

LISTADO DE SECUENCIAS

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Título de la Invención: TERAPIA DE COMBINACIÓN PARA EL TRATAMIENTO DE
CÁNCER CEREBRAL

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Información para la SEQ ID No: 1
I.-Características de la secuencia
(A) Longitud 117
II.-Tipo de molécula: PRT
(A) Organismo: Secuencia artificial

Característica:
Otras informaciones: Descripción de secuencia artificial: Polipéptido
sintético

Secuencia SEQ ID No: 1

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

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

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

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

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

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

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

Val Thr Val Ser Ser
115

Información para la SEQ ID No: 2
I.-Características de la secuencia
(A) Longitud: 107
II.-Tipo de molécula: PRT
(A) Organismo: Secuencia artificial

Característica:
Otras informaciones: Descripción de secuencia artificial: Polipéptido sintético

Secuencia SEQ ID No: 2
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Pro Gly Thr Val Val Asp Phe Arg
100 105

Información para la SEQ ID No: 3
I.-Características de la secuencia
(A) Longitud: 8
II.-Tipo de molécula: PRT
(A) Organismo: Secuencia artificial

Característica:
Otras informaciones: Descripción de secuencia artificial: Péptido

sintético

Secuencia SEQ ID No: 3

Gly Phe Thr Phe Ser Asn Phe Gly

1 5

Información para la SEQ ID No: 4

I.-Características de la secuencia

(A) Longitud: 8

II.-Tipo de molécula: PRT

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Péptido sintético

Secuencia SEQ ID No: 4

Ile Ser Gly Gly Gly Arg Asp Thr

1 5

Información para la SEQ ID No: 5

I.-Características de la secuencia

(A) Longitud: 10

PRT

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Péptido sintético

Secuencia SEQ ID No: 5

Val Lys Trp Gly Asn Ile Tyr Phe Asp Tyr

1 5 10

Información para la SEQ ID No: 6

I.-Características de la secuencia

(A) Longitud: 6

II.-Tipo de molécula: PRT

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Péptido sintético

Secuencia SEQ ID No: 6

Leu Ser Ile Asn Thr Phe

1 5

Información para la SEQ ID No: 7

I.-Características de la secuencia

(A) Longitud: 3

II.-Tipo de molécula: PRT

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Péptido sintético

Secuencia SEQ ID No: 7

Ala Ala Ser

1

Información para la SEQ ID No: 8

I.-Características de la secuencia

(A) Longitud: 9

II.-Tipo de molécula: PRT

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Péptido sintético

Secuencia SEQ ID No: 8

Gln Gln Ser Ser Asn Thr Pro Phe Thr

1

5

Información para la SEQ ID No: 9

I.-Características de la secuencia

(A) Longitud: 444

II.-Tipo de molécula: PRT

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polipéptido sintético

Secuencia SEQ ID No: 9

Glu Val Gln Leu Leu Glu Ser Gly Gly Val Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Phe

20

25

30

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

35

40

45

Ser Gly Ile Ser Gly Gly Gly Arg Asp Thr Tyr Phe Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Lys Gly Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Val Lys Trp Gly Asn Ile Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu

100

105

110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu

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

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

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

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

Información para la SEQ ID No: 10

I.-Características de la secuencia

(A) Longitud: 214

II.-Tipo de molécula: PRT

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polipéptido sintético

Secuencia SEQ ID No: 10

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

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

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

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

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

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

Thr Phe Gly Pro Gly Thr Val Val Asp Phe Arg Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

Información para la SEQ ID No: 11
I.-Características de la secuencia
(A) Longitud: 2283
II.-Tipo de molécula: ADN
(A) Organismo: Secuencia artificial

Característica:
Otras informaciones: Descripción de secuencia artificial: Polinucleótido sintético

Secuencia SEQ ID No: 11
atgtggaacg cactgcatga gactgattct gctgtcgcac tgggacggag accccggtgg
60

