

LISTA DE SECUENCIAS

<110> AMGEN INC.

<120> RECEPTORES QUÍMICOS DE STEAP1 Y MÉTODOS DE USO DE LOS MISMOS

<130> A-2280-WO-PCT

<140> PCT/US2019/042245

<141> 17/07/2019

<150> 62/700,178

<151> 2018-07-18

<160> 147

<170> PatentIn versión 3.5

<210> 1

<211> 294

<212> ADN

<213> Desconocido

<220>

<221> fuente

<223> /nota= "Descripción de lo desconocido: Secuencia de CD28T"

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ctcgcttgtt actctctgct cgtcaccgtg gcttttataa tcttctgggt tagatccaaa 180

agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgccc tggccccaca 240

aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagc 294

<210> 2

<211> 98

<212> PRT

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<221> fuente

<223> /nota= "Descripción de lo desconocido: Secuencia de CD28T"

<400> 2

Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys
1 5 10 15

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp

20

25

30

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
 35 40 45

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
 50 55 60

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
 65 70 75 80

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
 85 90 95

Arg Ser

<210> 3

<211> 90

<212> ADN

<213> Desconocido

<220>

<221> fuente

<223> /nota= "Descripción de lo desconocido: Secuencia de CD28T"

<400> 3

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tcacccttgt tccctggtcc atccaagcca 90

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<211> 30

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<223> /nota= "Descripción de lo desconocido: Secuencia de CD28T"

<400> 4

Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys
 1 5 10 15

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro
 20 25 30

<210> 5
<211> 81
<212> ADN
<213> Desconocido

<220>
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<223> /nota= "Descripción de lo desconocido: Secuencia de CD28"

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gcttttataa tcttctgggt t 81

<210> 6
<211> 27
<212> PRT
<213> Desconocido

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<223> /nota= "Descripción de lo desconocido: Secuencia de CD28"

<400> 6
Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 7
<211> 123
<212> ADN
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<223> /nota= "Descripción de lo desconocido: Secuencia de CD28"

<400> 7
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agc 123

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<211> 41

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<213> Desconocido

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<400> 8
Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
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Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 9
<211> 336
<212> ADN
<213> Desconocido

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<223> /nota= "Descripción de lo desconocido: secuencia zeta CD3"

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cgggaccctg agatgggtgg caaaccaaga cgaaaaaacc cccaggaggg tctctataat 180
gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg 240
agaaggggaa aagggcacga cggtttgtac cagggactca gcactgctac gaaggatact 300
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<210> 10
<211> 112
<212> PRT
<213> Desconocido

<220>
<221> fuente
<223> /nota= "Descripción de lo desconocido: secuencia zeta CD3"

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Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly

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

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 <213> Desconocido

<220>
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 <223> /nota= "Descripción de lo desconocido: Secuencia de CD28"

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cacgtgaaag gtaaacacct gtgtccttct cccctcttcc ccgggccatc aaagccc	117

<210> 12
 <211> 39
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 <213> Desconocido

<220>
 <221> fuente
 <223> /nota= "Descripción de lo desconocido: Secuencia de CD28"

<400> 12	
Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn	
1	5 10 15

Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu
20 25 30

Phe Pro Gly Pro Ser Lys Pro
35

<210> 13
<211> 288
<212> ADN
<213> Desconocido

<220>
<221> fuente
<223> /nota= "Descripción de lo desconocido: Secuencia de CD8"

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cagcctctgt ccctgcgccc agaggcttgc cgaccggccg cagggggcgc tgttcataacc 180
agaggactgg atttcgcctg cgatatctat atctgggcac ccctggccgg aacctgcggc 240
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<211> 96
<212> PRT
<213> Desconocido

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<221> fuente
<223> /nota= "Descripción de lo desconocido: Secuencia de CD8"

<400> 14
Ala Ala Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro
1 5 10 15

Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
20 25 30

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
35 40 45

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp

50

55

60

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
65 70 75 80

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
85 90 95

<210> 15

<211> 141

<212> ADN

<213> Desconocido

<220>

<221> fuente

<223> /nota= "Descripción de lo desconocido: Secuencia de 4-1BB"

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atgaggccgg tccaaacgac tcaggaagag gacggctgct cctgccgctt tcctgaggag 120

gaggagggcg ggtgcgaact g 141

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<223> /nota= "Descripción de lo desconocido: Secuencia de 4-1BB"

