcgg cagcctgaac 1620
agcgacggca ttgtctatct ggcagatacc gaccaatccg gcgcaaacga aaccgtacac 1680
atcaaaggca gtctgcagct ggacggcaaa ggtacgctgt acacacgttt gggcaaactg 1740
ctgaaagtgg acggtacggc gattatcggc ggcaagctgt acatgtcggc acgcggcaag 1800
ggggcaggct atctcaacag taccggacga cgtgttccct tcctgagtgc cgccaaaatc 1860
gggcaggatt attctttctt cacaaacatc gaaaccgacg gcggcctgct ggcttccctc 1920
gacagcgtcg aaaaaacagc gggcagtgaa ggcgacacgc tgtcctatta tgtccgtcgc 1980
ggcaatgcgg cacggactgc ttcggcagcg gcacattccg cgcccgccgg tctgaaacac 2040
gccgtagaac agggcggcag caatctggaa aacctgatgg tcgaactgga tgcctccgaa 2100
tcatccgcaa cacccgagac ggttgaaact gcggcagccg accgcacaga tatgccgggc 2160
atccgcccct acggcgcaac tttccgcgca gcggcagccg tacagcatgc gaatgccgcc 2220
gacggtgtac gcatcttcaa cagtctcgcc gctaccgtct atgccgacag taccgccgcc 2280
catgccgata tgcagggacg ccgcctgaaa gccgtatcgg acgggttgga ccacaacggc 2340
acgggtctgc gcgtcatcgc gcaaacccaa caggacggtg gaacgtggga acagggcggt 2400
gttgaaggca aaatgcgcgg cagtacccaa accgtcggca ttgccgcgaa aaccggcgaa 2460
aatacgacag cagccgccac actgggcatg ggacgcagca catggagcga aaacagtgca 2520
aatgcaaaaa ccgacagcat tagtctgttt gcaggcatac ggcacgatgc gggcgatatc 2580
ggctatctca aaggcctgtt ctcctacgga cgctacaaaa acagcatcag ccgcagcacc 2640
ggtgcggacg aacatgcgga aggcagcgtc aacggcacgc tgatgcagct gggcgcactg 2700
ggcggtgtca acgttccgtt tgccgcaacg ggagatttga cggtcgaagg cggtctgcgc 2760
tacgacctgc tcaaacagga tgcattcgcc gaaaaaggca gtgctttggg ctggagcggc 2820
aacagcctca ctgaaggcac gctggtcgga ctcgcgggtc tgaagctgtc gcaacccttg 2880
agcgataaag ccgtcctgtt tgcaacggcg ggcgtggaac gcgacctgaa cggacgcgac 2940
tacacggtaa cgggcggctt taccggcgcg actgcagcaa ccggcaagac gggggcacgc 3000
aatatgccgc acacccgtct ggttgccggc ctgggcgcgg atgtcgaatt cggcaacggc 3060
tggaacggct tggcacgtta cagctacgcc ggttccaaac agtacggcaa ccacagcgga 3120
cgagtcggcg taggctaccg gttcctcgag ggatccggag gggtggtgt cgccgccgac  3180
```

```
atcggtgcgg ggcttgccga tgcactaacc gcaccgctcg accataaaga caaaggtttg   3240
cagtctttga cgctggatca gtccgtcagg aaaaacgaga aactgaagct ggcggcacaa   3300
ggtgcggaaa aaacttatgg aaacggtgac agcctcaata cgggcaaatt gaagaacgac   3360
aaggtcagcc gtttcgactt tatccgccaa atcgaagtgg acgggcagct cattaccttg   3420
gagagtggag agttccaagt atacaaacaa agccattccg ccttaaccgc ctttcagacc   3480
gagcaaatac aagattcgga gcattccggg aagatggttg cgaaacgcca gttcagaatc   3540
ggcgacatag cgggcgaaca tacatctttt gacaagcttc ccgaaggcgg cagggcgaca   3600
tatcgcggga cggcgttcgg ttcagacgat gccggcggaa aactgaccta caccatagat   3660
ttcgccgcca agcagggaaa cggcaaaatc gaacatttga aatcgccaga actcaatgtc   3720
gacctggccg ccgccgatat caagccggat ggaaaacgcc atgccgtcat cagcggttcc   3780
gtcctttaca accaagccga gaaaggcagt tactccctcg gtatctttgg cggaaaagcc   3840
caggaagttg ccggcagcgc ggaagtgaaa accgtaaacg gcatacgcca tatcggcctt   3900
gccgccaagc aactcgagca ccaccaccac caccactga                         3939
```

<210> 20

<211> 1312

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG983-741

<400> 20

```
Met Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser
1               5                   10                  15

Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly
            20                  25                  30

Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg
        35                  40                  45

Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro
    50                  55                  60

Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys
65                  70                  75                  80

Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg
                85                  90                  95

Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile
            100                 105                 110

Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn
        115                 120                 125

Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly
    130                 135                 140

Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu
145                 150                 155                 160

Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His
                165                 170                 175

Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg
            180                 185                 190

Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr
        195                 200                 205
```

```
Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg Asn Ala
    210                 215                 220

Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe
225                 230                 235                 240

Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn
                245                 250                 255

Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly Gly Asp
            260                 265                 270

Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn
        275                 280                 285

Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr
    290                 295                 300

Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe
305                 310                 315                 320

Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp
                325                 330                 335

Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr
            340                 345                 350

Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp
        355                 360                 365

Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn
    370                 375                 380

Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly
385                 390                 395                 400

Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn
                405                 410                 415

Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly
            420                 425                 430

Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met
        435                 440                 445

Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys
    450                 455                 460

Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr
465                 470                 475                 480

Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn
                485                 490                 495

Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu
            500                 505                 510

Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu
        515                 520                 525
```

```
Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile
    530                 535                 540

Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His
545                 550                 555                 560

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

Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys
            580                 585                 590

Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr
        595                 600                 605

Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr
    610                 615                 620

Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu
625                 630                 635                 640

Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr
                645                 650                 655

Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His
            660                 665                 670

Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn
        675                 680                 685

Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr
    690                 695                 700

Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly
705                 710                 715                 720

Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His
                725                 730                 735

Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr
            740                 745                 750

Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly Arg Arg
        755                 760                 765

Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg
    770                 775                 780

Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly
785                 790                 795                 800

Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala
                805                 810                 815

Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg
            820                 825                 830

Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser
        835                 840                 845

Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys
```

```
    850                 855                 860

Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr
865                 870                 875                 880

Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln
                885                 890                 895

Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp
            900                 905                 910

Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala
        915                 920                 925

Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr
    930                 935                 940

Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu
945                 950                 955                 960

Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu
                965                 970                 975

Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala
            980                 985                 990

Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val
        995                 1000                1005

Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu
    1010                1015                1020

Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly
1025                1030                1035                1040

Arg Val Gly Val Gly Tyr Arg Phe Leu Glu Gly Ser Gly Gly Gly Gly
                1045                1050                1055

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
            1060                1065                1070

Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser
        1075                1080                1085

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
    1090                1095                1100

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
1105                1110                1115                1120

Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln
                1125                1130                1135

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His
            1140                1145                1150

Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His
        1155                1160                1165

Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala
    1170                1175                1180
```

```
Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr
1185                1190                1195                1200

Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr
                1205                1210                1215

Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His
            1220                1225                1230

Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys
        1235                1240                1245

Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn
    1250                1255                1260

Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala
1265                1270                1275                1280

Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg
                1285                1290                1295

His Ile Gly Leu Ala Ala Lys Gln Leu Glu His His His His His His
            1300                1305                1310
```

<210> 21

<211> 4344

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG983-961

<400> 21

```
atgacttctg cgcccgactt caatgcaggc ggtaccggta tcggcagcaa cagcagagca   60
acaacagcga aatcagcagc agtatcttac gccggtatca agaacgaaat gtgcaaagac  120
agaagcatgc tctgtgccgg tcgggatgac gttgcggtta cagacaggga tgccaaaatc  180
aatgcccccc ccccgaatct gcataccgga gactttccaa acccaaatga cgcatacaag  240
aatttgatca acctcaaacc tgcaattgaa gcaggctata caggacgcgg ggtagaggta  300
ggtatcgtcg acacaggcga atccgtcggc agcatatcct ttcccgaact gtatggcaga  360
aaagaacacg gctataacga aaattacaaa aactatacgg cgtatatgcg gaaggaagcg  420
cctgaagacg gaggcggtaa agacattgaa gcttctttcg acgatgaggc cgttatagag  480
actgaagcaa agccgacgga tatccgccac gtaaaagaaa tcggacacat cgatttggtc  540
tcccatatta ttggcgggcg ttccgtggac ggcagacctg caggcggtat tgcgcccgat  600
gcgacgctac acataatgaa tacgaatgat gaaaccaaga acgaaatgat ggttgcagcc  660
atccgcaatg catgggtcaa gctgggcgaa cgtggcgtgc gcatcgtcaa taacagtttt  720
ggaacaacat cgagggcagg cactgccgac cttttccaaa tagccaattc ggaggagcag  780
taccgccaag cgttgctcga ctattccggc ggtgataaaa cagacgaggg tatccgcctg  840
atgcaacaga gcgattacgg caacctgtcc taccacatcc gtaataaaaa catgcttttc  900
atcttttcga caggcaatga cgcacaagct cagcccaaca catatgccct attgccattt  960
tatgaaaaag acgctcaaaa aggcattatc acagtcgcag gcgtagaccg cagtggagaa 1020
aagttcaaac gggaaatgta tggagaaccg ggtacagaac cgcttgagta tggctccaac 1080
cattgcggaa ttactgccat gtggtgcctg tcggcaccct atgaagcaag cgtccgtttc 1140
acccgtacaa acccgattca aattgccgga acatcctttt ccgcacccat cgtaaccggc 1200
acggcggctc tgctgctgca gaaatacccg tggatgagca acgacaacct gcgtaccacg 1260
ttgctgacga cggctcagga catcggtgca gtcggcgtgg acagcaagtt cggctgggga 1320
ctgctggatg cgggtaaggc catgaacgga cccgcgtcct ttccgttcgg cgactttacc 1380
gccgatacga aaggtacatc cgatattgcc tactccttcc gtaacgacat ttcaggcacg 1440
ggcggcctga tcaaaaaagg cggcagccaa ctgcaactgc acggcaacaa cacctatacg 1500
ggcaaaacca ttatcgaagg cggttcgctg gtgttgtacg gcaacaacaa atcggatatg 1560
```

```
cgcgtcgaaa ccaaaggtgc gctgatttat aacggggcgg catccggcgg cagcctgaac   1620
agcgacggca ttgtctatct ggcagatacc gaccaatccg gcgcaaacga aaccgtacac   1680
atcaaaggca gtctgcagct ggacggcaaa ggtacgctgt acacacgttt gggcaaactg   1740
ctgaaagtgg acggtacggc gattatcggc ggcaagctgt acatgtcggc acgcggcaag   1800
ggggcaggct atctcaacag taccggacga cgtgttccct tcctgagtgc cgccaaaatc   1860
gggcaggatt attctttctt cacaaacatc gaaaccgacg gcggcctgct ggcttccctc   1920
gacagcgtcg aaaaaacagc gggcagtgaa ggcgacacgc tgtcctatta tgtccgtcgc   1980
ggcaatgcgg cacggactgc ttcggcagcg gcacattccg cgcccgccgg tctgaaacac   2040
gccgtagaac agggcggcag caatctggaa aacctgatgg tcgaactgga tgcctccgaa   2100
tcatccgcaa cacccgagac ggttgaaact gcggcagccg accgcacaga tatgccgggc   2160
atccgcccct acggcgcaac tttccgcgca gcggcagccg tacagcatgc gaatgccgcc   2220
gacggtgtac gcatcttcaa cagtctcgcc gctaccgtct atgccgacag taccgccgcc   2280
catgccgata tgcagggacg ccgcctgaaa gccgtatcgg acgggttgga ccacaacggc   2340
acgggtctgc gcgtcatcgc gcaaacccaa caggacggtg gaacgtggga acagggcggt   2400
gttgaaggca aaatgcgcgg cagtacccaa accgtcggca ttgccgcgaa aaccggcgaa   2460
aatacgacag cagccgccac actgggcatg ggacgcagca catggagcga aaacagtgca   2520
aatgcaaaaa ccgacagcat tagtctgttt gcaggcatac ggcacgatgc gggcgatatc   2580
ggctatctca aaggcctgtt ctcctacgga cgctacaaaa acagcatcag ccgcagcacc   2640
ggtgcggacg aacatgcgga aggcagcgtc aacggcacgc tgatgcagct gggcgcactg   2700
ggcggtgtca acgttccgtt tgccgcaacg ggagatttga cggtcgaagg cggtctgcgc   2760
tacgacctgc tcaaacagga tgcattcgcc gaaaaaggca gtgctttggg ctggagcggc   2820
aacagcctca ctgaaggcac gctggtcgga ctcgcgggtc tgaagctgtc gcaacccttg   2880
agcgataaag ccgtcctgtt tgcaacggcg ggcgtggaac gcgacctgaa cggacgcgac   2940
tacacggtaa cgggcggctt taccggcgcg actgcagcaa ccggcaagac gggggcacgc   3000
aatatgccgc acacccgtct ggttgccggc ctgggcgcgg atgtcgaatt cggcaacggc   3060
tggaacggct tggcacgtta cagctacgcc ggttccaaac agtacggcaa ccacagcgga   3120
cgagtcggcg taggctaccg gttcctcgag ggtggcggag gcactggatc cgccacaaac   3180
gacgacgatg ttaaaaaagc tgccactgtg gccattgctg ctgcctacaa caatggccaa   3240
gaaatcaacg gtttcaaagc tggagagacc atctacgaca ttgatgaaga cggcacaatt   3300
accaaaaaag acgcaactgc agccgatgtt gaagccgacg actttaaagg tctgggtctg   3360
aaaaaagtcg tgactaacct gaccaaaacc gtcaatgaaa acaaacaaaa cgtcgatgcc   3420
aaagtaaaag ctgcagaatc tgaaatagaa aagttaacaa ccaagttagc agacactgat   3480
gccgctttag cagatactga tgccgctctg gatgcaacca ccaacgcctt gaataaattg   3540
ggagaaaata taacgacatt tgctgaagag actaagacaa atatcgtaaa aattgatgaa   3600
aaattagaag ccgtggctga taccgtcgac aagcatgccg aagcattcaa cgatatcgcc   3660
gattcattgg atgaaaccaa cactaaggca gacgaagccg tcaaaaccgc caatgaagcc   3720
aaacagacgg ccgaagaaac caaacaaaac gtcgatgcca aagtaaaagc tgcagaaact   3780
gcagcaggca aagccgaagc tgccgctggc acagctaata ctgcagccga caaggccgaa   3840
gctgtcgctg caaaagttac cgacatcaaa gctgatatcg ctacgaacaa agataatatt   3900
gctaaaaaag caaacagtgc cgacgtgtac accagagaag agtctgacag caaatttgtc   3960
agaattgatg gtctgaacgc tactaccgaa aaattggaca cacgcttggc ttctgctgaa   4020
aaatccattg ccgatcacga tactcgcctg aacggtttgg ataaaacagt gtcagacctg   4080
cgcaaagaaa cccgccaagg ccttgcagaa caagccgcgc tctccggtct gttccaacct   4140
tacaacgtgg gtcggttcaa tgtaacggct gcagtcggcg gctacaaatc cgaatcggca   4200
gtcgccatcg gtaccggctt ccgctttacc gaaaactttg ccgccaaagc aggcgtggca   4260
gtcggcactt cgtccggttc ttccgcagcc taccatgtcg gcgtcaatta cgagtggctc   4320
gagcaccacc accaccacca ctga                                          4344
```

<210> 22

<211> 1447

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG983-961

<400> 22

```
Met Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser
1               5                   10                  15

Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly
```

```
            20                  25                  30

Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg
        35                  40                  45

Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro
    50                  55                  60

Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys
65                  70                  75                  80

Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg
                85                  90                  95

Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile
            100                 105                 110

Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn
        115                 120                 125

Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly
    130                 135                 140

Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu
145                 150                 155                 160

Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His
                165                 170                 175

Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg
            180                 185                 190

Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr
        195                 200                 205

Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg Asn Ala
    210                 215                 220

Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe
225                 230                 235                 240

Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn
                245                 250                 255

Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly Gly Asp
            260                 265                 270

Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn
        275                 280                 285

Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr
    290                 295                 300

Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe
305                 310                 315                 320

Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp
                325                 330                 335

Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr
            340                 345                 350
```

```
Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp
        355                 360                 365

Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn
    370                 375                 380

Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly
385                 390                 395                 400

Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn
                405                 410                 415

Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly
            420                 425                 430

Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met
        435                 440                 445

Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys
    450                 455                 460

Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr
465                 470                 475                 480

Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn
                485                 490                 495

Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu
            500                 505                 510

Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu
        515                 520                 525

Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile
    530                 535                 540

Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His
545                 550                 555                 560

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

Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys
            580                 585                 590

Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr
        595                 600                 605

Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr
    610                 615                 620

Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu
625                 630                 635                 640

Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr
                645                 650                 655

Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His
            660                 665                 670
```

```
Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn
        675                 680                 685

Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr
    690                 695                 700

Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly
705                 710                 715                 720

Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His
                725                 730                 735

Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr
            740                 745                 750

Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly Arg Arg
        755                 760                 765

Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg
    770                 775                 780

Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly
785                 790                 795                 800

Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala
                805                 810                 815

Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg
            820                 825                 830

Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser
        835                 840                 845

Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys
    850                 855                 860

Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr
865                 870                 875                 880

Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln
                885                 890                 895

Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp
            900                 905                 910

Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala
        915                 920                 925

Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr
    930                 935                 940

Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu
945                 950                 955                 960

Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu
                965                 970                 975

Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala
            980                 985                 990

Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val
```

```
        995                 1000                1005

Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu
    1010                1015                1020

Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly
1025                1030                1035                1040

Arg Val Gly Val Gly Tyr Arg Phe Leu Glu Gly Gly Gly Gly Thr Gly
                1045                1050                1055

Ser Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
            1060                1065                1070

Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
        1075                1080                1085

Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
    1090                1095                1100

Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu
1105                1110                1115                1120

Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
                1125                1130                1135

Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
            1140                1145                1150

Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
        1155                1160                1165

Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile
    1170                1175                1180

Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
1185                1190                1195                1200

Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
                1205                1210                1215

Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu
            1220                1225                1230

Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
        1235                1240                1245

Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
    1250                1255                1260

Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
1265                1270                1275                1280

Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
                1285                1290                1295

Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
            1300                1305                1310

Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
        1315                1320                1325
```

Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
1330 1335 1340

Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
1345 1350 1355 1360

Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
1365 1370 1375

Leu Phe Gln Pro Tyr Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val
1380 1385 1390

Gly Gly Tyr Lys Ser Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg
1395 1400 1405

Phe Thr Glu Asn Phe Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser
1410 1415 1420

Ser Gly Ser Ser Ala Ala Tyr His Val Gly Val Asn Tyr Glu Trp Leu
1425 1430 1435 1440

Glu His His His His His His
1445

<210> 23

<211> 4179

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG983-961c

<400> 23

```
atgacttctg cgcccgactt caatgcaggc ggtaccggta tcggcagcaa cagcagagca   60
acaacagcga aatcagcagc agtatcttac gccggtatca agaacgaaat gtgcaaagac   120
agaagcatgc tctgtgccgg tcgggatgac gttgcggtta cagacaggga tgccaaaatc   180
aatgcccccc ccccgaatct gcataccgga gactttccaa acccaaatga cgcatacaag   240
aatttgatca acctcaaacc tgcaattgaa gcaggctata caggacgcgg ggtagaggta   300
ggtatcgtcg acacaggcga atccgtcggc agcatatcct ttcccgaact gtatggcaga   360
aaagaacacg gctataacga aaattacaaa aactatacgg cgtatatgcg gaaggaagcg   420
cctgaagacg gaggcggtaa agacattgaa gcttctttcg acgatgaggc cgttatagag   480
actgaagcaa agccgacgga tatccgccac gtaaaagaaa tcggacacat cgatttggtc   540
tcccatatta ttggcgggcg ttccgtggac ggcagacctg caggcggtat tgcgcccgat   600
gcgacgctac acataatgaa tacgaatgat gaaaccaaga acgaaatgat ggttgcagcc   660
atccgcaatg catgggtcaa gctgggcgaa cgtggcgtgc gcatcgtcaa taacagtttt   720
ggaacaacat cgagggcagg cactgccgac cttttccaaa tagccaattc ggaggagcag   780
taccgccaag cgttgctcga ctattccggc ggtgataaaa cagacgaggg tatccgcctg   840
atgcaacaga gcgattacgg caacctgtcc taccacatcc gtaataaaaa catgcttttc   900
atcttttcga caggcaatga cgcacaagct cagcccaaca catatgccct attgccattt   960
tatgaaaaag acgctcaaaa aggcattatc acagtcgcag gcgtagaccg cagtggagaa   1020
aagttcaaac gggaaatgta tggagaaccg ggtacagaac cgcttgagta tggctccaac   1080
cattgcggaa ttactgccat gtggtgcctg tcggcaccct atgaagcaag cgtccgtttc   1140
acccgtacaa acccgattca aattgccgga acatcctttt ccgcacccat cgtaaccggc   1200
acggcggctc tgctgctgca gaaatacccg tggatgagca acgacaacct gcgtaccacg   1260
ttgctgacga cggctcagga catcggtgca gtcggcgtgg acagcaagtt cggctgggga   1320
ctgctggatg cgggtaaggc catgaacgga cccgcgtcct ttccgttcgg cgactttacc   1380
gccgatacga aaggtacatc cgatattgcc tactccttcc gtaacgacat ttcaggcacg   1440
ggcggcctga tcaaaaaagg cggcagccaa ctgcaactgc acggcaacaa cacctatacg   1500
ggcaaaacca ttatcgaagg cggttcgctg gtgttgtacg gcaacaacaa atcggatatg   1560
cgcgtcgaaa ccaaaggtgc gctgatttat aacggggcgg catccggcgg cagcctgaac   1620
```