ctgtgcgctg gagcactggt gctggccggc gggggattcc tgctgggatt cctgtttggc
120

tggtttatca aaagctccag cgaggctacc aatattaccc ctaagcaca taagaaagca
180

ttcctggatg aactgaaagc cgagaacatc aagaaattcc tgtacaactt cacaagaatt
240

ccacatctgg ctggcactga gcagaacttc cagctggcaa aacagatcca gagtcagtgg
300

aaggaatttg ggctggactc agtggagctg acccactacg atgtcctgct gtcctatcca
360

aataagactc atcccaacta catctctatc attaacgaag acggaaatga gattttcaac
420

acctctctgt ttgaaccccc tccaccggc tatgagaatg tcagtgcgt ggtccctcca
480

ttctcagcct tcagcccccga ggggatgcct gagggagatc tgggtgtacgt caattatgct
540

agaacagaag acttcttttaa gctggagagg gatatgaaaa tcaactgttc cggcaagatc
600

gtgattgccc ggtacgggaa ggtgttcaga ggaaataagg tcaaaaacgc tcagctggcc
660

ggagctaccg gcgtgatcct gtacagcgac cccgctgatt attttgcacc tggcgtgaag
720

tcctatccag acggatggaa tctgcccggc gggggagtgc agaggggaaa catcctgaac
780

ctgaatggag ccggcgatcc tctgactcca ggataccccc ccaacgaata cgcttatcgc
840

cggggaattg cagaggccgt gggcctgcct agcatcccag tccatcccat tggctattac
900

gatgcccaga agctgctgga gaaaatgggc gggagcgctc cccctgactc tagttggaag
960

ggctccctga aagtgcctta caatgtcggg ccaggattca ctgggaactt ttctaccag
1020

aaggtgaaaa tgcacatcca tagtaccagc gaggtgacac gaatctacaa cgtcattggc
1080

accctgagag gcgccgtgga gcctgatcgc tatgtcattc tgggaggcca cagagactca
1140

tgggtgttcg ggggaatcga tccacagagc ggagcagctg tgggtccatga aattgtgcgc
1200

agctttggga ccctgaagaa agagggatgg cgaccaggc gcacaatcct gttcgcaccc
1260

tgggacgccg aggaatttgg gctgctgggc agcacagaat gggccgagga aaattctcgc
1320

ctgctgcagg agcgaggggt ggcttacatc aatgcagact caagcattga aggaaactat
1380

accctgcggg tggattgcac acccctgatg tacagtctgg tctataacct gacaaaggag
1440

ctgaaatcac ctgacgaggg cttcgaaggg aaaagcctgt acgaatcctg gactgagaag
1500

agcccatccc ccgaattcag cggcatgcct aggatctcta agctgggcag tgggaacgat
1560

tttgaggtgt tctttcagcg cctgggaatt gcctctggcc gagctcggta cacaaaaaat
1620

tgggagacta acaagttctc ctcttaccca ctgtatcaca gcgtgtacga gacttatgaa
1680

ctgggtcgaga aattctacga cccactttt aagtatcatc tgaccgtggc acaggtcagg
1740

ggcgggatgg tgttcgaact ggccaatagc atcgtcctgc catttgactg tcgagattac
1800

gctgtggtcc tgcggaagta cgcagacaag atctataaca tctccatgaa gcacccccag
1860

gagatgaagg cctattctgt gagtttcgat tccctgtttt ctgccgtcaa aaatttcacc
1920

gaaatcgcta gtaagttttc agagcgcctg caggacctgg ataagtcaa tcccatcctg
1980

ctgcggatta tgaacgatca gctgatgttc ctggaaagag cctttatcga ccctctgggc
2040

ctgcctgata gaccattcta caggcacgtg atctacgcac ctagttcaca taacaagtac
2100

gccggcgagt ctttcccagg gatctatgac gctctgtttg atattgaatc aaaggtggac
2160

cccagcaaag catggggcga ggtcaagaga cagatcagca ttgcagcctt tacagtgcag
2220

gccgccgccc aaaccctgtc cgaagtcgct taccatacgc atgtccccga ttacgcatga
2280

taa
2283

Información para la SEQ ID No: 12

I.-Características de la secuencia

(A) Longitud: 2334

II.-Tipo de molécula: ADN

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polinucleótido
sintético

Secuencia SEQ ID No: 12

atggactgga catggattct gttcctggtc gccgccgcaa ctgcgctgca ttcttggaac
60

gcactgcatg agactgattc tgctgtcgca ctgggacgga gaccccggtg gctgtgcgct
120

ggagcactgg tgctggccgg cgggggatcc ctgctgggat tcctgttttg ctggtttacc
180

aaaagctcca gcgaggctac caatattacc cctaagcaca ataagaaagc attcctggat
240

gaactgaaag ccgagaacat caagaaattc ctgtacaact tcacaagaat tccacatctg
300

gctggcactg agcagaactt ccagctggca aaacagatcc agagtcagtg gaaggaattt
360

gggctggact cagtggagct gaccactac gatgtcctgc tgtcctatcc aaataagact
420

catcccaact acatctctat cattaacgaa gacggaaatg agattttcaa cacctctctg
480

tttgaacccc ctccacccgg ctatgagaat gtcagtgcg tggtcctcc attctcagcc
540

ttcagccccc aggggatgcc tgaggagat ctgggtgtacg tcaattatgc tagaacagaa
600

gacttcttta agctggagag ggatatgaaa atcaactgtt ccggcaagat cgtgattgcc
660

cggtacggga aggtgttcag aggaaataag gtcaaaaacg ctcagctggc cggagctacc
720

ggcgtgatcc tgtacagcga ccccgctgat tattttgcac ctggcgtgaa gtcctatcca
780

gacggatgga atctgcccgg cgggggagtg cagaggggaa acatcctgaa cctgaatgga
840

gccggcgatc ctctgactcc aggatacccc gccaacgaat acgcttatcg ccggggaatt
900

gcagaggccg tgggcctgcc tagcatccca gtccatccca ttggctatta cgatgccag
960

aagctgctgg agaaaatggg cgggagcgct ccccctgact ctagttggaa gggctccctg
1020

aaagtgcctt acaatgtcgg gccaggattc actgggaact tttctaccca gaaggtgaaa
1080

atgcacatcc atagtaccag cgaggtgaca cgaatctaca acgtcattgg caccctgaga
1140

ggcgccgtgg agcctgatcg ctatgtcatt ctgggaggcc acagagactc atgggtgttc
1200

gggggaatcg atccacagag cggagcagct gtggtccatg aaattgtgcg cagctttggg
1260

accctgaaga aagagggatg gcgaccagg cgcacaatcc tgttcgcac ctgggacgcc
1320

gaggaatttg ggctgctggg cagcacagaa tgggccgagg aaaattctcg cctgctgcag
1380

gagcgagggg tggcttacat caatgcagac tcaagcattg aaggaaacta taccctgcgg
1440

gtggattgca caccctgat gtacagtctg gtctataacc tgacaaagga gctgaaatca
1500

cctgacgagg gcttcgaagg gaaaagcctg tacgaatcct ggactgagaa gagcccatcc
1560

cccgaattca gcggcatgcc taggatctct aagctgggca gtgggaacga ttttgaggtg
1620

ttctttcagc gcctgggaat tgcctctggc cgagctcggc acacaaaaaa ttgggagact
1680

aacaagttct cctcttacct actgtatcac agcgtgtacg agacttatga actggctcag
1740

aaattctacg accccacttt taagtatcat ctgaccgtgg cacaggtcag gggcgggatg
1800

gtgttcgaac tggccaatag catcgtcctg ccatttgact gtcgagatta cgctgtggtc
1860

ctgcggaagt acgcagacaa gatctataac atctccatga agcaccacca ggagatgaag
1920

gcctattctg tgagtttcga ttccctgttt tctgccgtca aaaatttcac cgaaatcgct
1980

agtaagtttt cagagcgcct gcaggacctg gataagtcca atcccatcct gctgcggatt
2040

atgaacgatc agctgatggt cctggaaaga gcctttatcg accctctggg cctgcctgat
2100

agaccattct acaggcacgt gatctacga cctagttcac ataacaagta cgccggcgag
2160

tctttcccag ggatctatga cgctctgttt gatattgaat caaagggtgga cccagcaaa
2220

gcattggggc aggtcaagag acagatcagc attgcagcct ttacagtgca ggccgccgcc
2280

gaaaccctgt ccgaagtcgc ttaccatac gatgtccccg attacgcatg ataa
2334

Información para la SEQ ID No: 13

I.-Características de la secuencia

(A) Longitud: 750

II.-Tipo de molécula: PRT

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polipéptido sintético

Secuencia SEQ ID No: 13

Met	Trp	Asn	Ala	Leu	His	Glu	Thr	Asp	Ser	Ala	Val	Ala	Leu	Gly	Arg
1				5				10					15		

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

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

Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
515 520 525

Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
530 535 540

Lys Phe Ser Ser Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
545 550 555 560

Leu Val Glu Lys Phe Tyr Asp Pro Thr Phe Lys Tyr His Leu Thr Val
565 570 575

Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
580 585 590

Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
595 600 605

Asp Lys Ile Tyr Asn Ile Ser Met Lys His Pro Gln Glu Met Lys Ala
610 615 620

Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
625 630 635 640

Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Leu Asp Lys Ser
645 650 655

Asn Pro Ile Leu Leu Arg Ile Met Asn Asp Gln Leu Met Phe Leu Glu
660 665 670

Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
675 680 685

His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
690 695 700

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

Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Ser Ile Ala Ala
725 730 735

Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
740 745 750

Información para la SEQ ID No: 14
I.-Características de la secuencia
(A) Longitud: 767
II.-Tipo de molécula: PRT
(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polipéptido sintético

Secuencia SEQ ID No: 14

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Trp Asn Ala Leu His Glu Thr Asp Ser Ala Val Ala Leu Gly
20 25 30

Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly
35 40 45

Gly Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Ser
50 55 60

Glu Ala Thr Asn Ile Thr Pro Lys His Asn Lys Lys Ala Phe Leu Asp
65 70 75 80

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

Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln
100 105 110

Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Thr
115 120 125

His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr
130 135 140

Ile Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu
145 150 155 160

Phe Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Val Val Pro
165 170 175

Pro Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val
180 185 190

Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp

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

Thr Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val
450 455 460

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

Val Asp Cys Thr Pro Leu Met Tyr Ser Leu Val Tyr Asn Leu Thr Lys
485 490 495

Glu Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu
500 505 510

Ser Trp Thr Glu Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg
515 520 525

Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg
530 535 540

Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr
545 550 555 560

Asn Lys Phe Ser Ser Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr
565 570 575

Glu Leu Val Glu Lys Phe Tyr Asp Pro Thr Phe Lys Tyr His Leu Thr
580 585 590

Val Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile
595 600 605

Val Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr
610 615 620

Ala Asp Lys Ile Tyr Asn Ile Ser Met Lys His Pro Gln Glu Met Lys
625 630 635 640

Ala Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe
645 650 655

Thr Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Leu Asp Lys
660 665 670

Ser Asn Pro Ile Leu Leu Arg Ile Met Asn Asp Gln Leu Met Phe Leu
675 680 685

Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr
690 695 700

Arg His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu
705 710 715 720

Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val
725 730 735

Asp Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Ser Ile Ala
740 745 750

Ala Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
755 760 765

Información para la SEQ ID No: 15

I.-Características de la secuencia

(A) Longitud: 1332

II.-Tipo de molécula: ADN

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polinucleótido sintético

Secuencia SEQ ID No: 15

ggatccgccca ccatggactg gacctggatt ctgttctctg tgcgcgccgc aacacgggtg
60

catagtggga gtgatgtgag agacctgaac gccctgctgc cagcagtgcc atccctgcct
120

ggcgggggag gctgcgctct gccagtctct ggagcagctc agtgggctcc cgtgctggac
180

tttgacccc ctgcagcccc ttacggaagt ctgggcggcc cacactcatt catcaaacag
240

gagccaagct ggggcggggc agatcctcat gaggaacagt gcctgtcagc cttcacagtc
300

cacttttagcg ggcagttcac tggaaccgca ggagcttgta gatacggacc ctttgagca
360

ccacccctt cccaggcacc ttctggacag gcacgcatgt tcccaaacgc tccctatctg
420

cctaattgtc tggaaagcca gcccgctatt aggaaccagg gctactccac agtggcattt
480

gacgggactc ctagctatgg acatacccca tcccaccatg ctgcacagtt tcctaatac
540

tccttcaagc atgaggaccc catgggacag caggggtccc tgggagaaca gcagtactct
600

gtgccccctc ccgtgtacgg atgccacaca ccaactgaca gttgtacagg ctacaggcc
660

ctgctgctgc gaactccata caacagtgat aatctgtatc agatgacctc acagctggag
720

tgcattgacat ggaaccagat gaatctgggc agcacactga aaggccatgc cactgggtac
780

gaatctgaca accacaccac acctatgctg tacagttgtg gagcccagta tagaatccac
840

actcatggag tcttcagagg cattcaggat gtgcggagag tcccaggagt ggcaccaact
900

atcgtgcgga gcgcctccga gaccaacgaa aagcgcccct ttatggggcg ctaccctgga
960

ggcaataagc ggtatttcaa actgtctcac ctgcagatgg ggagtagaaa ggggaccgga
1020

gagaaacctt atcagggcga ctttaaagat ggggaaaggc gcttctctcg cagtgaccag
1080

ctgaagcgag gacagcgacg aggaaccggg gtgaagccat ttcagtgcaa aacatgtcag
1140

agaaagttct caaggagcga tcacctgaag acccatacaa gaactcacac cggcaagacc
1200

agcgagaaac cattttcctg ccgatggccc tcttgtcaga agaaattcgc ccgctccgac
1260

gaactgggtc gacaccacaa tatgcatcag agaaatatga caaaactgca gctggctctg
1320

tgataactcg ag
1332

Información para la SEQ ID No: 16

I.-Características de la secuencia

(A) Longitud: 436

II.-Tipo de molécula: PRT

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polipéptido
sintético

Secuencia SEQ ID No: 16

Met	Asp	Trp	Thr	Trp	Ile	Leu	Phe	Leu	Val	Ala	Ala	Ala	Thr	Arg	Val
1				5					10					15	

His	Ser	Gly	Ser	Asp	Val	Arg	Asp	Leu	Asn	Ala	Leu	Leu	Pro	Ala	Val
		20						25					30		

Pro Ser Leu Pro Gly Gly Gly Gly Cys Ala Leu Pro Val Ser Gly Ala

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

Arg Val Pro Gly Val Ala Pro Thr Ile Val Arg Ser Ala Ser Glu Thr
290 295 300

Asn Glu Lys Arg Pro Phe Met Gly Ala Tyr Pro Gly Gly Asn Lys Arg
305 310 315 320

Tyr Phe Lys Leu Ser His Leu Gln Met Gly Ser Arg Lys Gly Thr Gly
325 330 335

Glu Lys Pro Tyr Gln Gly Asp Phe Lys Asp Gly Glu Arg Arg Phe Ser
340 345 350

Arg Ser Asp Gln Leu Lys Arg Gly Gln Arg Arg Gly Thr Gly Val Lys
355 360 365

Pro Phe Gln Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser Asp His
370 375 380

Leu Lys Thr His Thr Arg Thr His Thr Gly Lys Thr Ser Glu Lys Pro
385 390 395 400

Phe Ser Cys Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser Asp
405 410 415