<400> 16

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
1 5 10 15

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
20 25 30

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40 45

<210> 17

<211> 2477

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

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gtgagctgca aagccagcgg ctacaccttc tccacctact ggatcgagtg ggtgagacag	180
gccccggaca gaggctggaa tggatgggag agatcctgcc cggcagcggc aacaccgact	240
tcaacgagaa gttccagggc agagtgcctt tcaccgccga taccagcagc gacaccgcct	300
acatggaact gagcagcctg agaagcgagg ataccgccgt ctactactgc accagatggg	360
gctactacgg caccaggggc tatttcaacg tgtggggcca gggaaccctc gtgaccgtga	420
gcagcggagg cggaggatct ggtggcggtg gttctggcgg cggaggctcc gagattgtgc	480
tgaccagag ccctgctaca ctgagcctga gccccggcga gagagccaca ctgagctgca	540
gagccagcag cagcgtgagc tacatgcact ggttccagca aaagcccggc caggccccta	600
ggctgctgat ctacagcaca tccaacctgg ccagcggcat ccctgccaga ttcagcggtt	660
ctggctccgg caccgactac accctgacca tctccagcct ggagcccag gactttgccg	720
tgtattactg ccagcagagg aggagcttcc cctacacatt cggccagggc accaaactgg	780
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tcgtagtggg tggagtcctc gcttgttact ctctgctcgt caccgtggct ttataatct	960
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gccgccctgg ccccaacaagg aaacactacc agccttacgc accacctaga gatttcgctg	1080
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gacgaaaaaa ccccaggag ggtctctata atgagctgca gaaggataag atggctgaag	1440

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acgtggaaga aaatccgggg cctatgggtg ccggcgccac ggggaagggt atggatggcc	1680
cgcgactgct tctcctgctg ttgttgggcg tgtctctcgg aggcgctaag gaggcctgtc	1740
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tcgcacaacc ttgtggtgct aaccagacag tctgtgaacc atgcctggat tcagtacat	1860
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attaccagga cgaaactacc gggcgggtgtg aggcctgccg ggtgtgtgaa gccggctctg	2040
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cctacagcga cgaggcgaac cacgtcgacc cttgcttgcc gtgcaccgtc tgcgaggata	2160
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aagaaccgga ggccccctca gagcaggacc tgatcgcttc tacagttgct ggcgtggtga	2340
cgacagtcac gggatcctca caaccagtcg tgacgcgggg cacaaccgac aatctgattc	2400
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agagatgacc taggtaa	2477

<210> 18

<211> 822

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 18

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
			20					25					30		

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Ser Thr Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Arg Leu Glu Trp Met Gly Glu Ile Leu Pro Gly Ser Gly Asn Thr Asp
65 70 75 80

Phe Asn Glu Lys Phe Gln Gly Arg Val Thr Phe Thr Ala Asp Thr Ser
85 90 95

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

Ala Val Tyr Tyr Cys Thr Arg Trp Gly Tyr Tyr Gly Thr Arg Gly Tyr
115 120 125

Phe Asn Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
145 150 155 160

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
165 170 175

Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe
180 185 190

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ser Thr Ser
195 200 205

Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
210 215 220

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
225 230 235 240

Val Tyr Tyr Cys Gln Gln Arg Arg Ser Phe Pro Tyr Thr Phe Gly Gln

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

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
465 470 475 480

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
485 490 495

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
500 505 510

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser Gly
515 520 525

Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
530 535 540

Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly
545 550 555 560

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

Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys
580 585 590

Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
595 600 605

Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val
610 615 620

Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu
625 630 635 640

Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg
645 650 655

Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala
660 665 670

Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp

675

680

685

Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp
690 695 700

Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp
705 710 715 720

Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys
725 730 735

Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly
740 745 750

Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu
755 760 765

Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met
770 775 780

Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile
785 790 795 800

Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala
805 810 815

Tyr Ile Ala Phe Lys Arg
820

<210> 19

<211> 2337

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 19

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gtgagctgca aagccagcgg ctacaccttc tccacctact ggatcgagtg ggtgagacag 180

gcccccgga	agaggctgga	atggatggga	gagatcctgc	ccggcagcgg	caacaccgac	240
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ctgaccaga	gccctgctac	actgagcctg	agccccggcg	agagagccac	actgagctgc	540
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gtgtattact	gccagcagag	gaggagcttc	ccctacacat	tcggccaggg	caccaaactg	780
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<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 20