```
agcgacggca ttgtctatct ggcagatacc gaccaatccg gcgcaaacga aaccgtacac   1680
atcaaaggca gtctgcagct ggacggcaaa ggtacgctgt acacacgttt gggcaaactg   1740
ctgaaagtgg acggtacggc gattatcggc ggcaagctgt acatgtcggc acgcggcaag   1800
ggggcaggct atctcaacag taccggacga cgtgttccct tcctgagtgc cgccaaaatc   1860
gggcaggatt attctttctt cacaaacatc gaaaccgacg gcggcctgct ggcttccctc   1920
gacagcgtcg aaaaaacagc gggcagtgaa ggcgacacgc tgtcctatta tgtccgtcgc   1980
ggcaatgcgg cacggactgc ttcggcagcg gcacattccg cgcccgccgg tctgaaacac   2040
gccgtagaac agggcggcag caatctggaa aacctgatgg tcgaactgga tgcctccgaa   2100
tcatccgcaa cacccgagac ggttgaaact gcggcagccg accgcacaga tatgccgggc   2160
atccgcccct acggcgcaac tttccgcgca gcggcagccg tacagcatgc gaatgccgcc   2220
gacggtgtac gcatcttcaa cagtctcgcc gctaccgtct atgccgacag taccgccgcc   2280
catgccgata tgcagggacg ccgcctgaaa gccgtatcgg acgggttgga ccacaacggc   2340
acgggtctgc gcgtcatcgc gcaaacccaa caggacggtg gaacgtggga acagggcggt   2400
gttgaaggca aaatgcgcgg cagtacccaa accgtcggca ttgccgcgaa aaccggcgaa   2460
aatacgacag cagccgccac actgggcatg ggacgcagca catggagcga aaacagtgca   2520
aatgcaaaaa ccgacagcat tagtctgttt gcaggcatac ggcacgatgc gggcgatatc   2580
ggctatctca aggcctgtt ctcctacgga cgctacaaaa acagcatcag ccgcagcacc   2640
ggtgcggacg aacatgcgga aggcagcgtc aacggcacgc tgatgcagct gggcgcactg   2700
ggcggtgtca acgttccgtt tgccgcaacg ggagatttga cggtcgaagg cggtctgcgc   2760
tacgacctgc tcaaacagga tgcattcgcc gaaaaaggca gtgctttggg ctggagcggc   2820
aacagcctca ctgaaggcac gctggtcgga ctcgcgggtc tgaagctgtc gcaacccttg   2880
agcgataaag ccgtcctgtt tgcaacggcg ggcgtggaac gcgacctgaa cggacgcgac   2940
tacacggtaa cgggcggctt taccggcgcg actgcagcaa ccggcaagac gggggcacgc   3000
aatatgccgc acacccgtct ggttgccggc ctgggcgcgg atgtcgaatt cggcaacggc   3060
tggaacggct tggcacgtta cagctacgcc ggttccaaac agtacggcaa ccacagcgga   3120
cgagtcggcg taggctaccg gttcctcgag ggtggcggag gcactggatc cgccacaaac   3180
gacgacgatg ttaaaaaagc tgccactgtg gccattgctg ctgcctacaa caatggccaa   3240
gaaatcaacg gtttcaaagc tggagagacc atctacgaca ttgatgaaga cggcacaatt   3300
accaaaaaag acgcaactgc agccgatgtt gaagccgacg actttaaagg tctgggtctg   3360
aaaaaagtcg tgactaacct gaccaaaacc gtcaatgaaa acaaacaaaa cgtcgatgcc   3420
aaagtaaaag ctgcagaatc tgaaatagaa aagttaacaa ccaagttagc agacactgat   3480
gccgctttag cagatactga tgccgctctg gatgcaacca ccaacgcctt gaataaattg   3540
ggagaaaata taacgacatt tgctgaagag actaagacaa atatcgtaaa aattgatgaa   3600
aaattagaag ccgtggctga taccgtcgac aagcatgccg aagcattcaa cgatatcgcc   3660
gattcattgg atgaaaccaa cactaaggca gacgaagccg tcaaaaccgc caatgaagcc   3720
aaacagacgg ccgaagaaac caaacaaaac gtcgatgcca aagtaaaagc tgcagaaact   3780
gcagcaggca aagccgaagc tgccgctggc acagctaata ctgcagccga caaggccgaa   3840
gctgtcgctg caaaagttac cgacatcaaa gctgatatcg ctacgaacaa agataatatt   3900
gctaaaaaag caaacagtgc cgacgtgtac accagagaag agtctgacag caaatttgtc   3960
agaattgatg gtctgaacgc tactaccgaa aaattggaca cacgcttggc ttctgctgaa   4020
aaatccattg ccgatcacga tactcgcctg aacggtttgg ataaaacagt gtcagacctg   4080
cgcaaagaaa cccgccaagg ccttgcagaa caagccgcgc tctccggtct gttccaacct   4140
tacaacgtgg gtctcgagca ccaccaccac caccactga                          4179
```

<210> 24

<211> 1392

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG983-961c

<400> 24

Met Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser
1 5 10 15

Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly
20 25 30

Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg
35 40 45

```
Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro
    50                  55                  60

Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys
65                  70                  75                  80

Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg
                85                  90                  95

Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile
            100                 105                 110

Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn
        115                 120                 125

Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly
    130                 135                 140

Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu
145                 150                 155                 160

Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His
                165                 170                 175

Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg
            180                 185                 190

Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr
        195                 200                 205

Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg Asn Ala
    210                 215                 220

Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe
225                 230                 235                 240

Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn
                245                 250                 255

Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly Gly Asp
            260                 265                 270

Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn
        275                 280                 285

Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr
    290                 295                 300

Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe
305                 310                 315                 320

Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp
                325                 330                 335

Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr
            340                 345                 350

Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp
        355                 360                 365
```

```
Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn
    370                 375                 380

Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly
385                 390                 395                 400

Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn
                405                 410                 415

Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly
            420                 425                 430

Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met
        435                 440                 445

Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys
    450                 455                 460

Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr
465                 470                 475                 480

Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn
                485                 490                 495

Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu
            500                 505                 510

Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu
        515                 520                 525

Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile
    530                 535                 540

Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His
545                 550                 555                 560

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

Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys
            580                 585                 590

Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr
        595                 600                 605

Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr
    610                 615                 620

Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu
625                 630                 635                 640

Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr
                645                 650                 655

Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His
            660                 665                 670

Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn
        675                 680                 685

Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr
```

```
    690                 695                 700

Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly
705                 710                 715                 720

Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His
                725                 730                 735

Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr
            740                 745                 750

Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly Arg Arg
        755                 760                 765

Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg
    770                 775                 780

Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly
785                 790                 795                 800

Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala
                805                 810                 815

Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg
            820                 825                 830

Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser
        835                 840                 845

Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys
    850                 855                 860

Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr
865                 870                 875                 880

Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln
                885                 890                 895

Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp
            900                 905                 910

Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala
        915                 920                 925

Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr
    930                 935                 940

Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu
945                 950                 955                 960

Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu
                965                 970                 975

Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala
            980                 985                 990

Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val
        995                 1000                1005

Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu
    1010                1015                1020
```

```
Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly
1025                1030                1035                1040

Arg Val Gly Val Gly Tyr Arg Phe Leu Glu Gly Gly Gly Gly Thr Gly
                1045                1050                1055

Ser Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
            1060                1065                1070

Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
        1075                1080                1085

Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
    1090                1095                1100

Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu
1105                1110                1115                1120

Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
                1125                1130                1135

Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
            1140                1145                1150

Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
        1155                1160                1165

Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile
    1170                1175                1180

Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
1185                1190                1195                1200

Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
                1205                1210                1215

Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu
            1220                1225                1230

Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
        1235                1240                1245

Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
    1250                1255                1260

Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
1265                1270                1275                1280

Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
                1285                1290                1295

Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
            1300                1305                1310

Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
        1315                1320                1325

Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
    1330                1335                1340
```

```
Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
1345                1350                1355                1360

Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
                1365                1370                1375

Leu Phe Gln Pro Tyr Asn Val Gly Leu Glu His His His His His His
            1380                1385                1390
```

<210> 25

<211> 274

<212> PRT

<213> Secuencia artificial

<220>

<223> 741

<400> 25

```
Val Asn Arg Thr Ala Phe Cys Cys Leu Ser Leu Thr Thr Ala Leu Ile
1               5                   10                  15

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

Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys
        35                  40                  45

Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys
    50                  55                  60

Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp
65                  70                  75                  80

Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp
                85                  90                  95

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

Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe
        115                 120                 125

Gln Thr Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala
    130                 135                 140

Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe
145                 150                 155                 160

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

Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala
            180                 185                 190

Ala Lys Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu
        195                 200                 205

Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His
    210                 215                 220

Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser
225                 230                 235                 240

Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser
                245                 250                 255

Ala Glu Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala
            260                 265                 270

Lys Gln
```

<210> 26

<211> 248

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG741

<400> 26

```
Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1               5                   10                  15

Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser
            20                  25                  30

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

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
    50                  55                  60

Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln
65                  70                  75                  80

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His
                85                  90                  95

Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His
            100                 105                 110

Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala
        115                 120                 125

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

Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr
145                 150                 155                 160

Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His
                165                 170                 175

Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys
            180                 185                 190

Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn
        195                 200                 205

Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala
```

```
    210                 215                 220

Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg
225                 230                 235                 240

His Ile Gly Leu Ala Ala Lys Gln
                245
```

<210> 27

<211> 1947

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG741-961

<400> 27

```
atggtcgccg ccgacatcgg tgcggggctt gccgatgcac taaccgcacc gctcgaccat    60
aaagacaaag gtttgcagtc tttgacgctg gatcagtccg tcaggaaaaa cgagaaactg   120
aagctggcgg cacaaggtgc ggaaaaaact tatggaaacg gtgacagcct caatacgggc   180
aaattgaaga acgacaaggt cagccgtttc gactttatcc gccaaatcga agtggacggg   240
cagctcatta ccttggagag tggagagttc caagtataca aacaaagcca ttccgcctta   300
accgcctttc agaccgagca aatacaagat tcggagcatt ccgggaagat ggttgcgaaa   360
cgccagttca gaatcggcga catagcgggc gaacatacat cttttgacaa gcttcccgaa   420
ggcggcaggg cgacatatcg cgggacggcg ttcggttcag acgatgccgg cggaaaactg   480
acctacacca tagatttcgc cgccaagcag ggaaacggca aaatcgaaca tttgaaatcg   540
ccagaactca atgtcgacct ggccgccgcc gatatcaagc cggatggaaa acgccatgcc   600
gtcatcagcg gttccgtcct ttacaaccaa gccgagaaag gcagttactc cctcggtatc   660
tttggcggaa aagcccagga agttgccggc agcgcggaag tgaaaaccgt aaacggcata   720
cgccatatcg gccttgccgc caagcaactc gagggtggcg gaggcactgg atccgccaca   780
aacgacgacg atgttaaaaa agctgccact gtggccattg ctgctgccta caacaatggc   840
caagaaatca acggtttcaa agctggagag accatctacg acattgatga agacggcaca   900
attaccaaaa aagacgcaac tgcagccgat gttgaagccg acgactttaa aggtctgggt   960
ctgaaaaaag tcgtgactaa cctgaccaaa accgtcaatg aaaacaaaca aaacgtcgat  1020
gccaaagtaa aagctgcaga atctgaaata gaaaagttaa caaccaagtt agcagacact  1080
gatgccgctt tagcagatac tgatgccgct ctggatgcaa ccaccaacgc cttgaataaa  1140
ttgggagaaa atataacgac atttgctgaa gagactaaga caaatatcgt aaaaattgat  1200
gaaaaattag aagccgtggc tgataccgtc gacaagcatg ccgaagcatt caacgatatc  1260
gccgattcat tggatgaaac caacactaag gcagacgaag ccgtcaaaac cgccaatgaa  1320
gccaaacaga cggccgaaga aaccaaacaa aacgtcgatg ccaaagtaaa agctgcagaa  1380
actgcagcag gcaaagccga agctgccgct ggcacagcta atactgcagc cgacaaggcc  1440
gaagctgtcg ctgcaaaagt taccgacatc aaagctgata tcgctacgaa caaagataat  1500
attgctaaaa aagcaaacag tgccgacgtg tacaccagag aagagtctga cagcaaattt  1560
gtcagaattg atggtctgaa cgctactacc gaaaaattgg acacacgctt ggcttctgct  1620
gaaaaatcca ttgccgatca cgatactcgc ctgaacggtt tggataaaac agtgtcagac  1680
ctgcgcaaag aaacccgcca aggccttgca gaacaagccg cgctctccgg tctgttccaa  1740
ccttacaacg tgggtcggtt caatgtaacg gctgcagtcg gcggctacaa atccgaatcg  1800
gcagtcgcca tcggtaccgg cttccgcttt accgaaaact ttgccgccaa agcaggcgtg  1860
gcagtcggca cttcgtccgg ttcttccgca gcctaccatg tcggcgtcaa ttacgagtgg  1920
ctcgagcacc accaccacca ccactga                                      1947
```

<210> 28

<211> 648

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG791-961

<400> 28

Met Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala

```
1               5                   10                  15

Pro Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln
            20                  25                  30

Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu
        35                  40                  45

Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn
    50                  55                  60

Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly
65                  70                  75                  80

Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser
                85                  90                  95

His Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu
            100                 105                 110

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

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

Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu
145                 150                 155                 160

Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu
                165                 170                 175

His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile
            180                 185                 190

Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr
        195                 200                 205

Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys
    210                 215                 220

Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile
225                 230                 235                 240

Arg His Ile Gly Leu Ala Ala Lys Gln Leu Glu Gly Gly Gly Gly Thr
                245                 250                 255

Gly Ser Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala
            260                 265                 270

Ile Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala
        275                 280                 285

Gly Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys
    290                 295                 300

Asp Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly
305                 310                 315                 320

Leu Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys
                325                 330                 335
```

```
Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys
            340                 345                 350

Leu Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp
        355                 360                 365

Ala Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn
    370                 375                 380

Ile Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp
385                 390                 395                 400

Glu Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala
                405                 410                 415

Phe Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp
            420                 425                 430

Glu Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr
        435                 440                 445

Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly
    450                 455                 460

Lys Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala
465                 470                 475                 480

Glu Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr
                485                 490                 495

Asn Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr
            500                 505                 510

Arg Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala
        515                 520                 525

Thr Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile
    530                 535                 540

Ala Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp
545                 550                 555                 560

Leu Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser
                565                 570                 575

Gly Leu Phe Gln Pro Tyr Asn Val Gly Arg Phe Asn Val Thr Ala Ala
            580                 585                 590

Val Gly Gly Tyr Lys Ser Glu Ser Ala Val Ala Ile Gly Thr Gly Phe
        595                 600                 605

Arg Phe Thr Glu Asn Phe Ala Ala Lys Ala Gly Val Ala Val Gly Thr
    610                 615                 620

Ser Ser Gly Ser Ser Ala Ala Tyr His Val Gly Val Asn Tyr Glu Trp
625                 630                 635                 640

Leu Glu His His His His His His
                645
```

<210> 29

<211> 1782

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG741-961c

<400> 29

```
atggtcgccg ccgacatcgg tgcggggctt gccgatgcac taaccgcacc gctcgaccat    60
aaagacaaag gtttgcagtc tttgacgctg gatcagtccg tcaggaaaaa cgagaaactg   120
aagctggcgg cacaaggtgc ggaaaaaact tatggaaacg gtgacagcct caatacgggc   180
aaattgaaga acgacaaggt cagccgtttc gactttatcc gccaaatcga agtggacggg   240
cagctcatta ccttggagag tggagagttc caagtataca aacaaagcca ttccgcctta   300
accgcctttc agaccgagca aatacaagat tcggagcatt ccgggaagat ggttgcgaaa   360
cgccagttca gaatcggcga catagcgggc gaacatacat cttttgacaa gcttcccgaa   420
ggcggcaggg cgacatatcg cgggacggcg ttcggttcag acgatgccgg cggaaaactg   480
acctacacca tagatttcgc cgccaagcag ggaaacggca aaatcgaaca tttgaaatcg   540
ccagaactca atgtcgacct ggccgccgcc gatatcaagc cggatggaaa acgccatgcc   600
gtcatcagcg gttccgtcct ttacaaccaa gccgagaaag gcagttactc cctcggtatc   660
tttggcggaa aagcccagga agttgccggc agcgcggaag tgaaaaccgt aaacggcata   720
cgccatatcg gccttgccgc caagcaactc gagggtggcg gaggcactgg atccgccaca   780
aacgacgacg atgttaaaaa agctgccact gtggccattg ctgctgccta caacaatggc   840
caagaaatca acggtttcaa agctggagag accatctacg acattgatga agacggcaca   900
attaccaaaa aagacgcaac tgcagccgat gttgaagccg acgactttaa aggtctgggt   960
ctgaaaaaag tcgtgactaa cctgaccaaa accgtcaatg aaaacaaaca aaacgtcgat  1020
gccaaagtaa aagctgcaga atctgaaata gaaaagttaa caaccaagtt agcagacact  1080
gatgccgctt tagcagatac tgatgccgct ctggatgcaa ccaccaacgc cttgaataaa  1140
ttgggagaaa atataacgac atttgctgaa gagactaaga caaatatcgt aaaaattgat  1200
gaaaaattag aagccgtggc tgataccgtc gacaagcatg ccgaagcatt caacgatatc  1260
gccgattcat tggatgaaac caacactaag gcagacgaag ccgtcaaaac cgccaatgaa  1320
gccaaacaga cggccgaaga aaccaaacaa aacgtcgatg ccaaagtaaa agctgcagaa  1380
actgcagcag gcaaagccga agctgccgct ggcacagcta atactgcagc cgacaaggcc  1440
gaagctgtcg ctgcaaaagt taccgacatc aaagctgata tcgctacgaa caaagataat  1500
attgctaaaa aagcaaacag tgccgacgtg tacaccagag aagagtctga cagcaaattt  1560
gtcagaattg atggtctgaa cgctactacc gaaaaattgg acacacgctt ggcttctgct  1620
gaaaaatcca ttgccgatca cgatactcgc ctgaacggtt tggataaaac agtgtcagac  1680
ctgcgcaaag aaacccgcca aggccttgca gaacaagccg cgctctccgg tctgttccaa  1740
ccttacaacg tgggtctcga gcaccaccac caccaccact ga                     1782
```

<210> 30

<211> 593

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG741-961c

<400> 30

```
Met Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala
1               5                   10                  15

Pro Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln
            20                  25                  30

Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu
        35                  40                  45

Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn
    50                  55                  60
```

```
Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly
65                  70                  75                  80

Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser
                85                  90                  95

His Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu
            100                 105                 110

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

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

Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu
145                 150                 155                 160

Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu
                165                 170                 175

His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile
            180                 185                 190

Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr
        195                 200                 205

Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys
    210                 215                 220

Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile
225                 230                 235                 240

Arg His Ile Gly Leu Ala Ala Lys Gln Leu Glu Gly Gly Gly Gly Thr
                245                 250                 255

Gly Ser Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala
            260                 265                 270

Ile Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala
        275                 280                 285

Gly Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys
    290                 295                 300

Asp Ala Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly
305                 310                 315                 320

Leu Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys
                325                 330                 335

Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys
            340                 345                 350

Leu Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp
        355                 360                 365

Ala Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn
    370                 375                 380

Ile Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp
```

```
385                 390                 395                 400

Glu Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala
                405                 410                 415

Phe Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp
            420                 425                 430

Glu Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr
        435                 440                 445

Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly
    450                 455                 460

Lys Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala
465                 470                 475                 480

Glu Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr
                485                 490                 495

Asn Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr
            500                 505                 510

Arg Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala
        515                 520                 525

Thr Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile
    530                 535                 540

Ala Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp
545                 550                 555                 560

Leu Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser
                565                 570                 575

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

His
```

<210> 31

<211> 3939

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG741-983

<400> 31

```
atggtcgccg ccgacatcgg tgcggggctt gccgatgcac taaccgcacc gctcgaccat    60
aaagacaaag gtttgcagtc tttgacgctg gatcagtccg tcaggaaaaa cgagaaactg   120
aagctggcgg cacaaggtgc ggaaaaaact tatggaaacg gtgacagcct caatacgggc   180
aaattgaaga acgacaaggt cagccgtttc gactttatcc gccaaatcga agtggacggg   240
cagctcatta ccttggagag tggagagttc caagtataca aacaaagcca ttccgcctta   300
accgcctttc agaccgagca aatacaagat tcggagcatt ccgggaagat ggttgcgaaa   360
cgccagttca gaatcggcga catagcgggc gaacatacat cttttgacaa gcttcccgaa   420
ggcggcaggg cgacatatcg cgggacggcg ttcggttcag acgatgccgg cggaaaactg   480
acctacacca tagatttcgc cgccaagcag ggaaacggca aaatcgaaca tttgaaatcg   540
ccagaactca atgtcgacct ggccgccgcc gatatcaagc cggatggaaa acgccatgcc   600
gtcatcagcg gttccgtcct ttacaaccaa gccgagaaag gcagttactc cctcggtatc   660
```