Glu Leu Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu
420 425 430

Gln Leu Ala Leu
435

Información para la SEQ ID No: 17

I.-Características de la secuencia

(A) Longitud: 3447

II.-Tipo de molécula: ADN

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polinucleótido sintético

Secuencia SEQ ID No: 17

atggattgga catggattct gttcctgggc gcagccgcca cagcagtgca tagccctaga
60

gccccacggt gtagagcagt ccgcagcctg ctgcgcagcc gataccggga agtgctgcct
120

ctggccacct ttgtccggag actgggacca cagggcaggc gcctggtgca ggcgcggcgac
180

cccgcagctt tccgagcact ggtggcacag tgcctggtgt gcgtgccatg ggatgcacgg
240

ccccctccag cagcccctag ctttagacag gtgtcctgcc tgaaagaact ggtcgcaagg
300

gtggtccagc ggctgtgcga gagaggcgcc aggaacgtgc tggcattcgg ctttgcaactg
360

ctggacggag ctagggggcg gccccctgag gcattcacca caagcgtgcg ctctacctg
420

ccaaatacag tcaactgatac cctgcgaggc tccggagcat ggggactgct gctgcgacgg
480

gtgggggacg atgtgctggt ccacctgctg gctagatgcg cactgtatgt gctggtcgct
540

ccctcttgcg cataccaggt gtgcggacca cccctgtatg acctggggcg tgcaaccag
600

gcaagacctc caccacacgc ctctggcact agaaggggac tgggcaccga acaggcatgg
660

aaccatagtg tcagggaggc aggagtgcc a ctgggactgc cagcacctgg ggctcgccga
720

cggagaggga gtgccggacg gtcactgcc a ctggctaaga gaccaaggcg cggagccgct
780

ccagaaccag agaggacacc tgtgggacag ggaagctggg cacaccctgg aagaactagg
840

gggccaagtg ataggggctt ctgcgtggtc tcaccagcac gaccagcaga ggaagctact
900

tctctggagg gagctctgag tggcaccgg cactctcatc ctagtgtggg aagacagcac
960

catgcaggcc ctccaagcac cagccggcct ccccggccat gggacactcc ttgtccacc
1020

gtgtacgctg aaaccaaaaca ctttctgtat agctccggag ataaggagca gctgcggccc
1080

tctttcctgc tgtctagtct gagacctagt ctgaccggag cacgacggct ggtggaaaca
1140

atctttctgg ggtcccgccc ttggatgcc a ggaaccccca gaaggacacc tcgactgcc
1200

cagcggtaact ggcagatgcg gccactgttc ctggagctgc tgggcaatca cgctcagtgc
1260

ccctatgggg cactgctgcg aacacattgt cctctgcggg cagcctgac tccagctgca
1320

ggagtctgcg ccagggaaaa gccacagggc agcgtggcag ctctgagga agaggacacc
1380

gatccacgcc gactggtgca gctgctgaga cagcactcaa gcccctggca ggtgtacgga
1440

tttctgaggg cctgtctgcg gagactggtg cctccaggac tgtggggggtc caggcacaac
1500

gaaaggcgct ttctgcgcaa tactaagaaa ttcattcagcc tgggcaagca tgctaaactg
1560

tccctgcagg agctgacctg gaaaatgagt gtgcgcgact gcgcatggct gcgacgggtca
1620

ccaggagtgc ggtgcgtgcc tgcagccgag caccgcctgc gagaagagat tctggccaag
1680

tttctgcatt ggctgatgtc agtgtacgtg gtcgaaactgc tgcggagctt cttttatgtg
1740

acagagacta ccttccagaa aaactacctg ttcttttatc gcaagtcagt gtggagcaaa
1800

ctgcagtcaa tcggcattcg gcagcacctg aagagagtgc agctgaggga actgagtga
1860

gccgaggtcc ggcagcatag agaggcaagg cctgccctgc tgacctcccg gctgagattc
1920

ctgcctaagc cagacgggct gagaccaatc gtgaacatgg attacgtggt cggagcacgg
1980

accttccgga gggaaaaacg cgctgagcga ctgacatccc gcgtgaagac tctgttctct
2040

gtcctgaatt atgagcgagc tcgccgaccc ggactgctgg gagcatctgt gctgggactg
2100

gacgatattc accgggcttg gagagcattt gtcctgaggg tgcgcgcaca ggacctccc
2160

ccagaactgt acttcgtgaa agtcgccgtg accggggctt atgacacaat ccctcaggat
2220

cggtctgactg aagtgatcgc ctccatcatt aagccacaga atacctactg cgtgcggaga
2280

tatgctgtgg tcaggcgcgc tgcacacggc catgtgagga agagcttcaa gcgccacgtc
2340

agcacactga ctgatctgca gccctacatg agacagttcg tggctcatct gcaggagacc
2400

agccctctga gggacgcagt ggtcatcgaa cagtcctcta gtctgaacga ggcataaagc
2460

gggctgttcg atgtctttct gcggttcgtg tgccaccatg ccgtcagaat tggaggcaaa
2520

tcttacgtgc agtgtcaggg catccccag ggcagcattc tgtctaccct gctgtgcagc
2580

ctgtgctatg gcgacatgga aaataagctg tttgccggaa tccgacggga tggcctgctg
2640

ctgagactgg tggccgcttt tctgctggtc actccacacc tgacccatgc caaagctttc
2700

ctgcgcacac tgggtccgagg ggtgccagag tacggatgcg tgggtcaacct gaggaagacc
2760

gtgggtcaatt tcccagtgga agacgaggcc ctgggacggca cagcatttgt ccagctgcca
2820

gcacacggac tgttcccatg gtgtggactg ctgctggaca cccgcacact ggaggtgcag
2880

tccgattact cctcttatgc ccggacaagc atcagagctt ccctgacttt taacagaggc
2940

ttcaaggccg ggaggaatat gagaaggaaa ctgtttggcg tgctgcgct gaagtgccat
3000

tccctgttcc tgtatctgca ggtgaactct ctgcagactg tctgtaccaa cgtgtacaaa
3060

atttttctgc tgcaggccta tcggttcac gcttgctgc tgcagctgcc attccatcag
3120

caggtcagga agaaccacac cttctttctg cgcgtgatct ctgatacagc tagtctgtgc
3180

tactcaattc tgaaggccaa aaatgctggc atgagcctgg gagcaaaagg agcagcagga
3240

ccatttcctt ccgaggctgc acagtggctg tgccaccagg cattcctgct gaagctggcc
3300

cgacatcggg tgacatatag gtgcctgctg ggcgcactgc gaacagcaca gactcagctg
3360

tgcagaaagc tgcccggggc cactctggct gccctggaag ccgctgccga ccctgccctg
3420

acctccgatt tcaagactat tctggac
3447

Información para la SEQ ID No: 18

I.-Características de la secuencia

(A) Longitud: 1149

II.-Tipo de molécula: PRT

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polipéptido sintético

Secuencia SEQ ID No: 18

Met	Asp	Trp	Thr	Trp	Ile	Leu	Phe	Leu	Val	Ala	Ala	Ala	Thr	Arg	Val
1				5					10					15	

His Ser Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg
 20 25 30

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

Gly Pro Gln Gly Arg Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe
 50 55 60

Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg
 65 70 75 80

Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu
 85 90 95

Leu Val Ala Arg Val Val Gln Arg Leu Cys Glu Arg Gly Ala Arg Asn
 100 105 110

Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro
 115 120 125

Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val
 130 135 140

Thr Asp Thr Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg
 145 150 155 160

Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Tyr
 165 170 175

Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu
 180 185 190

Tyr Asp Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser
 195 200 205

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

Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg
 225 230 235 240

Arg Arg Gly Ser Ala Gly Arg Ser Leu Pro Leu Ala Lys Arg Pro Arg
 245 250 255

Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser

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

Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys
515 520 525

Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly
530 535 540

Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys
545 550 555 560

Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser
565 570 575

Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Tyr Leu Phe Phe
580 585 590

Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln
595 600 605

His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg
610 615 620

Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe
625 630 635 640

Leu Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val
645 650 655

Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr
660 665 670

Ser Arg Val Lys Thr Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg
675 680 685

Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His
690 695 700

Arg Ala Trp Arg Ala Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro
705 710 715 720

Pro Glu Leu Tyr Phe Val Lys Val Ala Val Thr Gly Ala Tyr Asp Thr
725 730 735

Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro
740 745 750

Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Arg Arg Ala Ala
755 760 765

His Gly His Val Arg Lys Ser Phe Lys Arg His Val Ser Thr Leu Thr
770 775 780

Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr
785 790 795 800

Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn
805 810 815

Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Val Cys His
820 825 830

His Ala Val Arg Ile Gly Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile
835 840 845

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
850 855 860

Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu
865 870 875 880

Leu Arg Leu Val Ala Ala Phe Leu Leu Val Thr Pro His Leu Thr His
885 890 895

Ala Lys Ala Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
900 905 910

Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
915 920 925

Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Leu Pro Ala His Gly Leu
930 935 940

Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
945 950 955 960

Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr
965 970 975

Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe
980 985 990

Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Tyr Leu Gln Val
 995 1000 1005

Asn Ser Leu Gln Thr Val Cys Thr Asn Val Tyr Lys Ile Phe Leu
 1010 1015 1020

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe
 1025 1030 1035

His Gln Gln Val Arg Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 1040 1045 1050

Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn
 1055 1060 1065

Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Phe Pro
 1070 1075 1080

Ser Glu Ala Ala Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys
 1085 1090 1095

Leu Ala Arg His Arg Val Thr Tyr Arg Cys Leu Leu Gly Ala Leu
 1100 1105 1110

Arg Thr Ala Gln Thr Gln Leu Cys Arg Lys Leu Pro Gly Ala Thr
 1115 1120 1125

Leu Ala Ala Leu Glu Ala Ala Ala Asp Pro Ala Leu Thr Ser Asp
 1130 1135 1140

Phe Lys Thr Ile Leu Asp
 1145

Información para la SEQ ID No: 19

I.-Características de la secuencia

(A) Longitud: 3399

II.-Tipo de molécula: ADN

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polinucleótido sintético

Secuencia SEQ ID No: 19

cctagagccc cacggtgtag agcagtccgc agcctgctgc gcagccgata ccgggaagtg
 60

ctgcctctgg ccacctttgt ccggagactg ggaccacagg gcaggcgcct ggtgcagcgc
 120

ggcgaccccc cagctttccg agcactggtg gcacagtgcc tgggtgtgcgt gccatgggat
180

gcacggcccc ctccagcagc ccctagcttt agacaggtgt cctgcctgaa agaactggtc
240

gcaaggggtg tccagcggct gtgcgagaga ggcgccagga acgtgctggc attcggcttt
300

gcactgctgg acggagctag ggcggggccc cctgaggcat tcaccacaag cgtgcgctcc
360

tacctgcaa atacagtcac tgataccctg cgaggctccg gagcatgggg actgctgctg
420

cgacgggtgg gggacgatgt gctggtccac ctgctggcta gatgcgcact gtatgtgctg
480

gtcgtccct cttgcgcata ccaggtgtgc ggaccacccc tgtatgacct ggcgctgca
540

accagggcaa gacctccacc ccacgcctct ggcactagaa ggggactggg caccgaacag
600

gcatggaacc atagtgtcag ggaggcagga gtgccactgg gactgccagc acctggggct
660

cgccgacgga gagggagtgc cggacggtca ctgccactgg ctaagagacc aaggcgcgga
720

gccgctccag aaccagagag gacacctgtg ggacaggga gctgggcaca ccctggaaga
780

actagggggc caagtgatag gggcttctgc gtggtctcac cagcacgacc agcagaggaa
840

gctacttctc tggagggagc tctgagtggc acccggcact ctcatcctag tgtgggaaga
900

cagcaccatg caggccctcc aagcaccagc cggcctcccc ggccatggga cactccttgt
960

ccaccctgtg acgctgaaac caaacacttt ctgtatagct ccggagataa ggagcagctg
1020

cggccctctt tcctgctgtc tagtctgaga cctagtctga ccggagcacg acggctgggtg
1080

gaaacaatct ttctggggtc ccgcccttgg atgccaggaa ccccagaag gacacctga
1140

ctgccacagc ggtactggca gatgcggcca ctgttcctgg agctgctggg caatcacgct
1200

cagtgccct atggggcact gctgcgaaca cattgtctc tgcgggcagc cgtgactcca
1260

gctgcaggag tctgcgccag ggaaaagcca cagggcagcg tggcagctcc tgaggaagag
1320

gacaccgatac caccgccgact ggtgcagctg ctgagacagc actcaagccc ctggcaggtg
1380

tacggatttc tgagggcctg tctgcggaga ctggtgcctc caggactgtg ggggtccagg
1440

cacaacgaaa ggcgcctttct gcgcaatact aagaaattca tcagcctggg caagcatgct
1500

aaactgtccc tgcaggagct gacctggaaa atgagtgtgc gcgactgcgc atggctgcga
1560

cggtcaccag gagtcgggtg cgtgcctgca gccgagcacc gcctgcgaga agagattctg
1620

gccaagtttc tgcattggct gatgtcagtg tacgtggtcg aactgctgcg gagcttcttt
1680

tatgtgacag agactacctt ccagaaaaac tacctgttct tttatcgcaa gtcagtgtgg
1740

agcaaactgc agtcaatcgg cattcggcag cacctgaaga gagtgcagct gagggaaactg
1800

agtgaagccg aggtccggca gcatagagag gcaaggcctg cctgctgac ctcccggctg
1860

agattcctgc ctaagccaga cgggctgaga ccaatcgtga acatggatta cgtggtcgga
1920

gcacggacct tccggaggga aaaacgcgct gagcgactga catcccgcgt gaagactctg
1980

ttctctgtcc tgaattatga gcgagctcgc cgacccggac tgctgggagc atctgtgctg
2040

ggactggacg atattcaccg ggcttgagga gcatttgtcc tgaggggtgcg cgcacaggac
2100

cctccccag aactgtactt cgtgaaagtc gccgtgaccg gggcttatga cacaatccct
2160

caggatcggc tgactgaagt gatcgctcc atcattaagc cacagaatac ctactgcgtg
2220

cggagatatg ctgtgggtcag gcgcgctgca cacggccatg tgaggaagag cttcaagcgc
2280

cacgtcagca cactgactga tctgcagccc tacatgagac agttcgtggc tcacttcgag
2340

gagaccagcc ctctgaggga cgcagtggtc atcgaacagt cctctagtct gaacgaggca
2400

tcaagcgggc tgttcgatgt ctttctgcgg ttcgtgtgcc accatgccgt cagaattgga
2460

ggcaaattctt acgtgcagtg tcagggcatc ccccagggca gcattctgtc taccctgctg
2520

tgcagcctgt gctatggcga catggaaaat aagctgtttg ccggaatccg acgggatggc
2580

ctgctgctga gactgggtggc cgcttttctg ctggtcactc cacacctgac ccatgccaaa
2640

gctttcctgc gcacactggg ccgaggggtg ccagagtacg gatgcgtggg caacctgagg
2700

aagaccgtgg tcaatttccc agtgaagac gaggccctgg gcggcacagc atttgtccag
2760

ctgccagcac acggactggt cccatggtgt ggactgctgc tggacacccg cacactggag
2820

gtgcagtccg attactcctc ttatgcccg acaagcatca gagcttcctt gacttttaac
2880

agaggcttca aggccgggag gaatatgaga aggaaactgt ttggcgtgct ggcctgaag
2940

tgccattccc tgttctgtga tctgcaggtg aactctctgc agactgtctg taccaacgtg
3000

tacaaaattt ttctgctgca ggcctatcgg ttccacgctt gcgtgctgca gctgccattc
3060

catcagcagg tcaggaagaa cccaccttc tttctgcgcg tgatctctga tacagctagt
3120

ctgtgctact caattctgaa ggccaaaaat gctggcatga gcctgggagc aaaaggagca
3180

gcaggaccat ttccttccga ggctgcacag tggctgtgcc accaggcatt cctgctgaag
3240

ctggcccgac atcgggtgac atataggtgc ctgctgggcg cactgcgaac agcacagact
3300

cagctgtgca gaaagctgcc cggggccact ctggctgccc tggaagccgc tgccgaccct
3360

gccctgacct ccgatttcaa gactattctg gactgataa
3399

Información para la SEQ ID No: 20

I.-Características de la secuencia

(A) Longitud: 1131

II.-Tipo de molécula: PRT

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polipéptido
sintético

Secuencia SEQ ID No: 20

Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser Arg
1 5 10 15

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

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

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

Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu
530 535 540

His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe
545 550 555 560

Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Tyr Leu Phe Phe Tyr Arg
565 570 575