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

Thr Phe Ser Thr Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Gln
 50 55 60

Arg Leu Glu Trp Met Gly Glu Ile Leu Pro Gly Ser Gly Asn Thr Asp
 65 70 75 80

Phe Asn Glu Lys Phe Gln Gly Arg Val Thr Phe Thr Ala Asp Thr Ser
 85 90 95

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

Ala Val Tyr Tyr Cys Thr Arg Trp Gly Tyr Tyr Gly Thr Arg Gly Tyr
115 120 125

Phe Asn Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
145 150 155 160

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
165 170 175

Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe
180 185 190

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ser Thr Ser
195 200 205

Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
210 215 220

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
225 230 235 240

Val Tyr Tyr Cys Gln Gln Arg Arg Ser Phe Pro Tyr Thr Phe Gly Gln
245 250 255

Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Leu Asp Asn Glu Lys Ser
260 265 270

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
275 280 285

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
290 295 300

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
305 310 315 320

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
325 330 335

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
340 345 350

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
355 360 365

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
370 375 380

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
385 390 395 400

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
405 410 415

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
420 425 430

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
435 440 445

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
450 455 460

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser
465 470 475 480

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
485 490 495

Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp
500 505 510

Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly
515 520 525

Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys
530 535 540

Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala
545 550 555 560

Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp
565 570 575

Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly
580 585 590

Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys
595 600 605

Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
610 615 620

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
625 630 635 640

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
645 650 655

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
660 665 670

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
675 680 685

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
690 695 700

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
705 710 715 720

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
725 730 735

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu
740 745 750

Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val
755 760 765

Ala Tyr Ile Ala Phe Lys Arg
770 775

<210> 21

<211> 2355

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 21

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gtgagctgca aagccagcgg ctacaccttc tccacctact ggatcgagtg ggtgagacag	180
gccccgggac agaggctgga atggatggga gagatcctgc ccggcagcgg caacaccgac	240
ttcaacgaga agttccaggg cagagtgacc ttcaccgccg ataccagcag cgacaccgcc	300
tacatggaac tgagcagcct gagaagcgag gataccgccg tctactactg caccagatgg	360
ggctactacg gcaccagggg ctatttcaac gtgtggggcc agggaaccct cgtgaccgtg	420
agcagcggag gcggaggatc tgggtggcggg gggttctggcg gcggaggctc cgagattgtg	480
ctgaccaga gccctgctac actgagcctg agccccggcg agagagccac actgagctgc	540
agagccagca gcagcgtgag ctacatgcac tggttccagc aaaagcccgg ccaggcccct	600
aggctgctga tctacagcac atccaacctg gccagcggca tccctgccag attcagcggg	660
tctggctccg gcaccgacta caccctgacc atctccagcc tggagcccga ggactttgcc	720
gtgtattact gccagcagag gaggagcttc ccctacacat tcggccaggg caccaaactg	780
gagatcaagg ccgctgccct tgataatgaa aagtcaaacg gaacaatcat tcacgtgaag	840
ggcaagcacc tctgtccgtc acccttgttc cctgggtccat ccaagccatt ctgggtgttg	900
gtcgtagtgg gtggagtcct cgcttgttac tctctgctcg tcaccgtggc ttttataatc	960
ttctgggttc gcttttccgt cgtttaagcgg gggagaaaaa agctgctgta cattttcaaa	1020

cagccgttta tgaggccggt ccaaacgact caggaagagg acggctgctc ctgccgcttt	1080
cctgaggagg aggagggcgg gtgcgaactg aggggtgaagt tttccagatc tgcagatgca	1140
ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa	1200
gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga	1260
cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc	1320
tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac	1380
cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcc	1440
cctagggcca agagaagtgg cagcggggag ggccggggat ctctccttac atgtggggac	1500
gtggaagaaa atccggggcc tatgggtgcc ggcgccacgg gaagggtat ggatggccc	1560
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gcacaacctt gtggtgctaa ccagacagtc tgtgaaccat gcctggattc agtgacattc	1740
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tccatgtccg cccctgtgt cgaagccgat gatgcagtgt gcagatgtgc ctatggatat	1860
taccaggacg aaactaccgg gcggtgtgag gcctgccggg tgtgtgaagc cggctctggc	1920
ctcgtgttca gttgccagga taagcaaac acagtatgtg aggagtgtcc agacggaacc	1980
tacagcgacg aggcgaacca cgtcgaccct tgcttgccgt gcaccgtctg cgaggatacc	2040
gaacgccagc tgagagagtg tacgcgctgg gcagacgctg agtgcgagga gatccctggg	2100
agatggatca cccggagcac acctcctgag ggatcagaca gtacagcccc gagtacccaa	2160
gaaccggagg cccctccaga gcaggacctg atcgcttcta cagttgctgg cgtggtgacg	2220
acagtcatgg gatcctcaca accagtcgtg acgcggggca caaccgacaa tctgattcct	2280
gtctactgta gcatcttggc agccgtggtc gtgggcctgg tagcctacat cgcctttaag	2340
agatgaccta ggtaa	2355