```
tttggcggaa aagcccagga agttgccggc agcgcggaag tgaaaaccgt aaacggcata   720
cgccatatcg gccttgccgc caagcaactc gagggatccg gcggaggcgg cacttctgcg   780
cccgacttca atgcaggcgg taccggtatc ggcagcaaca gcagagcaac aacagcgaaa   840
tcagcagcag tatcttacgc cggtatcaag aacgaaatgt gcaaagacag aagcatgctc   900
tgtgccggtc gggatgacgt tgcggttaca gacagggatg ccaaaatcaa tgcccccccc   960
ccgaatctgc ataccggaga ctttccaaac ccaaatgacg catacaagaa tttgatcaac  1020
ctcaaacctg caattgaagc aggctataca ggacgcgggg tagaggtagg tatcgtcgac  1080
acaggcgaat ccgtcggcag catatccttt cccgaactgt atggcagaaa agaacacggc  1140
tataacgaaa attacaaaaa ctatacggcg tatatgcgga aggaagcgcc tgaagacgga  1200
ggcggtaaag acattgaagc ttctttcgac gatgaggccg ttatagagac tgaagcaaag  1260
ccgacggata tccgccacgt aaaagaaatc ggacacatcg atttggtctc ccatattatt  1320
ggcgggcgtt ccgtggacgg cagacctgca ggcggtattg cgcccgatgc gacgctacac  1380
ataatgaata cgaatgatga aaccaagaac gaaatgatgg ttgcagccat ccgcaatgca  1440
tgggtcaagc tgggcgaacg tggcgtgcgc atcgtcaata acagttttgg aacaacatcg  1500
agggcaggca ctgccgacct tttccaaata gccaattcgg aggagcagta ccgccaagcg  1560
ttgctcgact attccggcgg tgataaaaca gacgagggta tccgcctgat gcaacagagc  1620
gattacggca acctgtccta ccacatccgt aataaaaaca tgcttttcat cttttcgaca  1680
ggcaatgacg cacaagctca gcccaacaca tatgccctat tgccatttta tgaaaaagac  1740
gctcaaaaag gcattatcac agtcgcaggc gtagaccgca gtggagaaaa gttcaaacgg  1800
gaaatgtatg gagaaccggg tacagaaccg cttgagtatg gctccaacca ttgcggaatt  1860
actgccatgt ggtgcctgtc ggcaccctat gaagcaagcg tccgtttcac ccgtacaaac  1920
ccgattcaaa ttgccggaac atccttttcc gcacccatcg taaccggcac ggcggctctg  1980
ctgctgcaga aatacccgtg gatgagcaac gacaacctgc gtaccacgtt gctgacgacg  2040
gctcaggaca tcggtgcagt cggcgtggac agcaagttcg gctggggact gctggatgcg  2100
ggtaaggcca tgaacggacc cgcgtccttt ccgttcggcg actttaccgc cgatacgaaa  2160
ggtacatccg atattgccta ctccttccgt aacgacattt caggcacggg cggcctgatc  2220
aaaaaaggcg gcagccaact gcaactgcac ggcaacaaca cctatacggg caaaaccatt  2280
atcgaaggcg gttcgctggt gttgtacggc aacaacaaat cggatatgcg cgtcgaaacc  2340
aaaggtgcgc tgatttataa cggggcggca tccggcggca gcctgaacag cgacggcatt  2400
gtctatctgg cagataccga ccaatccggc gcaaacgaaa ccgtacacat caaaggcagt  2460
ctgcagctgg acggcaaagg tacgctgtac acacgtttgg gcaaactgct gaaagtggac  2520
ggtacggcga ttatcggcgg caagctgtac atgtcggcac gcggcaaggg ggcaggctat  2580
ctcaacagta ccggacgacg tgttcccttc ctgagtgccg ccaaaatcgg gcaggattat  2640
tctttcttca caaacatcga aaccgacggc ggcctgctgg cttccctcga cagcgtcgaa  2700
aaaacagcgg gcagtgaagg cgacacgctg tcctattatg tccgtcgcgg caatgcggca  2760
cggactgctt cggcagcggc acattccgcg cccgccggtc tgaaacacgc cgtagaacag  2820
ggcggcagca atctggaaaa cctgatggtc gaactggatg cctccgaatc atccgcaaca  2880
cccgagacgg ttgaaactgc ggcagccgac cgcacagata tgccgggcat ccgcccctac  2940
ggcgcaactt tccgcgcagc ggcagccgta cagcatgcga atgccgccga cggtgtacgc  3000
atcttcaaca gtctcgccgc taccgtctat gccgacagta ccgccgccca tgccgatatg  3060
cagggacgcc gcctgaaagc cgtatcggac gggttggacc acaacggcac gggtctgcgc  3120
gtcatcgcgc aaacccaaca ggacggtgga acgtgggaac agggcggtgt tgaaggcaaa  3180
atgcgcggca gtacccaaac cgtcggcatt gccgcgaaaa ccggcgaaaa tacgacagca  3240
gccgccacac tgggcatggg acgcagcaca tggagcgaaa acagtgcaaa tgcaaaaacc  3300
gacagcatta gtctgtttgc aggcatacgg cacgatgcgg gcgatatcgg ctatctcaaa  3360
ggcctgttct cctacggacg ctacaaaaac agcatcagcc gcagcaccgg tgcggacgaa  3420
catgcggaag gcagcgtcaa cggcacgctg atgcagctgg gcgcactggg cggtgtcaac  3480
gttccgtttg ccgcaacggg agatttgacg gtcgaaggcg gtctgcgcta cgacctgctc  3540
aaacaggatg cattcgccga aaaaggcagt gctttgggct ggagcggcaa cagcctcact  3600
gaaggcacgc tggtcggact cgcgggtctg aagctgtcgc aacccttgag cgataaagcc  3660
gtcctgtttg caacggcggg cgtggaacgc gacctgaacg gacgcgacta cacggtaacg  3720
ggcggcttta ccggcgcgac tgcagcaacc ggcaagacgg gggcacgcaa tatgccgcac  3780
acccgtctgg ttgccggcct gggcgcggat gtcgaattcg gcaacggctg gaacggcttg  3840
gcacgttaca gctacgccgg ttccaaacag tacggcaacc acagcggacg agtcggcgta  3900
ggctaccggt tcctcgagca ccaccaccac caccactga                          3939
```

<210> 32

<211> 1312

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG741-983

<400> 32

```
Met Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala
1               5                   10                  15

Pro Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln
            20                  25                  30

Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu
        35                  40                  45

Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn
    50                  55                  60

Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly
65                  70                  75                  80

Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser
                85                  90                  95

His Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu
            100                 105                 110

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

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

Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu
145                 150                 155                 160

Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu
                165                 170                 175

His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile
            180                 185                 190

Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr
        195                 200                 205

Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys
    210                 215                 220

Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile
225                 230                 235                 240

Arg His Ile Gly Leu Ala Ala Lys Gln Leu Glu Gly Ser Gly Gly Gly
                245                 250                 255

Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser
            260                 265                 270

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

Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg
    290                 295                 300
```

```
Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro
305                 310                 315                 320

Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys
                325                 330                 335

Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg
            340                 345                 350

Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile
        355                 360                 365

Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn
    370                 375                 380

Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly
385                 390                 395                 400

Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu
                405                 410                 415

Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His
            420                 425                 430

Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg
        435                 440                 445

Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr
    450                 455                 460

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

Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe
                485                 490                 495

Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn
            500                 505                 510

Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser Gly Gly Asp
        515                 520                 525

Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn
    530                 535                 540

Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr
545                 550                 555                 560

Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe
                565                 570                 575

Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp
            580                 585                 590

Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr
        595                 600                 605

Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp
    610                 615                 620

Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn
```

```
625                 630                 635                 640

Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly
                645                 650                 655

Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn
            660                 665                 670

Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly
        675                 680                 685

Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met
    690                 695                 700

Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys
705                 710                 715                 720

Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr
                725                 730                 735

Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn
            740                 745                 750

Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu
        755                 760                 765

Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu
    770                 775                 780

Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile
785                 790                 795                 800

Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His
                805                 810                 815

Ile Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu Tyr Thr Arg
            820                 825                 830

Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys
        835                 840                 845

Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr
    850                 855                 860

Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr
865                 870                 875                 880

Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu
                885                 890                 895

Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr
            900                 905                 910

Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His
        915                 920                 925

Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn
    930                 935                 940

Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr
945                 950                 955                 960
```

```
Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly
                965                 970                 975

Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His
            980                 985                 990

Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr
        995                 1000                1005

Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly Arg Arg
    1010                1015                1020

Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg
1025                1030                1035                1040

Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly
                1045                1050                1055

Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala
            1060                1065                1070

Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg
        1075                1080                1085

Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser
    1090                1095                1100

Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys
1105                1110                1115                1120

Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr
                1125                1130                1135

Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln
            1140                1145                1150

Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp
        1155                1160                1165

Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala
    1170                1175                1180

Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr
1185                1190                1195                1200

Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu
                1205                1210                1215

Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu
            1220                1225                1230

Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala
        1235                1240                1245

Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val
    1250                1255                1260

Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu
1265                1270                1275                1280
```

Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly
1285 1290 1295

Arg Val Gly Val Gly Tyr Arg Phe Leu Glu His His His His His His
1300 1305 1310

<210> 33

<211> 2028

<212> ADN

<213> Secuencia artificial

<220>

<223> deltaG741-ORF46.1

<400> 33

atggtcgccg ccgacatcgg tgcggggctt gccgatgcac taaccgcacc gctcgaccat 60
aaagacaaag gtttgcagtc tttgacgctg gatcagtccg tcaggaaaaa cgagaaactg 120
aagctggcgg cacaaggtgc ggaaaaaact tatggaaacg gtgacagcct caatacgggc 180
aaattgaaga acgacaaggt cagccgtttc gactttatcc gccaaatcga agtggacggg 240
cagctcatta ccttggagag tggagagttc caagtataca aacaaagcca ttccgcctta 300
accgcctttc agaccgagca aatacaagat tcggagcatt ccgggaagat ggttgcgaaa 360
cgccagttca gaatcggcga catagcgggc gaacatacat cttttgacaa gcttcccgaa 420
ggcggcaggg cgacatatcg cgggacggcg ttcggttcag acgatgccgg cggaaaactg 480
acctacacca tagatttcgc cgccaagcag ggaaacggca aaatcgaaca tttgaaatcg 540
ccagaactca atgtcgacct ggccgccgcc gatatcaagc cggatggaaa acgccatgcc 600
gtcatcagcg gttccgtcct ttacaaccaa gccgagaaag gcagttactc cctcggtatc 660
tttggcggaa aagcccagga agttgccggc agcgcggaag tgaaaaccgt aaacggcata 720
cgccatatcg gccttgccgc caagcaactc gacggtggcg gaggcactgg atcctcagat 780
ttggcaaacg attcttttat ccggcaggtt ctcgaccgtc agcatttcga acccgacggg 840
aaataccacc tattcggcag caggggggaa cttgccgagc gcagcggcca tatcggattg 900
ggaaaaatac aaagccatca gttgggcaac ctgatgattc aacaggcggc cattaaagga 960
aatatcggct acattgtccg cttttccgat cacgggcacg aagtccattc ccccttcgac 1020
aaccatgcct cacattccga ttctgatgaa gccggtagtc ccgttgacgg atttagcctt 1080
taccgcatcc attgggacgg atacgaacac catcccgccg acggctatga cgggccacag 1140
ggcggcggct atcccgctcc caaaggcgcg agggatatat acagctacga cataaaaggc 1200
gttgcccaaa atatccgcct caacctgacc gacaaccgca gcaccggaca acggcttgcc 1260
gaccgtttcc acaatgccgg tagtatgctg acgcaaggag taggcgacgg attcaaacgc 1320
gccacccgat acagccccga gctggacaga tcgggcaatg ccgccgaagc cttcaacggc 1380
actgcagata tcgttaaaaa catcatcggc gcggcaggag aaattgtcgg cgcaggcgat 1440
gccgtgcagg gcataagcga aggctcaaac attgctgtca tgcacggctt gggtctgctt 1500
tccaccgaaa acaagatggc gcgcatcaac gatttggcag atatggcgca actcaaagac 1560
tatgccgcag cagccatccg cgattgggca gtccaaaacc ccaatgccgc acaaggcata 1620
gaagccgtca gcaatatctt tatggcagcc atccccatca aagggattgg agctgttcgg 1680
ggaaaatacg gcttgggcgg catcacggca catcctatca agcggtcgca gatgggcgcg 1740
atcgcattgc cgaaagggaa atccgccgtc agcgacaatt ttgccgatgc ggcatacgcc 1800
aaatacccgt ccccttacca ttcccgaaat atccgttcaa acttggagca gcgttacggc 1860
aaagaaaaca tcacctcctc aaccgtgccg ccgtcaaacg gcaaaaatgt caaactggca 1920
gaccaacgcc acccgaagac aggcgtaccg tttgacggta aagggtttcc gaattttgag 1980
aagcacgtga aatatgatac gctcgagcac caccaccacc accactga 2028

<210> 34

<211> 675

<212> PRT

<213> Secuencia artificial

<220>

<223> deltaG741-ORF46.1

<400> 34

Met Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala

```
1               5                   10                  15

Pro Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln
            20                  25                  30

Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu
        35                  40                  45

Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn
    50                  55                  60

Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly
65                  70                  75                  80

Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser
                85                  90                  95

His Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu
            100                 105                 110

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

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

Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu
145                 150                 155                 160

Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu
                165                 170                 175

His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile
            180                 185                 190

Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr
        195                 200                 205

Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys
    210                 215                 220

Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile
225                 230                 235                 240

Arg His Ile Gly Leu Ala Ala Lys Gln Leu Asp Gly Gly Gly Gly Thr
                245                 250                 255

Gly Ser Ser Asp Leu Ala Asn Asp Ser Phe Ile Arg Gln Val Leu Asp
            260                 265                 270

Arg Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe Gly Ser Arg
        275                 280                 285

Gly Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly Lys Ile Gln
    290                 295                 300

Ser His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala Ile Lys Gly
305                 310                 315                 320

Asn Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His Glu Val His
                325                 330                 335
```

```
Ser Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp Glu Ala Gly
            340                 345                 350

Ser Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp Asp Gly Tyr
        355                 360                 365

Glu His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly Gly Tyr
    370                 375                 380

Pro Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile Lys Gly
385                 390                 395                 400

Val Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser Thr Gly
                405                 410                 415

Gln Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met Leu Thr Gln
            420                 425                 430

Gly Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro Glu Leu
        435                 440                 445

Asp Arg Ser Gly Asn Ala Ala Glu Ala Phe Asn Gly Thr Ala Asp Ile
    450                 455                 460

Val Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly Ala Gly Asp
465                 470                 475                 480

Ala Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val Met His Gly
                485                 490                 495

Leu Gly Leu Leu Ser Thr Glu Asn Lys Met Ala Arg Ile Asn Asp Leu
            500                 505                 510

Ala Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ala Ile Arg Asp
        515                 520                 525

Trp Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala Val Ser
    530                 535                 540

Asn Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala Val Arg
545                 550                 555                 560

Gly Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile Lys Arg Ser
                565                 570                 575

Gln Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala Val Ser Asp
            580                 585                 590

Asn Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr His Ser
        595                 600                 605

Arg Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu Asn Ile
    610                 615                 620

Thr Ser Ser Thr Val Pro Pro Ser Asn Gly Lys Asn Val Lys Leu Ala
625                 630                 635                 640

Asp Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly Lys Gly Phe
                645                 650                 655
```

```
Pro Asn Phe Glu Lys His Val Lys Tyr Asp Thr Leu Glu His His His
            660                 665                 670

His His His
        675
```

<210> 35

<211> 2019

<212> ADN

<213> Secuencia artificial

<220>

<223> ORF46.1-741

<400> 35

```
atgtcagatt tggcaaacga ttcttttatc cggcaggttc tcgaccgtca gcatttcgaa    60
cccgacggga aataccacct attcggcagc aggggggaac ttgccgagcg cagcggccat   120
atcggattgg gaaaaataca aagccatcag ttgggcaacc tgatgattca acaggcggcc   180
attaaaggaa atatcggcta cattgtccgc ttttccgatc acgggcacga agtccattcc   240
cccttcgaca accatgcctc acattccgat tctgatgaag ccggtagtcc cgttgacgga   300
tttagccttt accgcatcca ttgggacgga tacgaacacc atcccgccga cggctatgac   360
gggccacagg gcggcggcta tcccgctccc aaaggcgcga gggatatata cagctacgac   420
ataaaaggcg ttgcccaaaa tatccgcctc aacctgaccg acaaccgcag caccggacaa   480
cggcttgccg accgtttcca caatgccggt agtatgctga cgcaaggagt aggcgacgga   540
ttcaaacgcg ccacccgata cagccccgag ctggacagat cgggcaatgc cgccgaagcc   600
ttcaacggca ctgcagatat cgttaaaaac atcatcggcg cggcaggaga aattgtcggc   660
gcaggcgatg ccgtgcaggg cataagcgaa ggctcaaaca ttgctgtcat gcacggcttg   720
ggtctgcttt ccaccgaaaa caagatggcg cgcatcaacg atttggcaga tatggcgcaa   780
ctcaaagact atgccgcagc agccatccgc gattgggcag tccaaaaccc caatgccgca   840
caaggcatag aagccgtcag caatatcttt atggcagcca tccccatcaa agggattgga   900
gctgttcggg gaaaatacgg cttgggcggc atcacggcac atcctatcaa gcggtcgcag   960
atgggcgcga tcgcattgcc gaaagggaaa tccgccgtca gcgacaattt tgccgatgcg  1020
gcatacgcca aatacccgtc cccttaccat tcccgaaata tccgttcaaa cttggagcag  1080
cgttacggca aagaaaacat cacctcctca accgtgccgc cgtcaaacgg caaaaatgtc  1140
aaactggcag accaacgcca cccgaagaca ggcgtaccgt ttgacggtaa agggtttccg  1200
aattttgaga agcacgtgaa atatgatacg ggatccggag gggtggtgt cgccgccgac   1260
atcggtgcgg ggcttgccga tgcactaacc gcaccgctcg accataaaga caaaggtttg  1320
cagtctttga cgctggatca gtccgtcagg aaaaacgaga aactgaagct ggcggcacaa  1380
ggtgcggaaa aaacttatgg aaacggtgac agcctcaata cgggcaaatt gaagaacgac  1440
aaggtcagcc gtttcgactt tatccgccaa atcgaagtgg acgggcagct cattaccttg  1500
gagagtggag agttccaagt atacaaacaa agccattccg ccttaaccgc ctttcagacc  1560
gagcaaatac aagattcgga gcattccggg aagatggttg cgaaacgcca gttcagaatc  1620
ggcgacatag cgggcgaaca tacatctttt gacaagcttc ccgaaggcgg cagggcgaca  1680
tatcgcggga cggcgttcgg ttcagacgat gccggcggaa aactgaccta caccatagat  1740
ttcgccgcca agcagggaaa cggcaaaatc gaacatttga aatcgccaga actcaatgtc  1800
gacctggccg ccgccgatat caagccggat ggaaaacgcc atgccgtcat cagcggttcc  1860
gtcctttaca accaagccga gaaaggcagt tactccctcg gtatctttgg cggaaaagcc  1920
caggaagttg ccggcagcgc ggaagtgaaa accgtaaacg gcatacgcca tatcggcctt  1980
gccgccaagc aactcgagca ccaccaccac caccactga                          2019
```

<210> 36

<211> 672

<212> PRT

<213> Secuencia artificial

<220>

<223> ORF46.1-741

<400> 36

```
Met Ser Asp Leu Ala Asn Asp Ser Phe Ile Arg Gln Val Leu Asp Arg
1               5                   10                  15
```

```
Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe Gly Ser Arg Gly
            20                  25                  30

Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly Lys Ile Gln Ser
        35                  40                  45

His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala Ile Lys Gly Asn
    50                  55                  60

Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His Glu Val His Ser
65                  70                  75                  80

Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp Glu Ala Gly Ser
                85                  90                  95

Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp Asp Gly Tyr Glu
            100                 105                 110

His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly Gly Tyr Pro
        115                 120                 125

Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile Lys Gly Val
    130                 135                 140

Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser Thr Gly Gln
145                 150                 155                 160

Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met Leu Thr Gln Gly
                165                 170                 175

Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro Glu Leu Asp
            180                 185                 190

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

Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly Ala Gly Asp Ala
    210                 215                 220

Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val Met His Gly Leu
225                 230                 235                 240

Gly Leu Leu Ser Thr Glu Asn Lys Met Ala Arg Ile Asn Asp Leu Ala
                245                 250                 255

Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ala Ile Arg Asp Trp
            260                 265                 270

Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala Val Ser Asn
        275                 280                 285

Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala Val Arg Gly
    290                 295                 300

Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile Lys Arg Ser Gln
305                 310                 315                 320

Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala Val Ser Asp Asn
                325                 330                 335
```

```
Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr His Ser Arg
            340                 345                 350

Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu Asn Ile Thr
        355                 360                 365

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

Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly Lys Gly Phe Pro
385                 390                 395                 400