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

Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His
595 600 605

Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Leu Pro
610 615 620

Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
625 630 635 640

Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
645 650 655

Val Lys Thr Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
660 665 670

Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala
675 680 685

Trp Arg Ala Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu
690 695 700

Leu Tyr Phe Val Lys Val Ala Val Thr Gly Ala Tyr Asp Thr Ile Pro
705 710 715 720

Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn
725 730 735

Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Arg Arg Ala Ala His Gly
740 745 750

His Val Arg Lys Ser Phe Lys Arg His Val Ser Thr Leu Thr Asp Leu
755 760 765

Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro
770 775 780

Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala
785 790 795 800

Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Val Cys His His Ala
805 810 815

Val Arg Ile Gly Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
820 825 830

Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
835 840 845

Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
850 855 860

Leu Val Ala Ala Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
865 870 875 880

Ala Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
885 890 895

Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
900 905 910

Leu Gly Gly Thr Ala Phe Val Gln Leu Pro Ala His Gly Leu Phe Pro
915 920 925

Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
930 935 940

Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
945 950 955 960

Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
965 970 975

Leu Arg Leu Lys Cys His Ser Leu Phe Leu Tyr Leu Gln Val Asn Ser
980 985 990

Leu Gln Thr Val Cys Thr Asn Val Tyr Lys Ile Phe Leu Leu Gln Ala
995 1000 1005

Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
1010 1015 1020

Val Arg Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr
1025 1030 1035

Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met
1040 1045 1050

Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Phe Pro Ser Glu Ala
1055 1060 1065