Asn Phe Glu Lys His Val Lys Tyr Asp Thr Gly Ser Gly Gly Gly Gly
                405                 410                 415

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
            420                 425                 430

Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser
        435                 440                 445

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
    450                 455                 460

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
465                 470                 475                 480

Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln
                485                 490                 495

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His
            500                 505                 510

Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His
        515                 520                 525

Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala
    530                 535                 540

Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr
545                 550                 555                 560

Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr
                565                 570                 575

Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His
            580                 585                 590

Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys
        595                 600                 605

Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn
    610                 615                 620

Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala
625                 630                 635                 640

Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg
                645                 650                 655

His Ile Gly Leu Ala Ala Lys Gln Leu Glu His His His His His His
```

```
            660                 665                 670
```

<210> 37

<211> 2421

<212> ADN

<213> Secuencia artificial

<220>

<223> ORF46.1-961

<400> 37

```
atgtcagatt tggcaaacga ttcttttatc cggcaggttc tcgaccgtca gcatttcgaa   60
cccgacggga aataccacct attcggcagc aggggggaac ttgccgagcg cagcggccat  120
atcggattgg gaaaaataca aagccatcag ttgggcaacc tgatgattca acaggcggcc  180
attaaaggaa atatcggcta cattgtccgc ttttccgatc acgggcacga agtccattcc  240
cccttcgaca accatgcctc acattccgat tctgatgaag ccggtagtcc cgttgacgga  300
tttagccttt accgcatcca ttgggacgga tacgaacacc atcccgccga cggctatgac  360
gggccacagg gcggcggcta tcccgctccc aaaggcgcga gggatatata cagctacgac  420
ataaaaggcg ttgcccaaaa tatccgcctc aacctgaccg acaaccgcag caccggacaa  480
cggcttgccg accgtttcca caatgccggt agtatgctga cgcaaggagt aggcgacgga  540
ttcaaacgcg ccacccgata cagccccgag ctggacagat cgggcaatgc cgccgaagcc  600
ttcaacggca ctgcagatat cgttaaaaac atcatcggcg cggcaggaga aattgtcggc  660
gcaggcgatg ccgtgcaggg cataagcgaa ggctcaaaca ttgctgtcat gcacggcttg  720
ggtctgcttt ccaccgaaaa caagatggcg cgcatcaacg atttggcaga tatggcgcaa  780
ctcaaagact atgccgcagc agccatccgc gattgggcag tccaaaaccc caatgccgca  840
caaggcatag aagccgtcag caatatcttt atggcagcca tccccatcaa agggattgga  900
gctgttcggg gaaaatacgg cttgggcggc atcacggcac atcctatcaa gcggtcgcag  960
atgggcgcga tcgcattgcc gaaagggaaa tccgccgtca gcgacaattt tgccgatgcg 1020
gcatacgcca aatacccgtc cccttaccat tcccgaaata tccgttcaaa cttggagcag 1080
cgttacggca aagaaaacat cacctcctca accgtgccgc cgtcaaacgg caaaaatgtc 1140
aaactggcag accaacgcca cccgaagaca ggcgtaccgt ttgacggtaa agggtttccg 1200
aattttgaga agcacgtgaa atatgatacg ggatccggag gaggaggagc cacaaacgac 1260
gacgatgtta aaaaagctgc cactgtggcc attgctgctg cctacaacaa tggccaagaa 1320
atcaacggtt tcaaagctgg agagaccatc tacgacattg atgaagacgg cacaattacc 1380
aaaaaagacg caactgcagc cgatgttgaa gccgacgact ttaaaggtct gggtctgaaa 1440
aaagtcgtga ctaacctgac caaaaccgtc aatgaaaaca aacaaaacgt cgatgccaaa 1500
gtaaaagctg cagaatctga aatagaaaag ttaacaacca agttagcaga cactgatgcc 1560
gctttagcag atactgatgc cgctctggat gcaaccacca acgccttgaa taaattggga 1620
gaaaatataa cgacatttgc tgaagagact aagacaaata tcgtaaaaat tgatgaaaaa 1680
ttagaagccg tggctgatac cgtcgacaag catgccgaag cattcaacga tatcgccgat 1740
tcattggatg aaaccaacac taaggcagac gaagccgtca aaaccgccaa tgaagccaaa 1800
cagacggccg aagaaaccaa acaaaacgtc gatgccaaag taaaagctgc agaaactgca 1860
gcaggcaaag ccgaagctgc cgctggcaca gctaatactg cagccgacaa ggccgaagct 1920
gtcgctgcaa aagttaccga catcaaagct gatatcgcta cgaacaaaga taatattgct 1980
aaaaaagcaa acagtgccga cgtgtacacc agagaagagt ctgacagcaa atttgtcaga 2040
attgatggtc tgaacgctac taccgaaaaa ttggacacac gcttggcttc tgctgaaaaa 2100
tccattgccg atcacgatac tcgcctgaac ggtttggata aaacagtgtc agacctgcgc 2160
aaagaaaccc gccaaggcct tgcagaacaa gccgcgctct ccggtctgtt ccaaccttac 2220
aacgtgggtc ggttcaatgt aacggctgca gtcggcggct acaaatccga atcggcagtc 2280
gccatcggta ccggcttccg ctttaccgaa aactttgccg ccaaagcagg cgtggcagtc 2340
ggcacttcgt ccggttcttc cgcagcctac catgtcggcg tcaattacga gtggctcgag 2400
caccaccacc accaccactg a                                            2421
```

<210> 38

<211> 806

<212> PRT

<213> Secuencia artificial

<220>

<223> ORF46.1-961

<400> 38

```
Met Ser Asp Leu Ala Asn Asp Ser Phe Ile Arg Gln Val Leu Asp Arg
1               5                   10                  15

Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe Gly Ser Arg Gly
            20                  25                  30

Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly Lys Ile Gln Ser
        35                  40                  45

His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala Ile Lys Gly Asn
    50                  55                  60

Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His Glu Val His Ser
65                  70                  75                  80

Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp Glu Ala Gly Ser
                85                  90                  95

Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp Asp Gly Tyr Glu
            100                 105                 110

His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly Gly Tyr Pro
        115                 120                 125

Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile Lys Gly Val
    130                 135                 140

Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser Thr Gly Gln
145                 150                 155                 160

Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met Leu Thr Gln Gly
                165                 170                 175

Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro Glu Leu Asp
            180                 185                 190

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

Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly Ala Gly Asp Ala
    210                 215                 220

Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val Met His Gly Leu
225                 230                 235                 240

Gly Leu Leu Ser Thr Glu Asn Lys Met Ala Arg Ile Asn Asp Leu Ala
                245                 250                 255

Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ala Ile Arg Asp Trp
            260                 265                 270

Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala Val Ser Asn
        275                 280                 285

Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala Val Arg Gly
    290                 295                 300

Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile Lys Arg Ser Gln
305                 310                 315                 320
```

```
Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala Val Ser Asp Asn
                325                 330                 335

Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr His Ser Arg
            340                 345                 350

Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu Asn Ile Thr
        355                 360                 365

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

Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly Lys Gly Phe Pro
385                 390                 395                 400

Asn Phe Glu Lys His Val Lys Tyr Asp Thr Gly Ser Gly Gly Gly Gly
                405                 410                 415

Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile Ala
            420                 425                 430

Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly Glu
        435                 440                 445

Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp Ala
    450                 455                 460

Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu Lys
465                 470                 475                 480

Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln Asn
                485                 490                 495

Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu Thr
            500                 505                 510

Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala Ala
        515                 520                 525

Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile Thr
    530                 535                 540

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

Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe Asn
                565                 570                 575

Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu Ala
            580                 585                 590

Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys Gln
        595                 600                 605

Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys Ala
    610                 615                 620

Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu Ala
625                 630                 635                 640
```

```
Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn Lys
                645                 650                 655

Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg Glu
            660                 665                 670

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

Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala Asp
    690                 695                 700

His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu Arg
705                 710                 715                 720

Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly Leu
                725                 730                 735

Phe Gln Pro Tyr Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val Gly
            740                 745                 750

Gly Tyr Lys Ser Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg Phe
        755                 760                 765

Thr Glu Asn Phe Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser Ser
    770                 775                 780

Gly Ser Ser Ala Ala Tyr His Val Gly Val Asn Tyr Glu Trp Leu Glu
785                 790                 795                 800

His His His His His His
                805
```

<210> 39

<211> 2256

<212> ADN

<213> Secuencia artificial

<220>

<223> ORF46.1-961c

<400> 39

```
atgtcagatt tggcaaacga ttcttttatc cggcaggttc tcgaccgtca gcatttcgaa    60
cccgacggga aataccacct attcggcagc aggggggaac ttgccgagcg cagcggccat   120
atcggattgg gaaaaataca aagccatcag ttgggcaacc tgatgattca acaggcggcc   180
attaaaggaa atatcggcta cattgtccgc ttttccgatc acgggcacga agtccattcc   240
cccttcgaca accatgcctc acattccgat tctgatgaag ccggtagtcc cgttgacgga   300
tttagccttt accgcatcca ttgggacgga tacgaacacc atcccgccga cggctatgac   360
gggccacagg gcggcggcta tcccgctccc aaaggcgcga gggatatata cagctacgac   420
ataaaaggcg ttgcccaaaa tatccgcctc aacctgaccg acaaccgcag caccggacaa   480
cggcttgccg accgtttcca caatgccggt agtatgctga cgcaaggagt aggcgacgga   540
ttcaaacgcg ccacccgata cagccccgag ctggacagat cgggcaatgc cgccgaagcc   600
ttcaacggca ctgcagatat cgttaaaaac atcatcggcg cggcaggaga aattgtcggc   660
gcaggcgatg ccgtgcaggg cataagcgaa ggctcaaaca ttgctgtcat gcacggcttg   720
ggtctgcttt ccaccgaaaa caagatggcg cgcatcaacg atttggcaga tatggcgcaa   780
ctcaaagact atgccgcagc agccatccgc gattgggcag tccaaaaccc caatgccgca   840
caaggcatag aagccgtcag caatatcttt atggcagcca tccccatcaa agggattgga   900
gctgttcggg gaaaatacgg cttgggcggc atcacggcac atcctatcaa gcggtcgcag   960
atgggcgcga tcgcattgcc gaaagggaaa tccgccgtca gcgacaattt tgccgatgcg  1020
gcatacgcca aatacccgtc cccttaccat tcccgaaata tccgttcaaa cttggagcag  1080
cgttacggca aagaaaacat cacctcctca accgtgccgc cgtcaaacgg caaaaatgtc  1140

aaactggcag accaacgcca cccgaagaca ggcgtaccgt ttgacggtaa agggtttccg  1200
aattttgaga agcacgtgaa atatgatacg ggatccggag gaggaggagc cacaaacgac  1260
gacgatgtta aaaaagctgc cactgtggcc attgctgctg cctacaacaa tggccaagaa  1320
atcaacggtt tcaaagctgg agagaccatc tacgacattg atgaagacgg cacaattacc  1380
aaaaaagacg caactgcagc cgatgttgaa gccgacgact ttaaaggtct gggtctgaaa  1440
aaagtcgtga ctaacctgac caaaaccgtc aatgaaaaca aacaaaacgt cgatgccaaa  1500
gtaaaagctg cagaatctga aatagaaaag ttaacaacca agttagcaga cactgatgcc  1560
gctttagcag atactgatgc cgctctggat gcaaccacca acgccttgaa taaattggga  1620
gaaaatataa cgacatttgc tgaagagact aagacaaata tcgtaaaaat tgatgaaaaa  1680
ttagaagccg tggctgatac cgtcgacaag catgccgaag cattcaacga tatcgccgat  1740
tcattggatg aaaccaacac taaggcagac gaagccgtca aaaccgccaa tgaagccaaa  1800
cagacggccg aagaaaccaa acaaaacgtc gatgccaaag taaaagctgc agaaactgca  1860
gcaggcaaag ccgaagctgc cgctggcaca gctaatactg cagccgacaa ggccgaagct  1920
gtcgctgcaa aagttaccga catcaaagct gatatcgcta cgaacaaaga taatattgct  1980
aaaaaagcaa acagtgccga cgtgtacacc agagaagagt ctgacagcaa atttgtcaga  2040
attgatggtc tgaacgctac taccgaaaaa ttggacacac gcttggcttc tgctgaaaaa  2100
tccattgccg atcacgatac tcgcctgaac ggtttggata aaacagtgtc agacctgcgc  2160
aaagaaaccc gccaaggcct tgcagaacaa gccgcgctct ccggtctgtt ccaaccttac  2220
aacgtgggtc tcgagcacca ccaccaccac cactga                            2256
```

<210> 40

<211> 751

<212> PRT

<213> Secuencia artificial

<220>

<223> ORF46.1-961c

<400> 40

```
Met Ser Asp Leu Ala Asn Asp Ser Phe Ile Arg Gln Val Leu Asp Arg
1               5                   10                  15

Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe Gly Ser Arg Gly
            20                  25                  30

Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly Lys Ile Gln Ser
        35                  40                  45

His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala Ile Lys Gly Asn
    50                  55                  60

Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His Glu Val His Ser
65                  70                  75                  80

Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp Glu Ala Gly Ser
                85                  90                  95

Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp Asp Gly Tyr Glu
            100                 105                 110

His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly Gly Tyr Pro
        115                 120                 125

Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile Lys Gly Val
    130                 135                 140

Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser Thr Gly Gln
145                 150                 155                 160

Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met Leu Thr Gln Gly
                165                 170                 175
```

```
Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro Glu Leu Asp
            180                 185                 190

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

Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly Ala Gly Asp Ala
    210                 215                 220

Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val Met His Gly Leu
225                 230                 235                 240

Gly Leu Leu Ser Thr Glu Asn Lys Met Ala Arg Ile Asn Asp Leu Ala
                245                 250                 255

Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ala Ile Arg Asp Trp
            260                 265                 270

Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala Val Ser Asn
        275                 280                 285

Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala Val Arg Gly
    290                 295                 300

Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile Lys Arg Ser Gln
305                 310                 315                 320

Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala Val Ser Asp Asn
                325                 330                 335

Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr His Ser Arg
            340                 345                 350

Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu Asn Ile Thr
        355                 360                 365

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

Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly Lys Gly Phe Pro
385                 390                 395                 400

Asn Phe Glu Lys His Val Lys Tyr Asp Thr Gly Ser Gly Gly Gly Gly
                405                 410                 415

Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile Ala
            420                 425                 430

Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly Glu
        435                 440                 445

Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp Ala
    450                 455                 460

Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu Lys
465                 470                 475                 480

Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln Asn
                485                 490                 495
```

```
Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu Thr
            500                 505                 510

Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala Ala
        515                 520                 525

Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile Thr
    530                 535                 540

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

Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe Asn
                565                 570                 575

Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu Ala
            580                 585                 590

Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys Gln
        595                 600                 605

Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys Ala
    610                 615                 620

Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu Ala
625                 630                 635                 640

Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn Lys
                645                 650                 655

Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg Glu
            660                 665                 670

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

Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala Asp
    690                 695                 700

His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu Arg
705                 710                 715                 720

Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly Leu
                725                 730                 735

Phe Gln Pro Tyr Asn Val Gly Leu Glu His His His His His His
            740                 745                 750
```

<210> 41

<211> 2421

<212> ADN

<213> Secuencia artificial

<220>

<223> 961-ORF46.1

<400> 41

```
atggccacaa acgacgacga tgttaaaaaa gctgccactg tggccattgc tgctgcctac    60
aacaatggcc aagaaatcaa cggtttcaaa gctggagaga ccatctacga cattgatgaa   120
gacggcacaa ttaccaaaaa agacgcaact gcagccgatg ttgaagccga cgactttaaa   180
ggtctgggtc tgaaaaaagt cgtgactaac ctgaccaaaa ccgtcaatga aaacaaacaa   240

aacgtcgatg ccaaagtaaa agctgcagaa tctgaaatag aaaagttaac aaccaagtta   300
gcagacactg atgccgcttt agcagatact gatgccgctc tggatgcaac caccaacgcc   360
ttgaataaat tgggagaaaa tataacgaca tttgctgaag agactaagac aaatatcgta   420
aaaattgatg aaaaattaga agccgtggct gataccgtcg acaagcatgc cgaagcattc   480
aacgatatcg ccgattcatt ggatgaaacc aacactaagg cagacgaagc cgtcaaaacc   540
gccaatgaag ccaaacagac ggccgaagaa accaaacaaa acgtcgatgc caaagtaaaa   600
gctgcagaaa ctgcagcagg caaagccgaa gctgccgctg gcacagctaa tactgcagcc   660
gacaaggccg aagctgtcgc tgcaaaagtt accgacatca aagctgatat cgctacgaac   720
aaagataata ttgctaaaaa agcaaacagt gccgacgtgt acaccagaga agagtctgac   780
agcaaatttg tcagaattga tggtctgaac gctactaccg aaaaattgga cacacgcttg   840
gcttctgctg aaaaatccat tgccgatcac gatactcgcc tgaacggttt ggataaaaca   900
gtgtcagacc tgcgcaaaga aacccgccaa ggccttgcag aacaagccgc gctctccggt   960
ctgttccaac cttacaacgt gggtcggttc aatgtaacgg ctgcagtcgg cggctacaaa  1020
tccgaatcgg cagtcgccat cggtaccggc ttccgcttta ccgaaaactt tgccgccaaa  1080
gcaggcgtgg cagtcggcac ttcgtccggt tcttccgcag cctaccatgt cggcgtcaat  1140
tacgagtggg gatccggagg aggaggatca gatttggcaa acgattcttt tatccggcag  1200
gttctcgacc gtcagcattt cgaacccgac gggaaatacc acctattcgg cagcaggggg  1260
gaacttgccg agcgcagcgg ccatatcgga ttgggaaaaa tacaaagcca tcagttgggc  1320
aacctgatga ttcaacaggc ggccattaaa ggaaatatcg gctacattgt ccgcttttcc  1380
gatcacgggc acgaagtcca ttcccccttc gacaaccatg cctcacattc cgattctgat  1440
gaagccggta gtcccgttga cggatttagc ctttaccgca tccattggga cggatacgaa  1500
caccatcccg ccgacggcta tgacgggcca cagggcggcg gctatcccgc tcccaaaggc  1560
gcgagggata tatacagcta cgacataaaa ggcgttgccc aaaatatccg cctcaacctg  1620
accgacaacc gcagcaccgg acaacggctt gccgaccgtt tccacaatgc cggtagtatg  1680
ctgacgcaag gagtaggcga cggattcaaa cgcgccaccc gatacagccc cgagctggac  1740
agatcgggca atgccgccga agccttcaac ggcactgcag atatcgttaa aaacatcatc  1800
ggcgcggcag gagaaattgt cggcgcaggc gatgccgtgc agggcataag cgaaggctca  1860
aacattgctg tcatgcacgg cttgggtctg ctttccaccg aaaacaagat ggcgcgcatc  1920
aacgatttgg cagatatggc gcaactcaaa gactatgccg cagcagccat ccgcgattgg  1980
gcagtccaaa accccaatgc cgcacaaggc atagaagccg tcagcaatat ctttatggca  2040
gccatcccca tcaaagggat tggagctgtt cggggaaaat acggcttggg cggcatcacg  2100
gcacatccta tcaagcggtc gcagatgggc gcgatcgcat tgccgaaagg gaaatccgcc  2160
gtcagcgaca attttgccga tgcggcatac gccaaatacc cgtcccctta ccattcccga  2220
aatatccgtt caaacttgga gcagcgttac ggcaaagaaa acatcacctc ctcaaccgtg  2280
ccgccgtcaa acggcaaaaa tgtcaaactg gcagaccaac gccacccgaa gacaggcgta  2340
ccgtttgacg gtaaagggtt tccgaatttt gagaagcacg tgaaatatga tacgctcgag  2400
caccaccacc accaccactg a                                            2421
```

<210> 42

<211> 806

<212> PRT

<213> Secuencia artificial

<220>

<223> 961-ORF46.1

<400> 42

```
Met Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
1               5                   10                  15

Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
            20                  25                  30

Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
        35                  40                  45

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

Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
65                  70                  75                  80
```

```
Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
                85                  90                  95

Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
            100                 105                 110

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

Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
    130                 135                 140

Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
145                 150                 155                 160

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

Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
            180                 185                 190

Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
        195                 200                 205

Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
    210                 215                 220

Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
225                 230                 235                 240

Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
                245                 250                 255

Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
            260                 265                 270

Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
        275                 280                 285

Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
    290                 295                 300

Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
305                 310                 315                 320

Leu Phe Gln Pro Tyr Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val
                325                 330                 335

Gly Gly Tyr Lys Ser Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg
            340                 345                 350

Phe Thr Glu Asn Phe Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser
        355                 360                 365

Ser Gly Ser Ser Ala Ala Tyr His Val Gly Val Asn Tyr Glu Trp Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Leu Ala Asn Asp Ser Phe Ile Arg Gln
385                 390                 395                 400
```

```
Val Leu Asp Arg Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe
                405                 410                 415

Gly Ser Arg Gly Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly
            420                 425                 430

Lys Ile Gln Ser His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala
        435                 440                 445

Ile Lys Gly Asn Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His
    450                 455                 460

Glu Val His Ser Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp
465                 470                 475                 480

Glu Ala Gly Ser Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp
                485                 490                 495

Asp Gly Tyr Glu His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly
            500                 505                 510

Gly Gly Tyr Pro Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp
        515                 520                 525

Ile Lys Gly Val Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg
    530                 535                 540

Ser Thr Gly Gln Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met
545                 550                 555                 560

Leu Thr Gln Gly Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser
                565                 570                 575

Pro Glu Leu Asp Arg Ser Gly Asn Ala Ala Glu Ala Phe Asn Gly Thr
            580                 585                 590

Ala Asp Ile Val Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly
        595                 600                 605

Ala Gly Asp Ala Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val
    610                 615                 620

Met His Gly Leu Gly Leu Leu Ser Thr Glu Asn Lys Met Ala Arg Ile
625                 630                 635                 640

Asn Asp Leu Ala Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ala
                645                 650                 655

Ile Arg Asp Trp Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu
            660                 665                 670

Ala Val Ser Asn Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly
        675                 680                 685

Ala Val Arg Gly Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile
    690                 695                 700

Lys Arg Ser Gln Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala
705                 710                 715                 720

Val Ser Asp Asn Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro
```

```
                    725                      730                      735

Tyr His Ser Arg Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys
            740                     745                     750

Glu Asn Ile Thr Ser Ser Thr Val Pro Pro Ser Asn Gly Lys Asn Val
        755                     760                     765

Lys Leu Ala Asp Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly
    770                     775                     780

Lys Gly Phe Pro Asn Phe Glu Lys His Val Lys Tyr Asp Thr Leu Glu
785                     790                     795                     800

His His His His His His
                805
```

<210> 43

<211> 1938

<212> ADN

<213> Secuencia artificial

<220>

<223> 961-741

<400> 43

```
atggccacaa acgacgacga tgttaaaaaa gctgccactg tggccattgc tgctgcctac   60
aacaatggcc aagaaatcaa cggtttcaaa gctggagaga ccatctacga cattgatgaa  120
gacggcacaa ttaccaaaaa agacgcaact gcagccgatg ttgaagccga cgactttaaa  180
ggtctgggtc tgaaaaaagt cgtgactaac ctgaccaaaa ccgtcaatga aaacaaacaa  240
aacgtcgatg ccaaagtaaa agctgcagaa tctgaaatag aaaagttaac aaccaagtta  300
gcagacactg atgccgcttt agcagatact gatgccgctc tggatgcaac caccaacgcc  360
ttgaataaat tgggagaaaa tataacgaca tttgctgaag agactaagac aaatatcgta  420
aaaattgatg aaaaattaga agccgtggct gataccgtcg acaagcatgc cgaagcattc  480
aacgatatcg ccgattcatt ggatgaaacc aacactaagg cagacgaagc cgtcaaaacc  540
gccaatgaag ccaaacagac ggccgaagaa accaaacaaa acgtcgatgc caaagtaaaa  600
gctgcagaaa ctgcagcagg caaagccgaa gctgccgctg gcacagctaa tactgcagcc  660
gacaaggccg aagctgtcgc tgcaaaagtt accgacatca aagctgatat cgctacgaac  720
aaagataata ttgctaaaaa agcaaacagt gccgacgtgt acaccagaga agagtctgac  780
agcaaatttg tcagaattga tggtctgaac gctactaccg aaaaattgga cacacgcttg  840
gcttctgctg aaaaatccat tgccgatcac gatactcgcc tgaacggttt ggataaaaca  900
gtgtcagacc tgcgcaaaga aacccgccaa ggccttgcag aacaagccgc gctctccggt  960
ctgttccaac cttacaacgt gggtcggttc aatgtaacgg ctgcagtcgg cggctacaaa 1020
tccgaatcgg cagtcgccat cggtaccggc ttccgcttta ccgaaaactt tgccgccaaa 1080
gcaggcgtgg cagtcggcac ttcgtccggt tcttccgcag cctaccatgt cggcgtcaat 1140
tacgagtggg gatccggagg gggtggtgtc gccgccgaca tcggtgcggg gcttgccgat 1200
gcactaaccg caccgctcga ccataaagac aaaggtttgc agtctttgac gctggatcag 1260
tccgtcagga aaaacgagaa actgaagctg gcggcacaag gtgcggaaaa aacttatgga 1320
aacggtgaca gcctcaatac gggcaaattg aagaacgaca aggtcagccg tttcgacttt 1380
atccgccaaa tcgaagtgga cgggcagctc attaccttgg agagtggaga- gttccaagta 1440
tacaaacaaa gccattccgc cttaaccgcc tttcagaccg agcaaataca agattcggag 1500
cattccggga agatggttgc gaaacgccag ttcagaatcg gcgacatagc gggcgaacat 1560
acatcttttg acaagcttcc cgaaggcggc agggcgacat atcgcgggac ggcgttcggt 1620
tcagacgatg ccggcggaaa actgacctac accatagatt tcgccgccaa gcagggaaac 1680
ggcaaaatcg aacatttgaa atcgccagaa ctcaatgtcg acctggccgc cgccgatatc 1740
aagccggatg gaaaacgcca tgccgtcatc agcggttccg tcctttacaa ccaagccgag 1800
aaaggcagtt actccctcgg tatctttggc ggaaaagccc aggaagttgc cggcagcgcg 1860
gaagtgaaaa ccgtaaacgg catacgccat atcggccttg ccgccaagca actcgagcac 1920
caccaccacc accactga                                                1938
```

<210> 44

<211> 645

<212> PRT

<213> Secuencia artificial

<220>

<223> 961-741

<400> 44

```
Met Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
1               5                   10                  15

Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
            20                  25                  30

Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
        35                  40                  45

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

Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
65                  70                  75                  80

Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
                85                  90                  95

Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
            100                 105                 110

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

Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
    130                 135                 140

Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
145                 150                 155                 160

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

Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
            180                 185                 190

Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
        195                 200                 205

Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
    210                 215                 220

Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
225                 230                 235                 240

Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
                245                 250                 255

Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
            260                 265                 270

Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
        275                 280                 285
```

```
Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
    290                 295                 300

Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
305                 310                 315                 320

Leu Phe Gln Pro Tyr Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val
                325                 330                 335

Gly Gly Tyr Lys Ser Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg
            340                 345                 350

Phe Thr Glu Asn Phe Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser
        355                 360                 365

Ser Gly Ser Ser Ala Ala Tyr His Val Gly Val Asn Tyr Glu Trp Gly
    370                 375                 380

Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp
385                 390                 395                 400

Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu
                405                 410                 415

Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala
            420                 425                 430

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

Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile
    450                 455                 460

Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val
465                 470                 475                 480

Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile
                485                 490                 495

Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg
            500                 505                 510

Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu
        515                 520                 525

Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala
    530                 535                 540

Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn
545                 550                 555                 560

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

Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly
            580                 585                 590

Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile
        595                 600                 605
```

Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr
610 615 620

Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln Leu Glu His
625 630 635 640

His His His His His
645

<210> 45

<211> 4335

<212> ADN

<213> Secuencia artificial

<220>

<223> 961-983

<400> 45

atggccacaa acgacgacga tgttaaaaaa gctgccactg tggccattgc tgctgcctac 60
aacaatggcc aagaaatcaa cggtttcaaa gctggagaga ccatctacga cattgatgaa 120
gacggcacaa ttaccaaaaa agacgcaact gcagccgatg ttgaagccga cgactttaaa 180
ggtctgggtc tgaaaaaagt cgtgactaac ctgaccaaaa ccgtcaatga aaacaaacaa 240
aacgtcgatg ccaaagtaaa agctgcagaa tctgaaatag aaaagttaac aaccaagtta 300
gcagacactg atgccgcttt agcagatact gatgccgctc tggatgcaac caccaacgcc 360
ttgaataaat tgggagaaaa tataacgaca tttgctgaag agactaagac aaatatcgta 420
aaaattgatg aaaaattaga agccgtggct gataccgtcg acaagcatgc cgaagcattc 480
aacgatatcg ccgattcatt ggatgaaacc aacactaagg cagacgaagc cgtcaaaacc 540
gccaatgaag ccaaacagac ggccgaagaa accaaacaaa acgtcgatgc caaagtaaaa 600
gctgcagaaa ctgcagcagg caaagccgaa gctgccgctg gcacagctaa tactgcagcc 660
gacaaggccg aagctgtcgc tgcaaaagtt accgacatca aagctgatat cgctacgaac 720
aaagataata ttgctaaaaa agcaaacagt gccgacgtgt acaccagaga agagtctgac 780
agcaaatttg tcagaattga tggtctgaac gctactaccg aaaaattgga cacacgcttg 840
gcttctgctg aaaaatccat tgccgatcac gatactcgcc tgaacggttt ggataaaaca 900
gtgtcagacc tgcgcaaaga aacccgccaa ggccttgcag aacaagccgc gctctccggt 960
ctgttccaac cttacaacgt gggtcggttc aatgtaacgg ctgcagtcgg cggctacaaa 1020
tccgaatcgg cagtcgccat cggtaccggc ttccgcttta ccgaaaactt tgccgccaaa 1080
gcaggcgtgg cagtcggcac ttcgtccggt tcttccgcag cctaccatgt cggcgtcaat 1140
tacgagtggg gatccggcgg aggcggcact tctgcgcccg acttcaatgc aggcggtacc 1200
ggtatcggca gcaacagcag agcaacaaca gcgaaatcag cagcagtatc ttacgccggt 1260
atcaagaacg aaatgtgcaa agacagaagc atgctctgtg ccggtcggga tgacgttgcg 1320
gttacagaca gggatgccaa aatcaatgcc cccccccga atctgcatac cggagacttt 1380
ccaaacccaa atgacgcata caagaatttg atcaacctca aacctgcaat tgaagcaggc 1440
tatacaggac gcggggtaga ggtaggtatc gtcgacacag gcgaatccgt cggcagcata 1500
tcctttcccg aactgtatgg cagaaaagaa cacggctata acgaaaatta caaaaactat 1560
acggcgtata tgcggaagga agcgcctgaa gacggaggcg gtaaagacat tgaagcttct 1620
ttcgacgatg aggccgttat agagactgaa gcaaagccga cggatatccg ccacgtaaaa 1680
gaaatcggac acatcgattt ggtctcccat attattggcg ggcgttccgt ggacggcaga 1740
cctgcaggcg gtattgcgcc cgatgcgacg ctacacataa tgaatacgaa tgatgaaacc 1800
aagaacgaaa tgatggttgc agccatccgc aatgcatggg tcaagctggg cgaacgtggc 1860
gtgcgcatcg tcaataacag ttttggaaca acatcgaggg caggcactgc cgaccttttc 1920
caaatagcca attcggagga gcagtaccgc caagcgttgc tcgactattc cggcggtgat 1980
aaaacagacg agggtatccg cctgatgcaa cagagcgatt acggcaacct gtcctaccac 2040
atccgtaata aaaacatgct tttcatcttt tcgacaggca atgacgcaca agctcagccc 2100
aacacatatg ccctattgcc attttatgaa aaagacgctc aaaaaggcat tatcacagtc 2160
gcaggcgtag accgcagtgg agaaaagttc aaacgggaaa tgtatggaga accgggtaca 2220
gaaccgcttg agtatggctc caaccattgc ggaattactg ccatgtggtg cctgtcggca 2280
ccctatgaag caagcgtccg tttcacccgt acaaacccga ttcaaattgc cggaacatcc 2340
ttttccgcac ccatcgtaac cggcacggcg gctctgctgc tgcagaaata cccgtggatg 2400
agcaacgaca acctgcgtac cacgttgctg acgacggctc aggacatcgg tgcagtcggc 2460
gtggacagca agttcggctg gggactgctg gatgcgggta aggccatgaa cggacccgcg 2520
tcctttccgt tcggcgactt taccgccgat acgaaaggta catccgatat tgcctactcc 2580

```
ttccgtaacg acatttcagg cacgggcggc ctgatcaaaa aaggcggcag ccaactgcaa   2640
ctgcacggca acaacaccta tacgggcaaa accattatcg aaggcggttc gctggtgttg   2700
tacggcaaca acaaatcgga tatgcgcgtc gaaaccaaag gtgcgctgat ttataacggg   2760
gcggcatccg gcggcagcct gaacagcgac ggcattgtct atctggcaga taccgaccaa   2820
tccggcgcaa acgaaaccgt acacatcaaa ggcagtctgc agctggacgg caaaggtacg   2880
ctgtacacac gtttgggcaa actgctgaaa gtggacggta cggcgattat cggcggcaag   2940
ctgtacatgt cggcacgcgg caaggggggca ggctatctca acagtaccgg acgacgtgtt   3000
cccttcctga gtgccgccaa aatcgggcag gattattctt tcttcacaaa catcgaaacc   3060
gacggcggcc tgctggcttc cctcgacagc gtcgaaaaaa cagcgggcag tgaaggcgac   3120
acgctgtcct attatgtccg tcgcggcaat gcggcacgga ctgcttcggc agcggcacat   3180
tccgcgcccg ccggtctgaa acacgccgta gaacagggcg gcagcaatct ggaaaacctg   3240
atggtcgaac tggatgcctc cgaatcatcc gcaacacccg agacggttga aactgcggca   3300
gccgaccgca cagatatgcc gggcatccgc ccctacggcg caactttccg cgcagcggca   3360
gccgtacagc atgcgaatgc cgccgacggt gtacgcatct tcaacagtct cgccgctacc   3420
gtctatgccg acagtaccgc cgcccatgcc gatatgcagg gacgccgcct gaaagccgta   3480
tcggacgggt tggaccacaa cggcacgggt ctgcgcgtca tcgcgcaaac ccaacaggac   3540
ggtggaacgt gggaacaggg cggtgttgaa ggcaaaatgc gcggcagtac ccaaaccgtc   3600
ggcattgccg cgaaaaccgg cgaaaatacg acagcagccg ccacactggg catggacgc   3660
agcacatgga gcgaaaacag tgcaaatgca aaaaccgaca gcattagtct gtttgcaggc   3720
atacggcacg atgcgggcga tatcggctat ctcaaaggcc tgttctccta cggacgctac   3780
aaaaacagca tcagccgcag caccggtgcg gacgaacatg cggaaggcag cgtcaacggc   3840
acgctgatgc agctgggcgc actgggcggt gtcaacgttc cgtttgccgc aacgggagat   3900
ttgacggtcg aaggcggtct gcgctacgac ctgctcaaac aggatgcatt cgccgaaaaa   3960
ggcagtgctt tgggctggag cggcaacagc ctcactgaag gcacgctggt cggactcgcg   4020
ggtctgaagc tgtcgcaacc cttgagcgat aaagccgtcc tgtttgcaac ggcgggcgtg   4080
gaacgcgacc tgaacggacg cgactacacg gtaacgggcg gctttaccgg cgcgactgca   4140
gcaaccggca agacgggggc acgcaatatg ccgcacaccc gtctggttgc cggcctgggc   4200
gcggatgtcg aattcggcaa cggctggaac ggcttggcac gttacagcta cgccggttcc   4260
aaacagtacg gcaaccacag cggacgagtc ggcgtaggct accggttcct cgagcaccac   4320
caccaccacc actga                                                    4335
```

<210> 46

<211> 1444

<212> PRT

<213> Secuencia artificial

<220>

<223> 961-983

<400> 46

```
Met Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
1               5                   10                  15

Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
            20                  25                  30

Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
        35                  40                  45

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

Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
65                  70                  75                  80

Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
                85                  90                  95

Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
            100                 105                 110
```

```
Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile
        115                 120                 125

Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
    130                 135                 140

Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
145                 150                 155                 160

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

Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
            180                 185                 190

Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
        195                 200                 205

Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
    210                 215                 220

Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
225                 230                 235                 240

Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
                245                 250                 255

Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
            260                 265                 270

Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
        275                 280                 285

Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
    290                 295                 300

Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
305                 310                 315                 320

Leu Phe Gln Pro Tyr Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val
                325                 330                 335

Gly Gly Tyr Lys Ser Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg
            340                 345                 350

Phe Thr Glu Asn Phe Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser
        355                 360                 365

Ser Gly Ser Ser Ala Ala Tyr His Val Gly Val Asn Tyr Glu Trp Gly
    370                 375                 380

Ser Gly Gly Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr
385                 390                 395                 400

Gly Ile Gly Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val
                405                 410                 415

Ser Tyr Ala Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu
            420                 425                 430

Cys Ala Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile
```

```
        435                 440                 445

Asn Ala Pro Pro Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn
    450                 455                 460

Asp Ala Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly
465                 470                 475                 480

Tyr Thr Gly Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser
                485                 490                 495

Val Gly Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly
            500                 505                 510

Tyr Asn Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala
        515                 520                 525

Pro Glu Asp Gly Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu
    530                 535                 540

Ala Val Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys
545                 550                 555                 560

Glu Ile Gly His Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser
                565                 570                 575

Val Asp Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His
            580                 585                 590

Ile Met Asn Thr Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala
        595                 600                 605

Ile Arg Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val
    610                 615                 620

Asn Asn Ser Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe
625                 630                 635                 640

Gln Ile Ala Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr
                645                 650                 655

Ser Gly Gly Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser
            660                 665                 670

Asp Tyr Gly Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe
        675                 680                 685

Ile Phe Ser Thr Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala
    690                 695                 700

Leu Leu Pro Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val
705                 710                 715                 720

Ala Gly Val Asp Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly
                725                 730                 735

Glu Pro Gly Thr Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile
            740                 745                 750

Thr Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe
        755                 760                 765
```

```
Thr Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro
    770                 775                 780

Ile Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met
785                 790                 795                 800

Ser Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile
                805                 810                 815

Gly Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala
            820                 825                 830

Gly Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr
        835                 840                 845

Ala Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp
    850                 855                 860

Ile Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln
865                 870                 875                 880

Leu His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly
                885                 890                 895

Ser Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr
            900                 905                 910

Lys Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn
        915                 920                 925

Ser Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn
    930                 935                 940

Glu Thr Val His Ile Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr
945                 950                 955                 960

Leu Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile
                965                 970                 975

Ile Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr
            980                 985                 990

Leu Asn Ser Thr Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile
        995                 1000                1005

Gly Gln Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu
    1010                1015                1020

Leu Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp
1025                1030                1035                1040

Thr Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser
                1045                1050                1055

Ala Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln
            1060                1065                1070

Gly Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu
        1075                1080                1085
```

```
Ser Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr
    1090                1095                1100

Asp Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala
1105                1110                1115                1120

Ala Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser
                1125                1130                1135

Leu Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met
            1140                1145                1150

Gln Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly
        1155                1160                1165

Thr Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp
    1170                1175                1180

Glu Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val
1185                1190                1195                1200

Gly Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu
                1205                1210                1215

Gly Met Gly Arg Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr
            1220                1225                1230

Asp Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile
        1235                1240                1245

Gly Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile
    1250                1255                1260

Ser Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly
1265                1270                1275                1280

Thr Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala
                1285                1290                1295

Ala Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu
            1300                1305                1310

Lys Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly
        1315                1320                1325

Asn Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu
    1330                1335                1340

Ser Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val
1345                1350                1355                1360

Glu Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr
                1365                1370                1375

Gly Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His
            1380                1385                1390

Thr Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly
        1395                1400                1405

Trp Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly
```

```
    1410                1415                1420

Asn His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe Leu Glu His His
1425                1430                1435                1440

His His His His
```

<210> 47

<211> 2256

<212> ADN

<213> Secuencia artificial

<220>

<223> 961c-ORF46.1

<400> 47

```
atggccacaa acgacgacga tgttaaaaaa gctgccactg tggccattgc tgctgcctac     60
aacaatggcc aagaaatcaa cggtttcaaa gctggagaga ccatctacga cattgatgaa    120
gacggcacaa ttaccaaaaa agacgcaact gcagccgatg ttgaagccga cgactttaaa    180
ggtctgggtc tgaaaaaagt cgtgactaac ctgaccaaaa ccgtcaatga aaacaaacaa    240
aacgtcgatg ccaaagtaaa agctgcagaa tctgaaatag aaaagttaac aaccaagtta    300
gcagacactg atgccgcttt agcagatact gatgccgctc tggatgcaac caccaacgcc    360
ttgaataaat tgggagaaaa tataacgaca tttgctgaag agactaagac aaatatcgta    420
aaaattgatg aaaaattaga agccgtggct gataccgtcg acaagcatgc cgaagcattc    480
aacgatatcg ccgattcatt ggatgaaacc aacactaagg cagacgaagc cgtcaaaacc    540
gccaatgaag ccaaacagac ggccgaagaa accaaacaaa acgtcgatgc caaagtaaaa    600
gctgcagaaa ctgcagcagg caaagccgaa gctgccgctg gcacagctaa tactgcagcc    660
gacaaggccg aagctgtcgc tgcaaaagtt accgacatca aagctgatat cgctacgaac    720
aaagataata ttgctaaaaa agcaaacagt gccgacgtgt acaccagaga agagtctgac    780
agcaaatttg tcagaattga tggtctgaac gctactaccg aaaaattgga cacacgcttg    840
gcttctgctg aaaaatccat tgccgatcac gatactcgcc tgaacggttt ggataaaaca    900
gtgtcagacc tgcgcaaaga aacccgccaa ggccttgcag aacaagccgc gctctccggt    960
ctgttccaac cttacaacgt gggtggatcc ggaggaggag gatcagattt ggcaaacgat   1020
tcttttatcc ggcaggttct cgaccgtcag catttcgaac ccgacgggaa ataccaccta   1080
ttcggcagca gggggggaact tgccgagcgc agcggccata tcggattggg aaaaatacaa   1140
agccatcagt tgggcaacct gatgattcaa caggcggcca ttaaaggaaa tatcggctac   1200
attgtccgct tttccgatca cgggcacgaa gtccattccc ccttcgacaa ccatgcctca   1260
cattccgatt ctgatgaagc cggtagtccc gttgacggat ttagccttta ccgcatccat   1320
tgggacggat acgaacacca tcccgccgac ggctatgacg ggccacaggg cggcggctat   1380
cccgctccca aaggcgcgag ggatatatac agctacgaca taaaaggcgt tgcccaaaat   1440
atccgcctca acctgaccga caaccgcagc accggacaac ggcttgccga ccgtttccac   1500
aatgccggta gtatgctgac gcaaggagta ggcgacggat tcaaacgcgc cacccgatac   1560
agccccgagc tggacagatc gggcaatgcc gccgaagcct tcaacggcac tgcagatatc   1620
gttaaaaaca tcatcggcgc ggcaggagaa attgtcggcg caggcgatgc cgtgcagggc   1680
ataagcgaag gctcaaacat tgctgtcatg cacggcttgg gtctgctttc caccgaaaac   1740
aagatggcgc gcatcaacga tttggcagat atggcgcaac tcaaagacta tgccgcagca   1800
gccatccgcg attgggcagt ccaaaacccc aatgccgcac aaggcataga agccgtcagc   1860
aatatcttta tggcagccat ccccatcaaa gggattggag ctgttcgggg aaaatacggc   1920
ttgggcggca tcacggcaca tcctatcaag cggtcgcaga tgggcgcgat cgcattgccg   1980
aaagggaaat ccgccgtcag cgacaatttt gccgatgcgg catacgccaa atacccgtcc   2040
ccttaccatt cccgaaatat ccgttcaaac ttggagcagc gttacggcaa agaaaacatc   2100
acctcctcaa ccgtgccgcc gtcaaacggc aaaaatgtca aactggcaga ccaacgccac   2160
ccgaagacag gcgtaccgtt tgacggtaaa gggtttccga attttgagaa gcacgtgaaa   2220
tatgatacgc tcgagcacca ccaccaccac cactga                             2256
```

<210> 48

<211> 751

<212> PRT

<213> Secuencia artificial

<220>

<223> 961c-ORF46.1

<400> 48