Ala Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Ala Arg
1070 1075 1080

His Arg Val Thr Tyr Arg Cys Leu Leu Gly Ala Leu Arg Thr Ala
1085 1090 1095

Gln Thr Gln Leu Cys Arg Lys Leu Pro Gly Ala Thr Leu Ala Ala
1100 1105 1110

Leu Glu Ala Ala Ala Asp Pro Ala Leu Thr Ser Asp Phe Lys Thr
1115 1120 1125

Ile Leu Asp
1130

Información para la SEQ ID No: 21

I.-Características de la secuencia

(A) Longitud: 2307

II.-Tipo de molécula: ADN

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polinucleótido
sintético

Secuencia SEQ ID No: 21

atggactgga catggattct gttcctgggc gccgccgcaa ctgcgctgca ttcttggaac
60

gcactgcatg agactgattc tgctgtcgca ctgggacgga gaccccggtg gctgtgcgct
120

ggagcactgg tgctggccgg cgggggattc ctgctgggat tcctgttttg ctggtttatc
180

aaaagctcca gcgaggctac caatattacc cctaagcaca ataagaaagc attcctggat
240

gaactgaaag ccgagaacat caagaaattc ctgtacaact tcacaagaat tccacatctg
300

gctggcactg agcagaactt ccagctggca aaacagatcc agagtcagtg gaaggaattt
360

gggctggact cagtggagct gaccactac gatgtcctgc tgtcctatcc aaataagact
420

catcccaact acatctctat cattaacgaa gacggaaatg agattttcaa cacctctctg
480

tttgaacccc ctccaccggt ctatgagaat gtcagtgcgc tgggtccctcc attctcagcc
540

ttcagccccc aggggatgcc tgaggagat ctgggtgtacg tcaattatgc tagaacagaa
600

gacttcttta agctggagag ggatatgaaa atcaactgtt ccggcaagat cgtgattgcc
660

cggtacggga aggtgttcag aggaaataag gtcaaaaacg ctcagctggc cggagctacc
720

ggcgtgatcc tgtacagcga ccccgctgat tattttgcac ctggcgtgaa gtcctatcca
780

gacggatgga atctgcccgt cgggggagtg cagaggggaa acatcctgaa cctgaatgga
840

gccggcgatc ctctgactcc aggatacccc gccaacgaat acgcttatcg ccggggaatt
900

gcagaggccg tgggcctgcc tagcatccca gtccatccca ttggctatta cgatgccag
960

aagctgctgg agaaaatggg cgggagcgt cccctgact ctagttggaa gggctccctg
1020

aaagtgcctt acaatgtcgt gccaggattc actgggaact tttctaccca gaaggtgaaa
1080

atgcacatcc atagtaccag cgaggtgaca cgaatctaca acgtcattgg caccctgaga
1140

ggcgccgtgg agcctgatcg ctatgtcatt ctgggaggcc acagagactc atgggtgttc
1200

gggggaatcg atccacagag cggagcagct gtgggtccatg aaattgtgcg cagctttggg
1260

accctgaaga aagagggatg gcgaccagc cgcacaatcc tgttcgcac cctgggacgc
1320

gaggaatttg ggctgctggg cagcacagaa tgggccgagg aaaattctcg cctgctgcag
1380

gagcgagggg tggcttacat caatgcagac tcaagcattg aaggaaacta taccctgcgg
1440

gtggattgca caccctgat gtacagtctg gtctataacc tgacaaagga gctgaaatca
1500

cctgacgagg gcttcgaagg gaaaagcctg tacgaatcct ggactgagaa gagcccatcc
1560

cccgaattca gcggcatgcc taggatctct aagctgggca gtgggaacga ttttgagggtg
1620

ttctttcagc gcctgggaat tgcctctggc cgagctcggg acacaaaaaa ttgggagact
1680

aacaagttct cctcttacct actgtatcac agcgtgtacg agacttatga actggtcgag
1740

aaattctacg accccacttt taagtatcat ctgaccgtgg cacaggtcag gggcgggatg
1800

gtgttcgaac tggccaatag catcgtcctg ccatttgact gtcgagatta cgctgtggtc
1860

ctgcggaagt acgcagacaa gatctataac atctccatga agcaccacca ggagatgaag
1920

gcctattctg tgagtttcga ttccctgttt tctgccgtca aaaatttcac cgaaatcgct
1980

agtaagtttt cagagcgcct gcaggacctg gataagtcca atcccatcct gctgcggatt
2040

atgaacgatc agctgatggt cctggaaaga gcctttatcg accctctggg cctgcctgat
2100

agaccattct acaggcacgt gatctacgca cctagttcac ataacaagta cgccggcgag
2160

tctttcccag ggatctatga cgctctgttt gatattgaat caaagggtgga cccagcaaa
2220

gcattggggcg aggtcaagag acagatcagc attgcagcct ttacagtgca ggccgccgcc
2280

gaaaccctgt ccgaagtcgc ttgataa
2307

Información para la SEQ ID No: 22

I.-Características de la secuencia

(A) Longitud: 660

II.-Tipo de molécula: ADN

(A) Organismo: Homo sapiens

Secuencia SEQ ID No: 22

atgtgtccag cgcgagcct cctccttggt gctaccctgg tcctcctgga ccacctcagt
60

ttggccagaa acctccccgt ggccactcca gaccagga tgttcccatg ccttcaccac
120

tccccaaaacc tgctgagggc cgtcagcaac atgctccaga aggccagaca aactctagaa
180

ttttaccctt gcacttctga agagattgat catgaagata tcacaaaaga taaaaccagc
240

acagtggagg cctgtttacc attggaatta accaagaatg agagttgcct aaattccaga
300

gagacctctt tcataactaa tgggagttgc ctggcctcca gaaagacctc ttttatgatg
360

gccctgtgcc ttagtagtat ttatgaagac ttgaagatgt accaggtgga gttcaagacc
420

atgaatgcaa agcttctgat ggatcctaag aggcagatct ttctagatca aaacatgctg
480

gcagttattg atgagctgat gcaggccctg aatttcaaca gtgagactgt gccacaaaaa
540

tcctcccttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat
600

gctttcagaa ttcgggcagt gactattgat agagtgatga gctatctgaa tgcttcctaa
660

Información para la SEQ ID No: 23

I.-Características de la secuencia

(A) Longitud: 219

II.-Tipo de molécula: PRT

(A) Organismo: Homo sapiens

Secuencia SEQ ID No: 23

Met Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu
1 5 10 15

Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro
20 25 30

Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
35 40 45

Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys
50 55 60

Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
65 70 75 80

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys
85 90 95

Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala

100	105	110
Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr		
115	120	125
Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys		
130	135	140
Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu		
145	150	155
Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr		
165	170	175
Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys		
180	185	190
Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr		
195	200	205
Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser		
210	215	

Información para la SEQ ID No: 24
 I.-Características de la secuencia
 (A) Longitud: 987
 II.-Tipo de molécula: ADN
 (A) Organismo: Homo sapiens

Secuencia SEQ ID No: 24
 atgtgtcacc agcagttggt catctcttgg ttttccctgg tttttctggc atctcccctc
 60
 gtggccatat gggaactgaa gaaagatggt tatgtcgtag aattggattg gtatccggat
 120
 gcccttgagg aaatggtggt cctcacctgt gacaccctg aagaagatgg tatcacctgg
 180
 accttgacc agagcagtga ggtcttaggc tctggcaaaa ccctgaccat ccaagtcaaa
 240
 gagtttggag atgctggcca gtacacctgt cacaaggag gcgaggttct aagccattcg
 300
 ctctgtctgc ttcacaaaaa ggaagatgga atttgggtcca ctgatatttt aaaggaccag
 360
 aaagaacca aaaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc
 420
 acctgctggt ggctgacgac aatcagtact gatttgacat tcagtgtcaa aagcagcaga
 480

ggctcttctg accccaagg ggtgacgtgc ggagctgcta cactctctgc agagagagtc
540

agaggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgctgcca
600

gctgctgagg agagtctgcc cattgaggtc atggtggatg ccgttcacaa gctcaagtat
660

gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac
720

ttgcagctga agccattaaa gaattctcgg cagggtggagg tcagctggga gtaccctgac
780

acctggagta ctccacattc ctacttctcc ctgacattct gcgttcaggc ccagggcaag
840

agcaagagag aaaagaaaga tagagtcttc acggacaaga cctcagccac ggtcatctgc
900

cgcaaaaatg ccagcattag cgtgcggggc caggaccgct actatagctc atcttgagc
960

gaatgggcat ctgtgccctg cagttag
987

Información para la SEQ ID No: 25
I.-Características de la secuencia
(A) Longitud: 328
II.-Tipo de molécula: PRT
(A) Organismo: Homo sapiens

Secuencia SEQ ID No: 25

Met	Cys	His	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Phe	Leu
1				5					10					15	

Ala	Ser	Pro	Leu	Val	Ala	Ile	Trp	Glu	Leu	Lys	Lys	Asp	Val	Tyr	Val
			20					25					30		

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

Thr	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Leu	Asp	Gln
	50					55					60				

Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65					70					75					80

Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val
				85					90					95	

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp

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

Información para la SEQ ID No: 26
I.-Características de la secuencia

(A) Longitud: 418
II.-Tipo de molécula: PRT
(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polipéptido sintético

Secuencia SEQ ID No: 26

Gly Ser Asp Val Arg Asp Leu Asn Ala Leu Leu Pro Ala Val Pro Ser
1 5 10 15

Leu Pro Gly Gly Gly Gly Cys Ala Leu Pro Val Ser Gly Ala Ala Gln
20 25 30

Trp Ala Pro Val Leu Asp Phe Ala Pro Pro Ala Ala Pro Tyr Gly Ser
35 40 45

Leu Gly Gly Pro His Ser Phe Ile Lys Gln Glu Pro Ser Trp Gly Gly
50 55 60

Ala Asp Pro His Glu Glu Gln Cys Leu Ser Ala Phe Thr Val His Phe
65 70 75 80

Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala Cys Arg Tyr Gly Pro Phe
85 90 95

Gly Ala Pro Pro Pro Ser Gln Ala Pro Ser Gly Gln Ala Arg Met Phe
100 105 110

Pro Asn Ala Pro Tyr Leu Pro Asn Cys Leu Glu Ser Gln Pro Ala Ile
115 120 125

Arg Asn Gln Gly Tyr Ser Thr Val Ala Phe Asp Gly Thr Pro Ser Tyr
130 135 140

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

Lys His Glu Asp Pro Met Gly Gln Gln Gly Ser Leu Gly Glu Gln Gln
165 170 175

Tyr Ser Val Pro Pro Pro Val Tyr Gly Cys His Thr Pro Thr Asp Ser
180 185 190

Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg Thr Pro Tyr Asn Ser Asp
195 200 205

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

Ala Leu

Información para la SEQ ID No: 27
 I.-Características de la secuencia
 (A) Longitud: 1260
 II.-Tipo de molécula: ADN
 (A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polinucleótido sintético