```
Met Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
1               5                   10                  15

Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
            20                  25                  30

Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
        35                  40                  45

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

Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
65                  70                  75                  80

Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
                85                  90                  95

Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
            100                 105                 110

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

Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
    130                 135                 140

Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
145                 150                 155                 160

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

Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
            180                 185                 190

Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
        195                 200                 205

Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
    210                 215                 220

Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
225                 230                 235                 240

Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
                245                 250                 255

Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
            260                 265                 270

Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
        275                 280                 285

Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
    290                 295                 300
```

```
Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
305                 310                 315                 320

Leu Phe Gln Pro Tyr Asn Val Gly Gly Ser Gly Gly Gly Gly Ser Asp
                325                 330                 335

Leu Ala Asn Asp Ser Phe Ile Arg Gln Val Leu Asp Arg Gln His Phe
            340                 345                 350

Glu Pro Asp Gly Lys Tyr His Leu Phe Gly Ser Arg Gly Glu Leu Ala
        355                 360                 365

Glu Arg Ser Gly His Ile Gly Leu Gly Lys Ile Gln Ser His Gln Leu
    370                 375                 380

Gly Asn Leu Met Ile Gln Gln Ala Ala Ile Lys Gly Asn Ile Gly Tyr
385                 390                 395                 400

Ile Val Arg Phe Ser Asp His Gly His Glu Val His Ser Pro Phe Asp
                405                 410                 415

Asn His Ala Ser His Ser Asp Ser Asp Glu Ala Gly Ser Pro Val Asp
            420                 425                 430

Gly Phe Ser Leu Tyr Arg Ile His Trp Asp Gly Tyr Glu His His Pro
        435                 440                 445

Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly Gly Tyr Pro Ala Pro Lys
    450                 455                 460

Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile Lys Gly Val Ala Gln Asn
465                 470                 475                 480

Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser Thr Gly Gln Arg Leu Ala
                485                 490                 495

Asp Arg Phe His Asn Ala Gly Ser Met Leu Thr Gln Gly Val Gly Asp
            500                 505                 510

Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro Glu Leu Asp Arg Ser Gly
        515                 520                 525

Asn Ala Ala Glu Ala Phe Asn Gly Thr Ala Asp Ile Val Lys Asn Ile
    530                 535                 540

Ile Gly Ala Ala Gly Glu Ile Val Gly Ala Gly Asp Ala Val Gln Gly
545                 550                 555                 560

Ile Ser Glu Gly Ser Asn Ile Ala Val Met His Gly Leu Gly Leu Leu
                565                 570                 575

Ser Thr Glu Asn Lys Met Ala Arg Ile Asn Asp Leu Ala Asp Met Ala
            580                 585                 590

Gln Leu Lys Asp Tyr Ala Ala Ala Ala Ile Arg Asp Trp Ala Val Gln
        595                 600                 605

Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala Val Ser Asn Ile Phe Met
    610                 615                 620

Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala Val Arg Gly Lys Tyr Gly
```

```
625                 630                 635                 640

Leu Gly Gly Ile Thr Ala His Pro Ile Lys Arg Ser Gln Met Gly Ala
                645                 650                 655

Ile Ala Leu Pro Lys Gly Lys Ser Ala Val Ser Asp Asn Phe Ala Asp
            660                 665                 670

Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr His Ser Arg Asn Ile Arg
        675                 680                 685

Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu Asn Ile Thr Ser Ser Thr
    690                 695                 700

Val Pro Pro Ser Asn Gly Lys Asn Val Lys Leu Ala Asp Gln Arg His
705                 710                 715                 720

Pro Lys Thr Gly Val Pro Phe Asp Gly Lys Gly Phe Pro Asn Phe Glu
                725                 730                 735

Lys His Val Lys Tyr Asp Thr Leu Glu His His His His His His
            740                 745                 750
```

<210> 49

<211> 1773

<212> AND

<213> Secuencia artificial

<220>

<223> 961c-741

<400> 49

```
atggccacaa acgacgacga tgttaaaaaa gctgccactg tggccattgc tgctgcctac   60
aacaatggcc aagaaatcaa cggtttcaaa gctggagaga ccatctacga cattgatgaa   120
gacggcacaa ttaccaaaaa agacgcaact gcagccgatg ttgaagccga cgactttaaa   180
ggtctgggtc tgaaaaaagt cgtgactaac ctgaccaaaa ccgtcaatga aaacaaacaa   240
aacgtcgatg ccaaagtaaa agctgcagaa tctgaaatag aaaagttaac aaccaagtta   300
gcagacactg atgccgcttt agcagatact gatgccgctc tggatgcaac caccaacgcc   360
ttgaataaat tgggagaaaa tataacgaca tttgctgaag agactaagac aaatatcgta   420
aaaattgatg aaaaattaga agccgtggct gataccgtcg acaagcatgc cgaagcattc   480
aacgatatcg ccgattcatt ggatgaaacc aacactaagg cagacgaagc cgtcaaaacc   540
gccaatgaag ccaaacagac ggccgaagaa accaaacaaa acgtcgatgc caaagtaaaa   600
gctgcagaaa ctgcagcagg caaagccgaa gctgccgctg gcacagctaa tactgcagcc   660
gacaaggccg aagctgtcgc tgcaaaagtt accgacatca aagctgatat cgctacgaac   720
aaagataata ttgctaaaaa agcaaacagt gccgacgtgt acaccagaga agagtctgac   780
agcaaatttg tcagaattga tggtctgaac gctactaccg aaaaattgga cacacgcttg   840
gcttctgctg aaaaatccat tgccgatcac gatactcgcc tgaacggttt ggataaaaca   900
gtgtcagacc tgcgcaaaga aacccgccaa ggccttgcag aacaagccgc gctctccggt   960
ctgttccaac cttacaacgt gggtggatcc ggagggggtg gtgtcgccgc cgacatcggt   1020
gcggggcttg ccgatgcact aaccgcaccg ctcgaccata aagacaaagg tttgcagtct   1080
ttgacgctgg atcagtccgt caggaaaaac gagaaactga agctggcggc acaaggtgcg   1140
gaaaaaactt atggaaacgg tgacagcctc aatacgggca aattgaagaa cgacaaggtc   1200
agccgtttcg actttatccg ccaaatcgaa gtggacgggc agctcattac cttggagagt   1260
ggagagttcc aagtatacaa acaaagccat tccgccttaa ccgcctttca gaccgagcaa   1320
atacaagatt cggagcattc cgggaagatg gttgcgaaac gccagttcag aatcggcgac   1380
atagcgggcg aacatacatc ttttgacaag cttcccgaag gcggcagggc gacatatcgc   1440
gggacggcgt tcggttcaga cgatgccggc ggaaaactga cctacaccat agatttcgcc   1500
gccaagcagg gaaacggcaa aatcgaacat ttgaaatcgc cagaactcaa tgtcgacctg   1560
gccgccgccg atatcaagcc ggatggaaaa cgccatgccg tcatcagcgg ttccgtcctt   1620
tacaaccaag ccgagaaagg cagttactcc ctcggtatct ttggcggaaa agcccaggaa   1680
gttgccggca gcgcggaagt gaaaaccgta aacggcatac gccatatcgg ccttgccgcc   1740

aagcaactcg agcaccacca ccaccaccac tga                                1773
```

<210> 50

<211> 590

<212> PRT

<213> Secuencia artificial

<220>

<223> 961c-741

<400> 50

```
Met Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
1               5                   10                  15

Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
            20                  25                  30

Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
        35                  40                  45

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

Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
65                  70                  75                  80

Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
                85                  90                  95

Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
            100                 105                 110

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

Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
    130                 135                 140

Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
145                 150                 155                 160

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

Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
            180                 185                 190

Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
        195                 200                 205

Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
    210                 215                 220

Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
225                 230                 235                 240

Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
                245                 250                 255

Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
            260                 265                 270
```

```
Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
        275                 280                 285

Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
    290                 295                 300

Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
305                 310                 315                 320

Leu Phe Gln Pro Tyr Asn Val Gly Gly Ser Gly Gly Gly Gly Val Ala
                325                 330                 335

Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp
            340                 345                 350

His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg
        355                 360                 365

Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr
    370                 375                 380

Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val
385                 390                 395                 400

Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile
                405                 410                 415

Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala
            420                 425                 430

Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His Ser Gly
        435                 440                 445

Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu
    450                 455                 460

His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg
465                 470                 475                 480

Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr
                485                 490                 495

Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His Leu Lys
            500                 505                 510

Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp
        515                 520                 525

Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala
    530                 535                 540

Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu
545                 550                 555                 560

Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg His Ile
                565                 570                 575

Gly Leu Ala Ala Lys Gln Leu Glu His His His His His His
            580                 585                 590
```

<210> 51

<211> 4170

<212> ADN

<213> Secuencia artificial

<220>

<223> 961c-983

<400> 51

```
atggccacaa acgacgacga tgttaaaaa gctgccactg tggccattgc tgctgcctac   60
aacaatggcc aagaaatcaa cggtttcaaa gctggagaga ccatctacga cattgatgaa  120
gacggcacaa ttaccaaaaa agacgcaact gcagccgatg ttgaagccga cgactttaaa  180
ggtctgggtc tgaaaaaagt cgtgactaac ctgaccaaaa ccgtcaatga aaacaaacaa  240
aacgtcgatg ccaaagtaaa agctgcagaa tctgaaatag aaaagttaac aaccaagtta  300
gcagacactg atgccgcttt agcagatact gatgccgctc tggatgcaac caccaacgcc  360
ttgaataaat tgggagaaaa tataacgaca tttgctgaag agactaagac aaatatcgta  420
aaaattgatg aaaaattaga agccgtggct gataccgtcg acaagcatgc cgaagcattc  480
aacgatatcg ccgattcatt ggatgaaacc aacactaagg cagacgaagc cgtcaaaacc  540
gccaatgaag ccaaacagac ggccgaagaa accaaacaaa acgtcgatgc caaagtaaaa  600
gctgcagaaa ctgcagcagg caaagccgaa gctgccgctg gcacagctaa tactgcagcc  660
gacaaggccg aagctgtcgc tgcaaaagtt accgacatca aagctgatat cgctacgaac  720
aaagataata ttgctaaaaa agcaaacagt gccgacgtgt acaccagaga agagtctgac  780
agcaaatttg tcagaattga tggtctgaac gctactaccg aaaaattgga cacacgcttg  840
gcttctgctg aaaaatccat tgccgatcac gatactcgcc tgaacggttt ggataaaaca  900
gtgtcagacc tgcgcaaaga aacccgccaa ggccttgcag aacaagccgc gctctccggt  960
ctgttccaac cttacaacgt gggtggatcc ggcggaggcg gcacttctgc gcccgacttc 1020
aatgcaggcg gtaccggtat cggcagcaac agcagagcaa caacagcgaa atcagcagca 1080
gtatcttacg ccggtatcaa gaacgaaatg tgcaaagaca gaagcatgct ctgtgccggt 1140
cgggatgacg ttgcggttac agacagggat gccaaaatca atgccccccc cccgaatctg 1200
cataccggag actttccaaa cccaaatgac gcatacaaga atttgatcaa cctcaaacct 1260
gcaattgaag caggctatac aggacgcggg gtagaggtag gtatcgtcga cacaggcgaa 1320
tccgtcggca gcatatcctt tcccgaactg tatggcagaa aagaacacgg ctataacgaa 1380
aattacaaaa actatacggc gtatatgcgg aaggaagcgc ctgaagacgg aggcggtaaa 1440
gacattgaag cttctttcga cgatgaggcc gttatagaga ctgaagcaaa gccgacggat 1500
atccgccacg taaaagaaat cggacacatc gatttggtct cccatattat tggcgggcgt 1560
tccgtggacg gcagacctgc aggcggtatt gcgcccgatg cgacgctaca cataatgaat 1620
acgaatgatg aaaccaagaa cgaaatgatg gttgcagcca tccgcaatgc atgggtcaag 1680
ctgggcgaac gtggcgtgcg catcgtcaat aacagttttg gaacaacatc gagggcaggc 1740
actgccgacc ttttccaaat agccaattcg gaggagcagt accgccaagc gttgctcgac 1800
tattccggcg gtgataaaac agacgagggt atccgcctga tgcaacagag cgattacggc 1860
aacctgtcct accacatccg taataaaaac atgcttttca tcttttcgac aggcaatgac 1920
gcacaagctc agcccaacac atatgcccta ttgccatttt atgaaaaaga cgctcaaaaa 1980
ggcattatca cagtcgcagg cgtagaccgc agtggagaaa agttcaaacg ggaaatgtat 2040
ggagaaccgg gtacagaacc gcttgagtat ggctccaacc attgcggaat tactgccatg 2100
tggtgcctgt cggcacccta tgaagcaagc gtccgtttca cccgtacaaa cccgattcaa 2160
attgccggaa catccttttc cgcacccatc gtaaccggca cggcggctct gctgctgcag 2220
aaatacccgt ggatgagcaa cgacaacctg cgtaccacgt tgctgacgac ggctcaggac 2280
atcggtgcag tcggcgtgga cagcaagttc ggctggggac tgctggatgc gggtaaggcc 2340
atgaacggac ccgcgtcctt tccgttcggc gactttaccg ccgatacgaa aggtacatcc 2400
gatattgcct actccttccg taacgacatt tcaggcacgg gcggcctgat caaaaaaggc 2460
ggcagccaac tgcaactgca cggcaacaac acctatacgg gcaaaaccat tatcgaaggc 2520
ggttcgctgg tgttgtacgg caacaacaaa tcggatatgc gcgtcgaaac caaaggtgcg 2580
ctgatttata acggggcggc atccggcggc agcctgaaca gcgacggcat tgtctatctg 2640
gcagataccg accaatccgg cgcaaacgaa accgtacaca tcaaaggcag tctgcagctg 2700
gacggcaaag gtacgctgta cacacgtttg ggcaaactgc tgaaagtgga cggtacggcg 2760
attatcggcg gcaagctgta catgtcggca cgcggcaagg gggcaggcta tctcaacagt 2820
accggacgac gtgttccctt cctgagtgcc gccaaaatcg ggcaggatta ttctttcttc 2880
acaaacatcg aaaccgacgg cggcctgctg gcttccctcg acagcgtcga aaaaacagcg 2940
ggcagtgaag gcgacacgct gtcctattat gtccgtcgcg gcaatgcggc acggactgct 3000
tcggcagcgg cacattccgc gcccgccggt ctgaaacacg ccgtagaaca gggcggcagc 3060
aatctggaaa acctgatggt cgaactggat gcctccgaat catccgcaac acccgagacg 3120
```

```
gttgaaactg cggcagccga ccgcacagat atgccgggca tccgccccta cggcgcaact   3180
ttccgcgcag cggcagccgt acagcatgcg aatgccgccg acggtgtacg catcttcaac   3240
agtctcgccg ctaccgtcta tgccgacagt accgccgccc atgccgatat gcagggacgc   3300
cgcctgaaag ccgtatcgga cgggttggac cacaacggca cgggtctgcg cgtcatcgcg   3360
caaacccaac aggacggtgg aacgtgggaa cagggcggtg ttgaaggcaa aatgcgcggc   3420
agtacccaaa ccgtcggcat tgccgcgaaa accggcgaaa atacgacagc agccgccaca   3480
ctgggcatgg gacgcagcac atggagcgaa aacagtgcaa atgcaaaaac cgacagcatt   3540
agtctgtttg caggcatacg gcacgatgcg ggcgatatcg gctatctcaa aggcctgttc   3600
tcctacggac gctacaaaaa cagcatcagc cgcagcaccg gtgcggacga acatgcggaa   3660
ggcagcgtca acggcacgct gatgcagctg ggcgcactgg gcggtgtcaa cgttccgttt   3720
gccgcaacgg gagatttgac ggtcgaaggc ggtctgcgct acgacctgct caaacaggat   3780
gcattcgccg aaaaaggcag tgctttgggc tggagcggca acagcctcac tgaaggcacg   3840
ctggtcggac tcgcgggtct gaagctgtcg caacccttga gcgataaagc cgtcctgttt   3900
gcaacggcgg gcgtggaacg cgacctgaac ggacgcgact acacggtaac gggcggcttt   3960
accggcgcga ctgcagcaac cggcaagacg gggcacgca atatgccgca cacccgtctg    4020
gttgccggcc tgggcgcgga tgtcgaattc ggcaacggct ggaacggctt ggcacgttac   4080
agctacgccg gttccaaaca gtacggcaac cacagcggac gagtcggcgt aggctaccgg   4140
ttcctcgagc accaccacca ccaccactga                                     4170
```

<210> 52

<211> 1389

<212> PRT

<213> Secuencia artificial

<220>

<223> 961c-983

<400> 52

```
Met Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile
1               5                   10                  15

Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly
            20                  25                  30

Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp
        35                  40                  45

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

Lys Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln
65                  70                  75                  80

Asn Val Asp Ala Lys Val Lys Ala Ala Glu Ser Glu Ile Glu Lys Leu
                85                  90                  95

Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala
            100                 105                 110

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

Thr Thr Phe Ala Glu Glu Thr Lys Thr Asn Ile Val Lys Ile Asp Glu
    130                 135                 140

Lys Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe
145                 150                 155                 160

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

```
Ala Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys
            180                 185                 190

Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys
        195                 200                 205

Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu
    210                 215                 220

Ala Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn
225                 230                 235                 240

Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg
                245                 250                 255

Glu Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr
            260                 265                 270

Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala
        275                 280                 285

Asp His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu
    290                 295                 300

Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly
305                 310                 315                 320

Leu Phe Gln Pro Tyr Asn Val Gly Gly Ser Gly Gly Gly Gly Thr Ser
                325                 330                 335

Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly Ser Asn Ser Arg
            340                 345                 350

Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala Gly Ile Lys Asn
        355                 360                 365

Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly Arg Asp Asp Val
    370                 375                 380

Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro Pro Pro Asn Leu
385                 390                 395                 400

His Thr Gly Asp Phe Pro Asn Pro Asn Asp Ala Tyr Lys Asn Leu Ile
                405                 410                 415

Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly Arg Gly Val Glu
            420                 425                 430

Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser Ile Ser Phe Pro
        435                 440                 445

Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu Asn Tyr Lys Asn
    450                 455                 460

Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp Gly Gly Gly Lys
465                 470                 475                 480

Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala Val Ile Glu Thr Glu Ala
                485                 490                 495

Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly His Ile Asp Leu
```

```
            500                 505                 510

Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly Arg Pro Ala Gly
        515                 520                 525

Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn Thr Asn Asp Glu
    530                 535                 540

Thr Lys Asn Glu Met Met Val Ala Ala Ile Arg Asn Ala Trp Val Lys
545                 550                 555                 560

Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser Phe Gly Thr Thr
                565                 570                 575

Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln Ile Ala Asn Ser Glu Glu
            580                 585                 590

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

Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly Asn Leu Ser Tyr
    610                 615                 620

His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser Thr Gly Asn Asp
625                 630                 635                 640

Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu Leu Pro Phe Tyr Glu Lys
                645                 650                 655

Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val Asp Arg Ser Gly
            660                 665                 670

Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu Pro Gly Thr Glu Pro Leu
        675                 680                 685

Glu Tyr Gly Ser Asn His Cys Gly Ile Thr Ala Met Trp Cys Leu Ser
    690                 695                 700

Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr Arg Thr Asn Pro Ile Gln
705                 710                 715                 720

Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile Val Thr Gly Thr Ala Ala
                725                 730                 735

Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser Asn Asp Asn Leu Arg Thr
            740                 745                 750

Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly Ala Val Gly Val Asp Ser
        755                 760                 765

Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly Lys Ala Met Asn Gly Pro
    770                 775                 780

Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala Asp Thr Lys Gly Thr Ser
785                 790                 795                 800

Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile Ser Gly Thr Gly Gly Leu
                805                 810                 815

Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu His Gly Asn Asn Thr Tyr
            820                 825                 830
```

```
Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser Leu Val Leu Tyr Gly Asn
        835                 840                 845

Asn Lys Ser Asp Met Arg Val Glu Thr Lys Gly Ala Leu Ile Tyr Asn
    850                 855                 860

Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser Asp Gly Ile Val Tyr Leu
865                 870                 875                 880

Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu Thr Val His Ile Lys Gly
                885                 890                 895

Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu Tyr Thr Arg Leu Gly Lys
            900                 905                 910

Leu Leu Lys Val Asp Gly Thr Ala Ile Ile Gly Gly Lys Leu Tyr Met
        915                 920                 925

Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu Asn Ser Thr Gly Arg Arg
    930                 935                 940

Val Pro Phe Leu Ser Ala Ala Lys Ile Gly Gln Asp Tyr Ser Phe Phe
945                 950                 955                 960

Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu Ala Ser Leu Asp Ser Val
                965                 970                 975

Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr Leu Ser Tyr Tyr Val Arg
            980                 985                 990

Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala Ala Ala His Ser Ala Pro
        995                 1000                1005

Ala Gly Leu Lys His Ala Val Glu Gln Gly Gly Ser Asn Leu Glu Asn
    1010                1015                1020

Leu Met Val Glu Leu Asp Ala Ser Glu Ser Ser Ala Thr Pro Glu Thr
1025                1030                1035                1040

Val Glu Thr Ala Ala Ala Asp Arg Thr Asp Met Pro Gly Ile Arg Pro
                1045                1050                1055

Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala Val Gln His Ala Asn Ala
            1060                1065                1070

Ala Asp Gly Val Arg Ile Phe Asn Ser Leu Ala Ala Thr Val Tyr Ala
        1075                1080                1085

Asp Ser Thr Ala Ala His Ala Asp Met Gln Gly Arg Arg Leu Lys Ala
    1090                1095                1100

Val Ser Asp Gly Leu Asp His Asn Gly Thr Gly Leu Arg Val Ile Ala
1105                1110                1115                1120

Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu Gln Gly Gly Val Glu Gly
                1125                1130                1135

Lys Met Arg Gly Ser Thr Gln Thr Val Gly Ile Ala Ala Lys Thr Gly
            1140                1145                1150
```

```
Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly Met Gly Arg Ser Thr Trp
        1155                1160                1165

Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp Ser Ile Ser Leu Phe Ala
    1170                1175                1180

Gly Ile Arg His Asp Ala Gly Asp Ile Gly Tyr Leu Lys Gly Leu Phe
1185                1190                1195                1200

Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser Arg Ser Thr Gly Ala Asp
                1205                1210                1215

Glu His Ala Glu Gly Ser Val Asn Gly Thr Leu Met Gln Leu Gly Ala
            1220                1225                1230

Leu Gly Gly Val Asn Val Pro Phe Ala Ala Thr Gly Asp Leu Thr Val
        1235                1240                1245

Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys Gln Asp Ala Phe Ala Glu
    1250                1255                1260

Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn Ser Leu Thr Glu Gly Thr
1265                1270                1275                1280

Leu Val Gly Leu Ala Gly Leu Lys Leu Ser Gln Pro Leu Ser Asp Lys
                1285                1290                1295

Ala Val Leu Phe Ala Thr Ala Gly Val Glu Arg Asp Leu Asn Gly Arg
            1300                1305                1310

Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly Ala Thr Ala Ala Thr Gly
        1315                1320                1325

Lys Thr Gly Ala Arg Asn Met Pro His Thr Arg Leu Val Ala Gly Leu
    1330                1335                1340

Gly Ala Asp Val Glu Phe Gly Asn Gly Trp Asn Gly Leu Ala Arg Tyr
1345                1350                1355                1360

Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn His Ser Gly Arg Val Gly
                1365                1370                1375

Val Gly Tyr Arg Phe Leu Glu His His His His His His
            1380                1385
```

<210> 53

<211> 2304

<212> ADN

<213> Secuencia artificial

<220>

<223> 961cL-ORF46.1

<400> 53

```
atgaaacact ttccatccaa agtactgacc acagccatcc ttgccacttt ctgtagcggc    60
gcactggcag ccacaaacga cgacgatgtt aaaaaagctg ccactgtggc cattgctgct   120
gcctacaaca atggccaaga aatcaacggt ttcaaagctg gagagaccat ctacgacatt   180
gatgaagacg gcacaattac caaaaaagac gcaactgcag ccgatgttga agccgacgac   240
tttaaaggtc tgggtctgaa aaaagtcgtg actaacctga ccaaaaccgt caatgaaaac   300
aaacaaaacg tcgatgccaa agtaaaagct gcagaatctg aaatagaaaa gttaacaacc   360
aagttagcag acactgatgc cgctttagca gatactgatg ccgctctgga tgcaaccacc   420

aacgccttga ataaattggg agaaaatata acgacatttg ctgaagagac taagacaaat   480
atcgtaaaaa ttgatgaaaa attagaagcc gtggctgata ccgtcgacaa gcatgccgaa   540
gcattcaacg atatcgccga ttcattggat gaaaccaaca ctaaggcaga cgaagccgtc   600
aaaaccgcca atgaagccaa acagacggcc gaagaaacca aacaaaacgt cgatgccaaa   660
gtaaaagctg cagaaactgc agcaggcaaa gccgaagctg ccgctggcac agctaatact   720
gcagccgaca aggccgaagc tgtcgctgca aaagttaccg acatcaaagc tgatatcgct   780
acgaacaaag ataatattgc taaaaaagca aacagtgccg acgtgtacac cagagaagag   840
tctgacagca aatttgtcag aattgatggt ctgaacgcta ctaccgaaaa attggacaca   900
cgcttggctt ctgctgaaaa atccattgcc gatcacgata ctcgcctgaa cggtttggat   960
aaaacagtgt cagacctgcg caaagaaacc cgccaaggcc ttgcagaaca agccgcgctc  1020
tccggtctgt tccaacctta caacgtgggt ggatccggag gaggaggatc agatttggca  1080
aacgattctt ttatccggca ggttctcgac cgtcagcatt tcgaacccga cgggaaatac  1140
cacctattcg gcagcagggg ggaacttgcc gagcgcagcg gccatatcgg attgggaaaa  1200
atacaaagcc atcagttggg caacctgatg attcaacagg cggccattaa aggaaatatc  1260
ggctacattg tccgcttttc cgatcacggg cacgaagtcc attccccctt cgacaaccat  1320
gcctcacatt ccgattctga tgaagccggt agtcccgttg acggatttag cctttaccgc  1380
atccattggg acggatacga acaccatccc gccgacggct atgacgggcc acagggcggc  1440
ggctatcccg ctcccaaagg cgcgagggat atatacagct acgacataaa aggcgttgcc  1500
caaaatatcc gcctcaacct gaccgacaac cgcagcaccg gacaacggct tgccgaccgt  1560
ttccacaatg ccggtagtat gctgacgcaa ggagtaggcg acggattcaa acgcgccacc  1620
cgatacagcc ccgagctgga cagatcgggc aatgccgccg aagccttcaa cggcactgca  1680
gatatcgtta aaaacatcat cggcgcggca ggagaaattg tcggcgcagg cgatgccgtg  1740
cagggcataa gcgaaggctc aaacattgct gtcatgcacg gcttgggtct gctttccacc  1800
gaaaacaaga tggcgcgcat caacgatttg gcagatatgg cgcaactcaa agactatgcc  1860
gcagcagcca tccgcgattg ggcagtccaa aaccccaatg ccgcacaagg catagaagcc  1920
gtcagcaata tctttatggc agccatcccc atcaaaggga ttggagctgt tcggggaaaa  1980
tacggcttgg gcggcatcac ggcacatcct atcaagcggt cgcagatggg cgcgatcgca  2040
ttgccgaaag ggaaatccgc cgtcagcgac aattttgccg atgcggcata cgccaaatac  2100
ccgtcccctt accattcccg aaatatccgt tcaaacttgg agcagcgtta cggcaaagaa  2160
aacatcacct cctcaaccgt gccgccgtca aacggcaaaa atgtcaaact ggcagaccaa  2220
cgccacccga agacaggcgt accgtttgac ggtaaagggt ttccgaattt tgagaagcac  2280
gtgaaatatg atacgtaact cgag                                          2304
```

<210> 54

<211> 765

<212> PRT

<213> Secuencia artificial

<220>

<223> 961cL-ORF46.1

<400> 54

```
Met Lys His Phe Pro Ser Lys Val Leu Thr Thr Ala Ile Leu Ala Thr
1               5                   10                  15

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

Ala Ala Thr Val Ala Ile Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile
        35                  40                  45

Asn Gly Phe Lys Ala Gly Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly
    50                  55                  60

Thr Ile Thr Lys Lys Asp Ala Thr Ala Ala Asp Val Glu Ala Asp Asp
65                  70                  75                  80

Phe Lys Gly Leu Gly Leu Lys Lys Val Val Thr Asn Leu Thr Lys Thr
                85                  90                  95

Val Asn Glu Asn Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu
```

```
            100                 105                 110

Ser Glu Ile Glu Lys Leu Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala
        115                 120                 125

Leu Ala Asp Thr Asp Ala Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn
    130                 135                 140

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

Ile Val Lys Ile Asp Glu Lys Leu Glu Ala Val Ala Asp Thr Val Asp
                165                 170                 175

Lys His Ala Glu Ala Phe Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr
            180                 185                 190

Asn Thr Lys Ala Asp Glu Ala Val Lys Thr Ala Asn Glu Ala Lys Gln
        195                 200                 205

Thr Ala Glu Glu Thr Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala
    210                 215                 220

Glu Thr Ala Ala Gly Lys Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr
225                 230                 235                 240

Ala Ala Asp Lys Ala Glu Ala Val Ala Ala Lys Val Thr Asp Ile Lys
                245                 250                 255

Ala Asp Ile Ala Thr Asn Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser
            260                 265                 270

Ala Asp Val Tyr Thr Arg Glu Glu Ser Asp Ser Lys Phe Val Arg Ile
        275                 280                 285

Asp Gly Leu Asn Ala Thr Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser
    290                 295                 300

Ala Glu Lys Ser Ile Ala Asp His Asp Thr Arg Leu Asn Gly Leu Asp
305                 310                 315                 320

Lys Thr Val Ser Asp Leu Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu
                325                 330                 335

Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Asn Val Gly Gly Ser
            340                 345                 350

Gly Gly Gly Gly Ser Asp Leu Ala Asn Asp Ser Phe Ile Arg Gln Val
        355                 360                 365

Leu Asp Arg Gln His Phe Glu Pro Asp Gly Lys Tyr His Leu Phe Gly
    370                 375                 380

Ser Arg Gly Glu Leu Ala Glu Arg Ser Gly His Ile Gly Leu Gly Lys
385                 390                 395                 400

Ile Gln Ser His Gln Leu Gly Asn Leu Met Ile Gln Gln Ala Ala Ile
                405                 410                 415

Lys Gly Asn Ile Gly Tyr Ile Val Arg Phe Ser Asp His Gly His Glu
            420                 425                 430
```

```
Val His Ser Pro Phe Asp Asn His Ala Ser His Ser Asp Ser Asp Glu
        435                 440                 445

Ala Gly Ser Pro Val Asp Gly Phe Ser Leu Tyr Arg Ile His Trp Asp
    450                 455                 460

Gly Tyr Glu His His Pro Ala Asp Gly Tyr Asp Gly Pro Gln Gly Gly
465                 470                 475                 480

Gly Tyr Pro Ala Pro Lys Gly Ala Arg Asp Ile Tyr Ser Tyr Asp Ile
                485                 490                 495

Lys Gly Val Ala Gln Asn Ile Arg Leu Asn Leu Thr Asp Asn Arg Ser
            500                 505                 510

Thr Gly Gln Arg Leu Ala Asp Arg Phe His Asn Ala Gly Ser Met Leu
        515                 520                 525

Thr Gln Gly Val Gly Asp Gly Phe Lys Arg Ala Thr Arg Tyr Ser Pro
    530                 535                 540

Glu Leu Asp Arg Ser Gly Asn Ala Ala Glu Ala Phe Asn Gly Thr Ala
545                 550                 555                 560

Asp Ile Val Lys Asn Ile Ile Gly Ala Ala Gly Glu Ile Val Gly Ala
                565                 570                 575

Gly Asp Ala Val Gln Gly Ile Ser Glu Gly Ser Asn Ile Ala Val Met
            580                 585                 590

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

Asp Leu Ala Asp Met Ala Gln Leu Lys Asp Tyr Ala Ala Ala Ala Ile
    610                 615                 620

Arg Asp Trp Ala Val Gln Asn Pro Asn Ala Ala Gln Gly Ile Glu Ala
625                 630                 635                 640

Val Ser Asn Ile Phe Met Ala Ala Ile Pro Ile Lys Gly Ile Gly Ala
                645                 650                 655

Val Arg Gly Lys Tyr Gly Leu Gly Gly Ile Thr Ala His Pro Ile Lys
            660                 665                 670

Arg Ser Gln Met Gly Ala Ile Ala Leu Pro Lys Gly Lys Ser Ala Val
        675                 680                 685

Ser Asp Asn Phe Ala Asp Ala Ala Tyr Ala Lys Tyr Pro Ser Pro Tyr
    690                 695                 700

His Ser Arg Asn Ile Arg Ser Asn Leu Glu Gln Arg Tyr Gly Lys Glu
705                 710                 715                 720

Asn Ile Thr Ser Ser Thr Val Pro Pro Ser Asn Gly Lys Asn Val Lys
                725                 730                 735

Leu Ala Asp Gln Arg His Pro Lys Thr Gly Val Pro Phe Asp Gly Lys
            740                 745                 750
```

```
Gly Phe Pro Asn Phe Glu Lys His Val Lys Tyr Asp Thr
        755                 760                 765
```

<210> 55

<211> 1839

<212> ADN

<213> Secuencia artificial

<220>

<223> 961cL-741

<400> 55

```
atgaaacact ttccatccaa agtactgacc acagccatcc ttgccacttt ctgtagcggc   60
gcactggcag ccacaaacga cgacgatgtt aaaaaagctg ccactgtggc cattgctgct  120
gcctacaaca atggccaaga aatcaacggt ttcaaagctg gagagaccat ctacgacatt  180
gatgaagacg gcacaattac caaaaaagac gcaactgcag ccgatgttga agccgacgac  240
tttaaaggtc tgggtctgaa aaaagtcgtg actaacctga ccaaaaccgt caatgaaaac  300
aaacaaaacg tcgatgccaa agtaaaagct gcagaatctg aaatagaaaa gttaacaacc  360
aagttagcag acactgatgc cgctttagca gatactgatg ccgctctgga tgcaaccacc  420
aacgccttga ataaattggg agaaaatata acgacatttg ctgaagagac taagacaaat  480
atcgtaaaaa ttgatgaaaa attagaagcc gtggctgata ccgtcgacaa gcatgccgaa  540
gcattcaacg atatcgccga ttcattggat gaaaccaaca ctaaggcaga cgaagccgtc  600
aaaaccgcca atgaagccaa acagacggcc gaagaaacca aacaaaacgt cgatgccaaa  660
gtaaaagctg cagaaactgc agcaggcaaa gccgaagctg ccgctggcac agctaatact  720
gcagccgaca aggccgaagc tgtcgctgca aaagttaccg acatcaaagc tgatatcgct  780
acgaacaaag ataatattgc taaaaaagca aacagtgccg acgtgtacac cagagaagag  840
tctgacagca aatttgtcag aattgatggt ctgaacgcta ctaccgaaaa attggacaca  900
cgcttggctt ctgctgaaaa atccattgcc gatcacgata ctcgcctgaa cggtttggat  960
aaaacagtgt cagacctgcg caaagaaacc cgccaaggcc ttgcagaaca agccgcgctc 1020
tccggtctgt tccaacctta caacgtgggt ggatccggag ggggtggtgt cgccgccgac 1080
atcggtgcgg ggcttgccga tgcactaacc gcaccgctcg accataaaga caaaggtttg 1140
cagtctttga cgctggatca gtccgtcagg aaaaacgaga aactgaagct ggcggcacaa 1200
ggtgcggaaa aaacttatgg aaacggtgac agcctcaata cgggcaaatt gaagaacgac 1260
aaggtcagcc gtttcgactt tatccgccaa atcgaagtgg acgggcagct cattaccttg 1320
gagagtggag agttccaagt atacaaacaa agccattccg ccttaaccgc ctttcagacc 1380
gagcaaatac aagattcgga gcattccggg aagatggttg cgaaacgcca gttcagaatc 1440
ggcgacatag cgggcgaaca tacatctttt gacaagcttc ccgaaggcgg cagggcgaca 1500
tatcgcggga cggcgttcgg ttcagacgat gccggcggaa aactgaccta caccatagat 1560
ttcgccgcca agcagggaaa cggcaaaatc gaacatttga aatcgccaga actcaatgtc 1620
gacctggccg ccgccgatat caagccggat ggaaaacgcc atgccgtcat cagcggttcc 1680
gtcctttaca accaagccga gaaaggcagt tactccctcg gtatctttgg cggaaaagcc 1740
caggaagttg ccggcagcgc ggaagtgaaa accgtaaacg gcatacgcca tatcggcctt 1800
gccgccaagc aactcgagca ccaccaccac caccactga                        1839
```

<210> 56

<211> 612

<212> PRT

<213> Secuencia artificial

<220>

<223> 961cL-741

<400> 56

```
Met Lys His Phe Pro Ser Lys Val Leu Thr Thr Ala Ile Leu Ala Thr
1               5                   10                  15

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

Ala Ala Thr Val Ala Ile Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile
        35                  40                  45
```

```
Asn Gly Phe Lys Ala Gly Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly
    50                  55                  60

Thr Ile Thr Lys Lys Asp Ala Thr Ala Ala Asp Val Glu Ala Asp Asp
65                  70                  75                  80

Phe Lys Gly Leu Gly Leu Lys Lys Val Val Thr Asn Leu Thr Lys Thr
                85                  90                  95

Val Asn Glu Asn Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu
            100                 105                 110

Ser Glu Ile Glu Lys Leu Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala
        115                 120                 125

Leu Ala Asp Thr Asp Ala Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn
    130                 135                 140

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

Ile Val Lys Ile Asp Glu Lys Leu Glu Ala Val Ala Asp Thr Val Asp
                165                 170                 175

Lys His Ala Glu Ala Phe Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr
            180                 185                 190

Asn Thr Lys Ala Asp Glu Ala Val Lys Thr Ala Asn Glu Ala Lys Gln
        195                 200                 205

Thr Ala Glu Glu Thr Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala
    210                 215                 220

Glu Thr Ala Ala Gly Lys Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr
225                 230                 235                 240

Ala Ala Asp Lys Ala Glu Ala Val Ala Ala Lys Val Thr Asp Ile Lys
                245                 250                 255

Ala Asp Ile Ala Thr Asn Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser
            260                 265                 270

Ala Asp Val Tyr Thr Arg Glu Glu Ser Asp Ser Lys Phe Val Arg Ile
        275                 280                 285

Asp Gly Leu Asn Ala Thr Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser
    290                 295                 300

Ala Glu Lys Ser Ile Ala Asp His Asp Thr Arg Leu Asn Gly Leu Asp
305                 310                 315                 320

Lys Thr Val Ser Asp Leu Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu
                325                 330                 335

Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Asn Val Gly Gly Ser
            340                 345                 350

Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala
        355                 360                 365
```

```
Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr
    370                 375                 380

Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln
385                 390                 395                 400

Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys
                405                 410                 415

Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu
            420                 425                 430

Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr
        435                 440                 445

Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln
    450                 455                 460

Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile
465                 470                 475                 480

Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly
                485                 490                 495

Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly
            500                 505                 510

Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly
        515                 520                 525

Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala
    530                 535                 540

Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser
545                 550                 555                 560

Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe
                565                 570                 575

Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val
            580                 585                 590

Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln Leu Glu His His
        595                 600                 605

His His His His
    610
```