Secuencia SEQ ID No: 27

gggagtgatg tgagagacct gaacgccctg ctgccagcag tgccatccct gcctggcggg
60

ggaggctgcg ctctgccagt ctctggagca gctcagtggg ctcccgtgct ggactttgca
120

ccccctgcag ccccttacgg aagtctgggc ggcccacact cattcatcaa acaggagcca
180

agctggggcg gggcagatcc tcatgaggaa cagtgcctgt cagccttcac agtccacttt
240

agcgggcagt tcaactggaac cgcaggagct tgtagatacg gaccctttgg agcaccaccc
300

ccttcccagg caccttctgg acaggcacgc atgttcccaa acgctcccta tctgcctaata
360

tgtctggaaa gccagcccg c tattaggaac cagggctact ccacagtggc atttgacggg
420

actcctagct atggacatac cccatccac catgctgcac agtttcctaa tcactccttc
480

aagcatgagg accccatggg acagcagggg tccctgggag aacagcagta ctctgtgccc
540

cctcccgtgt acggatgcca cacaccaact gacagttgta caggctcaca ggccctgctg
600

ctgcgaactc catacaacag tgataatctg tatcagatga cctcacagct ggagtgcattg
660

acatggaacc agatgaatct gggcagcaca ctgaaaggcc atgccactgg gtacgaatct
720

gacaaccaca ccacacctat gctgtacagt tgtggagccc agtatagaat ccacactcat
780

ggagtcttca gaggcattca ggatgtgcgg agagtcccag gagtggcacc aactatcgtg
840

cggagcgcct ccgagaccaa cgaaaagcgc ccctttatgg gcgcctaccc tggaggcaat
900

aagcgggtatt tcaaactgtc tcacctgcag atggggagta gaaaggggac cggagagaaa
960

ccttatcagg gcgactttaa agatggggaa aggcgcttct ctgcagtgga ccagctgaag
1020

cgaggacagc gacgaggaac cgggggtgaag ccatttcagt gcaaaacatg tcagagaaa
1080

ttctcaagga gcgatcacct gaagacccat acaagaactc acaccggcaa gaccagcgag
1140

aaaccatttt cctgccgatg gccctcttgt cagaagaaat tcgcccgcgc cgacgaactg
1200

gtccgacacc acaatatgca tcagagaaat atgacaaaac tgcagctggc tctgtgataa
1260

Información para la SEQ ID No: 28

I.-Características de la secuencia

(A) Longitud: 749

II.-Tipo de molécula: PRT

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polinucleótido
sintético

Secuencia SEQ ID No: 28

Trp	Asn	Ala	Leu	His	Glu	Thr	Asp	Ser	Ala	Val	Ala	Leu	Gly	Arg	Arg
1				5					10					15	

Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly	Gly	Gly	Phe
			20					25					30		

Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser	Ser	Ser	Glu	Ala
		35					40					45			

Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Lys	Lys	Ala	Phe	Leu	Asp	Glu	Leu
	50					55					60				

Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	Tyr	Asn	Phe	Thr	Arg	Ile	Pro
65				70						75				80	

His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe	Gln	Leu	Ala	Lys	Gln	Ile	Gln
			85						90					95	

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

Asp	Val	Leu	Leu	Ser	Tyr	Pro	Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser
		115					120					125			

Ile	Ile	Asn	Glu	Asp	Gly	Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu
	130					135					140				

Pro	Pro	Pro	Pro	Gly	Tyr	Glu	Asn	Val	Ser	Asp	Val	Val	Pro	Pro	Phe
145					150					155					160

Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val
 165 170 175

Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys
 180 185 190

Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe
 195 200 205

Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Thr Gly Val
 210 215 220

Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys Ser
 225 230 235

Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly Asn
 245 250 255

Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr Pro
 260 265 270

Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly Leu
 275 280 285

Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys Leu
 290 295 300

Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Lys Gly
 305 310 315 320

Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn Phe
 325 330 335

Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Ser Glu Val Thr
 340 345 350

Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro Asp
 355 360 365

Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly Gly
 370 375 380

Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg Ser
 385 390 395 400

Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile Leu

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

Pro Ile Leu Leu Arg Ile Met Asn Asp Gln Leu Met Phe Leu Glu Arg
660 665 670

Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg His
675 680 685

Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe
690 695 700

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

Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Ser Ile Ala Ala Phe
725 730 735

Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
740 745

Información para la SEQ ID No: 29

I.-Características de la secuencia

(A) Longitud: 2253

II.-Tipo de molécula: ADN

(A) Organismo: Secuencia artificial

Característica:

Otras informaciones: Descripción de secuencia artificial: Polinucleótido sintético

Secuencia SEQ ID No: 29

tggaacgcac tgcattgagac tgattctgct gtcgcactgg gacggagacc ccggtggctg
60

tgcgctggag cactgggtgct ggccggcggg ggattcctgc tgggattcct gtttggctgg
120

tttatcaaaa gctccagcga ggctaccaat attacccta agcacaataa gaaagcattc
180

ctggatgaac tgaaagccga gaacatcaag aaattcctgt acaacttcac aagaattcca
240

catctggctg gcactgagca gaacttcag ctggcaaac agatccagag tcagtggaag
300

gaatttgggc tggactcagt ggagctgacc cactacgatg tcttgctgtc ctatccaaat
360

aagactcatc ccaactacat ctctatcatt aacgaagacg gaaatgagat ttccaacacc
420

tctctgtttg aacccctcc acccggtat gagaatgtca gtgacgtggg cctccattc
480

tcagccttca gccccaggg gatgcctgag ggagatctgg tgtacgtcaa ttatgctaga
540

acagaagact tctttaagct ggagagggat atgaaaatca actgttccgg caagatcgtg
600

attgcccggg acgggaaggt gttcagagga aataaggtca aaaacgctca gctggccgga
660

gctaccggcg tgatcctgta cagcgacccc gctgattatt ttgcacctgg cgtgaagtcc
720

tatccagacg gatggaatct gcccggcggg ggagtgcaga ggggaaacat cctgaacctg
780

aatggagccg gcgatcctct gactccagga taccgccca acgaatacgc ttatcgccgg
840

ggaattgcag aggccgtggg cctgcctagc atcccagtc atcccattgg ctattacgat
900

gcccagaagc tgctggagaa aatgggcggg agcgctcccc ctgactctag ttggaagggc
960

tccctgaaag tgccttaca tgctgggcca ggattcactg ggaacttttc taccagaag
1020

gtgaaaatgc acatccatag taccagcgag gtgacacgaa tctacaacgt cattggcacc
1080

ctgagaggcg ccgtggagcc tgatcgctat gtcattctgg gaggccacag agactcatgg
1140

gtgttcgggg gaatcgatcc acagagcgga gcagctgtgg tccatgaaat tgtgcgcagc
1200

tttgggaccc tgaagaaaga gggatggcga cccaggcgca caatcctgtt cgcacacctg
1260

gacgccgagg aatttgggct gctgggcagc acagaatggg ccgaggaaaa ttctgcctg
1320

ctgcaggagc gaggggtggc ttacatcaat gcagactcaa gcattgaagg aaactatacc
1380

ctgcgggtgg attgcacacc cctgatgtac agtctggtct ataacctgac aaaggagctg
1440

aaatcacctg acgagggctt cgaagggaag agcctgtacg aatcctggac tgagaagagc
1500

ccatcccccg aattcagcgg catgcctagg atctctaagc tgggcagtgg gaacgatttt
1560

gaggtgttct ttcagcgctt gggaattgcc tctggccgag ctcggtacac aaaaaattgg
1620

gagactaaca agttctcctc ttaccactg tatcacagcg tgtacgagac ttatgaactg
1680

gtcgagaaat tctacgaccc cacttttaag tatcatctga ccgtggcaca ggtcaggggc
1740

gggatggtgt tcgaactggc caatagcatc gtcctgccat ttgactgtcg agattacgct
1800

gtggtcctgc ggaagtacgc agacaagatc tataacatct ccatgaagca cccccaggag
1860

atgaaggcct attctgtgag tttcgattcc ctgttttctg ccgtcaaaaa tttcaccgaa
1920

atcgctagta agttttcaga gcgcctgcag gacctggata agtccaatcc catcctgctg
1980

cggattatga acgatacagct gatgttcctg gaaagagcct ttatcgaccc tctgggcctg
2040

cctgatagac cattctacag gcacgtgac tacgcaccta gttcacataa caagtacgcc
2100

ggcgagtctt tcccagggat ctatgacgct ctgtttgata ttgaatcaaa ggtggacccc
2160

agcaaagcat ggggcgaggt caagagacag atcagcattg cagcctttac agtgcaggcc
2220

gccgccgaaa ccctgtccga agtcgcttga taa
2253