<210> 57

<211> 4218

<212> ADN

<213> Secuencia artificial

<220>

<223> 961cL-983

<400> 57

```
atgaaacact ttccatccaa agtactgacc acagccatcc ttgccacttt ctgtagcggc   60
gcactggcag ccacaaacga cgacgatgtt aaaaaagctg ccactgtggc cattgctgct  120
gcctacaaca atggccaaga aatcaacggt ttcaaagctg gagagaccat ctacgacatt  180
gatgaagacg gcacaattac caaaaaagac gcaactgcag ccgatgttga agccgacgac  240
```

```
tttaaaggtc tgggtctgaa aaaagtcgtg actaacctga ccaaaaccgt caatgaaaac   300
aaacaaaacg tcgatgccaa agtaaaagct gcagaatctg aaatagaaaa gttaacaacc   360
aagttagcag acactgatgc cgctttagca gatactgatg ccgctctgga tgcaaccacc   420
aacgccttga ataaattggg agaaaatata acgacatttg ctgaagagac taagacaaat   480
atcgtaaaaa ttgatgaaaa attagaagcc gtggctgata ccgtcgacaa gcatgccgaa   540
gcattcaacg atatcgccga ttcattggat gaaaccaaca ctaaggcaga cgaagccgtc   600
aaaaccgcca atgaagccaa acagacggcc gaagaaacca aacaaaacgt cgatgccaaa   660
gtaaaagctg cagaaactgc agcaggcaaa gccgaagctg ccgctggcac agctaatact   720
gcagccgaca aggccgaagc tgtcgctgca aaagttaccg acatcaaagc tgatatcgct   780
acgaacaaag ataatattgc taaaaaagca aacagtgccg acgtgtacac cagagaagag   840
tctgacagca aatttgtcag aattgatggt ctgaacgcta ctaccgaaaa attggacaca   900
cgcttggctt ctgctgaaaa atccattgcc gatcacgata ctcgcctgaa cggtttggat   960
aaaacagtgt cagacctgcg caaagaaacc cgccaaggcc ttgcagaaca agccgcgctc   1020
tccggtctgt tccaacctta caacgtgggt ggatccggcg gaggcggcac ttctgcgccc   1080
gacttcaatg caggcggtac cggtatcggc agcaacagca gagcaacaac agcgaaatca   1140
gcagcagtat cttacgccgg tatcaagaac gaaatgtgca aagacagaag catgctctgt   1200
gccggtcggg atgacgttgc ggttacagac agggatgcca aaatcaatgc cccccccccg   1260
aatctgcata ccggagactt tccaaaccca aatgacgcat acaagaattt gatcaacctc   1320
aaacctgcaa ttgaagcagg ctatacagga cgcggggtag aggtaggtat cgtcgacaca   1380
ggcgaatccg tcggcagcat atcctttccc gaactgtatg gcagaaaaga acacggctat   1440
aacgaaaatt acaaaaacta tacggcgtat atgcggaagg aagcgcctga agacggaggc   1500
ggtaaagaca ttgaagcttc tttcgacgat gaggccgtta tagagactga agcaaagccg   1560
acggatatcc gccacgtaaa agaaatcgga cacatcgatt tggtctccca tattattggc   1620
gggcgttccg tggacggcag acctgcaggc ggtattgcgc ccgatgcgac gctacacata   1680
atgaatacga atgatgaaac caagaacgaa atgatggttg cagccatccg caatgcatgg   1740
gtcaagctgg gcgaacgtgg cgtgcgcatc gtcaataaca gttttggaac aacatcgagg   1800
gcaggcactg ccgacctttt ccaaatagcc aattcggagg agcagtaccg ccaagcgttg   1860
ctcgactatt ccggcggtga taaaacagac gagggtatcc gcctgatgca acagagcgat   1920
tacggcaacc tgtcctacca catccgtaat aaaaacatgc ttttcatctt ttcgacaggc   1980
aatgacgcac aagctcagcc caacacatat gccctattgc cattttatga aaaagacgct   2040
caaaaaggca ttatcacagt cgcaggcgta gaccgcagtg gagaaaagtt caaacgggaa   2100
atgtatggag aaccgggtac agaaccgctt gagtatggct ccaaccattg cggaattact   2160
gccatgtggt gcctgtcggc accctatgaa gcaagcgtcc gtttcacccg tacaaacccg   2220
attcaaattg ccggaacatc cttttccgca cccatcgtaa ccggcacggc ggctctgctg   2280
ctgcagaaat acccgtggat gagcaacgac aacctgcgta ccacgttgct gacgacggct   2340
caggacatcg gtgcagtcgg cgtggacagc aagttcggct ggggactgct ggatgcgggt   2400
aaggccatga acggacccgc gtcctttccg ttcggcgact ttaccgccga tacgaaaggt   2460
acatccgata ttgcctactc cttccgtaac gacatttcag gcacgggcgg cctgatcaaa   2520
aaaggcggca gccaactgca actgcacggc aacaacacct atacgggcaa aaccattatc   2580
gaaggcggtt cgctggtgtt gtacggcaac aacaaatcgg atatgcgcgt cgaaaccaaa   2640
ggtgcgctga tttataacgg ggcggcatcc ggcggcagcc tgaacagcga cggcattgtc   2700
tatctggcag ataccgacca atccggcgca aacgaaaccg tacacatcaa aggcagtctg   2760
cagctggacg gcaaaggtac gctgtacaca cgtttgggca aactgctgaa agtggacggt   2820
acggcgatta tcggcggcaa gctgtacatg tcggcacgcg gcaagggggc aggctatctc   2880
aacagtaccg gacgacgtgt tcccttcctg agtgccgcca aaatcgggca ggattattct   2940
ttcttcacaa acatcgaaac cgacggcggc ctgctggctt ccctcgacag cgtcgaaaaa   3000
acagcgggca gtgaaggcga cacgctgtcc tattatgtcc gtcgcggcaa tgcggcacgg   3060
actgcttcgg cagcggcaca ttccgcgccc gccggtctga aacacgccgt agaacagggc   3120
ggcagcaatc tggaaaacct gatggtcgaa ctggatgcct ccgaatcatc cgcaacaccc   3180
gagacggttg aaactgcggc agccgaccgc acagatatgc cgggcatccg cccctacggc   3240
gcaactttcc gcgcagcggc agccgtacag catgcgaatg ccgccgacgg tgtacgcatc   3300
ttcaacagtc tcgccgctac cgtctatgcc gacagtaccg ccgcccatgc cgatatgcag   3360
ggacgccgcc tgaaagccgt atcggacggg ttggaccaca acggcacggg tctgcgcgtc   3420
atcgcgcaaa cccaacagga cggtggaacg tgggaacagg gcggtgttga aggcaaaatg   3480
cgcggcagta cccaaaccgt cggcattgcc gcgaaaaccg gcgaaaatac gacagcagcc   3540
gccacactgg gcatgggacg cagcacatgg agcgaaaaca gtgcaaatgc aaaaaccgac   3600
agcattagtc tgtttgcagg catacggcac gatgcgggcg atatcggcta tctcaaaggc   3660
ctgttctcct acggacgcta caaaaacagc atcagccgca gcaccggtgc ggacgaacat   3720
gcggaaggca gcgtcaacgg cacgctgatg cagctgggcg cactgggcgg tgtcaacgtt   3780
ccgtttgccg caacgggaga tttgacggtc gaaggcggtc tgcgctacga cctgctcaaa   3840
caggatgcat tcgccgaaaa aggcagtgct ttgggctgga gcggcaacag cctcactgaa   3900
```

```
ggcacgctgg tcggactcgc gggtctgaag ctgtcgcaac ccttgagcga taaagccgtc   3960
ctgtttgcaa cggcgggcgt ggaacgcgac ctgaacggac gcgactacac ggtaacgggc   4020
ggctttaccg gcgcgactgc agcaaccggc aagacggggg cacgcaatat gccgcacacc   4080
cgtctggttg ccggcctggg cgcggatgtc gaattcggca acggctggaa cggcttggca   4140
cgttacagct acgccggttc caaacagtac ggcaaccaca gcggacgagt cggcgtaggc   4200
taccggttct gactcgag                                                 4218
```

<210> 58

<211> 1403

<212> PRT

<213> Secuencia artificial

<220>

<223> 961cL-983

<400> 58

```
Met Lys His Phe Pro Ser Lys Val Leu Thr Thr Ala Ile Leu Ala Thr
1               5                   10                  15

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

Ala Ala Thr Val Ala Ile Ala Ala Ala Tyr Asn Asn Gly Gln Glu Ile
        35                  40                  45

Asn Gly Phe Lys Ala Gly Glu Thr Ile Tyr Asp Ile Asp Glu Asp Gly
    50                  55                  60

Thr Ile Thr Lys Lys Asp Ala Thr Ala Ala Asp Val Glu Ala Asp Asp
65                  70                  75                  80

Phe Lys Gly Leu Gly Leu Lys Lys Val Val Thr Asn Leu Thr Lys Thr
                85                  90                  95

Val Asn Glu Asn Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala Glu
            100                 105                 110

Ser Glu Ile Glu Lys Leu Thr Thr Lys Leu Ala Asp Thr Asp Ala Ala
        115                 120                 125

Leu Ala Asp Thr Asp Ala Ala Leu Asp Ala Thr Thr Asn Ala Leu Asn
    130                 135                 140

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

Ile Val Lys Ile Asp Glu Lys Leu Glu Ala Val Ala Asp Thr Val Asp
                165                 170                 175

Lys His Ala Glu Ala Phe Asn Asp Ile Ala Asp Ser Leu Asp Glu Thr
            180                 185                 190

Asn Thr Lys Ala Asp Glu Ala Val Lys Thr Ala Asn Glu Ala Lys Gln
        195                 200                 205

Thr Ala Glu Glu Thr Lys Gln Asn Val Asp Ala Lys Val Lys Ala Ala
    210                 215                 220

Glu Thr Ala Ala Gly Lys Ala Glu Ala Ala Ala Gly Thr Ala Asn Thr
225                 230                 235                 240
```

```
Ala Ala Asp Lys Ala Glu Ala Val Ala Ala Lys Val Thr Asp Ile Lys
                245                 250                 255

Ala Asp Ile Ala Thr Asn Lys Asp Asn Ile Ala Lys Lys Ala Asn Ser
            260                 265                 270

Ala Asp Val Tyr Thr Arg Glu Glu Ser Asp Ser Lys Phe Val Arg Ile
        275                 280                 285

Asp Gly Leu Asn Ala Thr Thr Glu Lys Leu Asp Thr Arg Leu Ala Ser
    290                 295                 300

Ala Glu Lys Ser Ile Ala Asp His Asp Thr Arg Leu Asn Gly Leu Asp
305                 310                 315                 320

Lys Thr Val Ser Asp Leu Arg Lys Glu Thr Arg Gln Gly Leu Ala Glu
                325                 330                 335

Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Asn Val Gly Gly Ser
            340                 345                 350

Gly Gly Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly
        355                 360                 365

Ile Gly Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser
    370                 375                 380

Tyr Ala Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys
385                 390                 395                 400

Ala Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn
                405                 410                 415

Ala Pro Pro Pro Asn Leu His Thr Gly Asp Phe Pro Asn Pro Asn Asp
            420                 425                 430

Ala Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr
        435                 440                 445

Thr Gly Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val
    450                 455                 460

Gly Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr
465                 470                 475                 480

Asn Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro
                485                 490                 495

Glu Asp Gly Gly Gly Lys Asp Ile Glu Ala Ser Phe Asp Asp Glu Ala
            500                 505                 510

Val Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu
        515                 520                 525

Ile Gly His Ile Asp Leu Val Ser His Ile Ile Gly Gly Arg Ser Val
    530                 535                 540

Asp Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile
545                 550                 555                 560

Met Asn Thr Asn Asp Glu Thr Lys Asn Glu Met Met Val Ala Ala Ile
```

```
                565                 570                 575

Arg Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn
            580                 585                 590

Asn Ser Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp Leu Phe Gln
        595                 600                 605

Ile Ala Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Asp Tyr Ser
    610                 615                 620

Gly Gly Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp
625                 630                 635                 640

Tyr Gly Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile
                645                 650                 655

Phe Ser Thr Gly Asn Asp Ala Gln Ala Gln Pro Asn Thr Tyr Ala Leu
            660                 665                 670

Leu Pro Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala
        675                 680                 685

Gly Val Asp Arg Ser Gly Glu Lys Phe Lys Arg Glu Met Tyr Gly Glu
    690                 695                 700

Pro Gly Thr Glu Pro Leu Glu Tyr Gly Ser Asn His Cys Gly Ile Thr
705                 710                 715                 720

Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr
                725                 730                 735

Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile
            740                 745                 750

Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser
        755                 760                 765

Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly
    770                 775                 780

Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly
785                 790                 795                 800

Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala
                805                 810                 815

Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile
            820                 825                 830

Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu
        835                 840                 845

His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser
    850                 855                 860

Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys
865                 870                 875                 880

Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser
                885                 890                 895
```

```
Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Gln Ser Gly Ala Asn Glu
            900                 905                 910

Thr Val His Ile Lys Gly Ser Leu Gln Leu Asp Gly Lys Gly Thr Leu
        915                 920                 925

Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Ile Ile
    930                 935                 940

Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu
945                 950                 955                 960

Asn Ser Thr Gly Arg Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly
                965                 970                 975

Gln Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu
            980                 985                 990

Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr
        995                 1000                1005

Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala
    1010                1015                1020

Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly
1025                1030                1035                1040

Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser
                1045                1050                1055

Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp
            1060                1065                1070

Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala
        1075                1080                1085

Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu
    1090                1095                1100

Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln
1105                1110                1115                1120

Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Gly Thr
                1125                1130                1135

Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu
            1140                1145                1150

Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly
        1155                1160                1165

Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly
    1170                1175                1180

Met Gly Arg Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp
1185                1190                1195                1200

Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly
                1205                1210                1215
```

Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser
1220 1225 1230

Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr
1235 1240 1245

Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala
1250 1255 1260

Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys
1265 1270 1275 1280

Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn
1285 1290 1295

Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser
1300 1305 1310

Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu
1315 1320 1325

Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly
1330 1335 1340

Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr
1345 1350 1355 1360

Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp
1365 1370 1375

Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn
1380 1385 1390

His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe
1395 1400

<210> 59

<211> 25

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 59

cgcggatccg gagggggtgg tgtcg 25

<210> 60

<211> 27

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 60

cccgctcgag ttgcttggcg gcaaggc 27

<210> 61

<211> 25

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 61

cgcggatccg gcggaggcgg cactt 25

<210> 62

<211> 26

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 62

cccgctcgag gaaccggtag cctacg 26

<210> 63

<211> 41

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 63

cgcggatccg gtggtggtgg ttcagatttg gcaaacgatt c 41

<210> 64

<211> 29

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 64

cccgctcgag cgtatcatat ttcacgtgc 29

<210> 65

<211> 25

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 65

cgcggatccg gagggggtgg tgtcg 25

<210> 66

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 66

cccgctcgag ttattgcttg gcggcaag 28

<210> 67

<211> 25

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 67

cgcggatccg gcggaggcgg cactt 25

<210> 68

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 68

cccgctcgag tcagaaccgg tagcctac 28

<210> 69

<211> 41

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 69

cgcggatccg gtggtggtgg ttcagatttg gcaaacgatt c 41

<210> 70

<211> 32

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 70

cccgctcgag ttacgtatca tatttcacgt gc 32

<210> 71

<211> 42

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 71

cgcggatccg gtggtggtgg tcaaagcaag agcatccaaa cc 42

<210> 72

<211> 30

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 72

cccaagcttt tcgggcggta ttcgggcttc 30

<210> 73

<211> 39

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 73

cgcggatccg gtggtggtgg tgccacctac aaagtggac 39

<210> 74

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 74

gcccaagctt ttgtttggct gcctcgat 28

<210> 75

<211> 34

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 75

cgcggatccg gtggtggtgg tacaagcgac gacg 34

<210> 76

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 76

gcccaagctt ccactcgtaa ttgacgcc 28

<210> 77

<211> 41

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 77

cgcggatccg gtggtggtgg ttcagatttg gcaaacgatt c 41

<210> 78

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 78

cccaagcttc gtatcatatt tcacgtgc 28

<210> 79

<211> 44

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 79

cccaagcttg gtggtggtgg tggttcagat ttggcaaacg attc 44

<210> 80

<211> 29

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 80

cccgctcgag cgtatcatat ttcacgtgc 29

<210> 81

<211> 45

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 81

cccaagcttg gtggtggtgg tggtcaaagc aagagcatcc aaacc 45

<210> 82

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 82

cccgctcgag cgggcggtat tcgggctt 28

<210> 83

<211> 32

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 83

cgcggatccg ctagccccga tgttaaatcg gc 32

<210> 84

<211> 29

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 84

cggggatcca tcctgctctt ttttgccgg 29

<210> 85

<211> 36

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 85

cgcggatccg ctagcggaca cacttatttc ggcatc 36

<210> 86

<211> 30

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 86

cgcggatccc cagcggtagc ctaatttgat 30

<210> 87

<211> 41

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 87

cgcggatccg gtggtggtgg ttcagatttg gcaaacgatt c 41

<210> 88

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 88

cccaagcttc gtatcatatt tcacgtgc 28

<210> 89

<211> 36

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 89

gcggcgtcga cggtggcgga ggcactggat cctcag 36

<210> 90

<211> 35

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 90

ggaggcactg gatcctcaga tttggcaaac gattc 35

<210> 91

<211> 29

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 91

cccgctcgag cgtatcatat ttcacgtgc 29

<210> 92

<211> 25

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 92

cggggatccg gggcggcgg tggcg 25

<210> 93

<211> 30

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 93

cccaagctta tcctgctctt ttttgccggc 30

<210> 94

<211> 42

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 94

cgcggatccg gtggtggtgg tcaaagcaag agcatccaaa cc 42

<210> 95

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 95

cccaagcttc gggcggtatt cgggcttc 28

<210> 96

<211> 26

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 96

ccccaagctt gggggcggcg gtggcg 26

<210> 97

<211> 31

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 97

cccgctcgag atcctgctct tttttgccgg c 31

<210> 98

<211> 45

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 98

cccaagcttg gtggtggtgg tggtcaaagc aagagcatcc aaacc 45

<210> 99

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 99

cccgctcgag cgggcggtat tcgggctt 28

<210> 100

<211> 35

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 100

ggaggcactg gatccgcagc cacaaacgac gacga 35

<210> 101

<211> 36

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 101

gcggcctcga gggtggcgga ggcactggat ccgcag 36

<210> 102

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 102

cccgctcgag acccaqcttg taaggttg 28

<210> 103

<211> 35

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 103

ggaggcactg gatccgcagc cacaaacgac gacga 35

<210> 104

<211> 36

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 104

gcggcctcga gggtggcgga ggcactggat ccgcag 36

<210> 105

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 105

cccgctcgag ccactcgtaa ttgacgcc 28

<210> 106

<211> 38

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 106

gcggcctcga gggatccggc ggaggcggca cttctgcg 38

<210> 107

<211> 26

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 107

cccgctcgag gaaccggtag cctacg 26

<210> 108

<211> 35

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 108

ggaggcactg gatcctcaga tttggcaaac gattc 35

<210> 109

<211> 37

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 109

gcggcgtcga cggtggcgga ggcactggat cctcaga 37

<210> 110

<211> 29

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 110

cccgctcgag cgtatcatat ttcacgtgc 29

<210> 111

<211> 35

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 111

gcggcctcga gggatccgga gggggtggtg tcgcc 35

<210> 112

<211> 25

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 112

cccgctcgag ttgcttggcg gcaag 25

<210> 113

<211> 35

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 113

ggaggcactg gatccgcagc cacaaacgac gacga 35

<210> 114

<211> 36

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 114

gcggcctcga gggtggcgga ggcactggat ccgcag 36

<210> 115

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 115

cccgctcgag acccagcttg taaggttg 28

<210> 116

<211> 35

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 116

ggaggcactg gatccgcagc cacaaacgac gacga 35

<210> 117

<211> 36

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 117

gcggcctcga gggtggcgga ggcactggat ccgcag 36

<210> 118

<211> 28

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 118

cccgctcgag ccactcgtaa ttgacgcc 28

<210> 119

<211> 35

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 119

ggaggcactg gatcctcaga tttggcaaac gattc 35

<210> 120

<211> 37

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 120

gcggcgtcga cggtggcgga ggcactggat cctcaga 37

<210> 121

<211> 29

<212> ADN

<213> Secuencia artificial

<220>

<223> Oligonucleótido

<400> 121

cccgctcgag cgtatcatat ttcacgtgc 29

REIVINDICACIONES

1.- Una proteína híbrida de fórmula NH_2-A-B-COOH, en la que A comprende la proteína ∆G287 de *Neisseria*, y B comprende la proteína 961 de *Neisseria*, y en la que la secuencia de aminoácidos de la proteína híbrida es la descrita en SEQ ID NO:8, o es una secuencia que tiene más de 70% de identidad de secuencia con ésta.

2.- La proteína de la reivindicación 1, en la que ∆G287 es de la cepa 2996 o 394/98

3.- La proteína de la reivindicación 1, en la que 961 es de la cepa 2996 o 394/98.

4.- La proteína de la reivindicación 1, en la que A y B son de la misma cepa.

5.- La proteína de la reivindicación 1, que comprende la secuencia de aminoácidos definida en SEQ ID NO:8.

FIGURA 1 — ΔG287—961

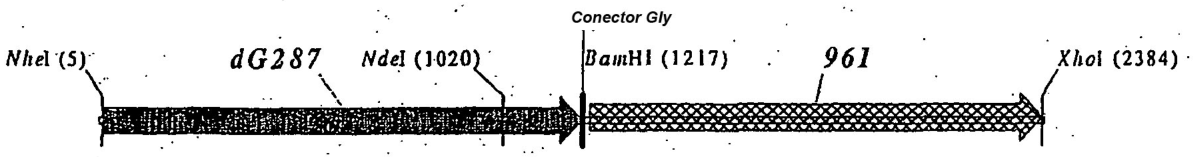


FIGURA 2 — ΔG287NZ—961