<210> 22

<211> 781

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 22

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Ser Thr Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Arg Leu Glu Trp Met Gly Glu Ile Leu Pro Gly Ser Gly Asn Thr Asp
65 70 75 80

Phe Asn Glu Lys Phe Gln Gly Arg Val Thr Phe Thr Ala Asp Thr Ser
85 90 95

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

Ala Val Tyr Tyr Cys Thr Arg Trp Gly Tyr Tyr Gly Thr Arg Gly Tyr
115 120 125

Phe Asn Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
145 150 155 160

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
165 170 175

Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe
180 185 190

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ser Thr Ser
195 200 205

Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
210 215 220

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
225 230 235 240

Val Tyr Tyr Cys Gln Gln Arg Arg Ser Phe Pro Tyr Thr Phe Gly Gln
245 250 255

Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Leu Asp Asn Glu Lys Ser
260 265 270

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
275 280 285

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
290 295 300

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
305 310 315 320

Phe Trp Val Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu
325 330 335

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
340 345 350

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
355 360 365

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
370 375 380

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
385 390 395 400

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
405 410 415

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu

420

425

430

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
 435 440 445

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
 450 455 460

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
 465 470 475 480

Pro Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
 485 490 495

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala
 500 505 510

Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu
 515 520 525

Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr
 530 535 540

Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val
 545 550 555 560

Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu Asp
 565 570 575

Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro
 580 585 590

Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu
 595 600 605

Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu
 610 615 620

Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly
 625 630 635 640

Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys
645 650 655

Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu
660 665 670

Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr
675 680 685

Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr
690 695 700

Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln
705 710 715 720

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

Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr Arg
740 745 750

Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala
755 760 765

Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe Lys Arg
770 775 780

<210> 23

<211> 2415

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 23

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ccgcaggtgc agctggtgca gagcggagcc gaggtgaaga agcccggagc cagcgtgaag 120

gtgagctgca aagccagcgg ctacaccttc tccacctact ggatcgagtg ggtgagacag 180

gccccggac agaggctgga atggatggga gagatcctgc ccggcagcgg caacaccgac 240

ttcaacgaga agttccaggg cagagtgacc ttcaccgccg ataccagcag cgacaccgcc	300
tacatggaac tgagcagcct gagaagcgag gataccgccg tctactactg caccagatgg	360
ggctactacg gcaccagggg ctatttcaac gtgtggggcc agggaaaccct cgtgaccgtg	420
agcagcggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgagattgtg	480
ctgaccaga gccctgctac actgagcctg agccccggcg agagagccac actgagctgc	540
agagccagca gcagcgtgag ctacatgcac tggttccagc aaaagcccgg ccaggcccct	600
aggctgctga tctacagcac atccaacctg gccagcggca tccctgccag attcagcggg	660
tctggctccg gcaccgacta caccctgacc atctccagcc tggagcccga ggactttgcc	720
gtgtattact gccagcagag gaggagcttc ccctacacat tcggccaggg caccaaactg	780
gagatcaagg ccgctgcctt cgtgcctgtt tttctgcccg cgaaaccac aactaccccc	840
gcccctcggc cccaactcc tgcaccaact atcgcttccc aaccctgtc tctgagacct	900
gaggcatgcc gcccgcggc aggcggcgcc gtgcacacta gaggcctgga cttgcctgc	960
gatatttata tctgggcccc ctttgccggg acatgcgggg tactgctgct gtctctggtg	1020
attaccctct actgcaacca cagaaacaga tccaaaagaa gccgcctgct ccatagcgat	1080
tacatgaata tgactccacg ccgccctggc ccacaagga aacactacca gccttacgca	1140
ccacctagag atttcgctgc ctatcggagc aggggtgaagt tttccagatc tgcagatgca	1200
ccagcgtatc agcagggcc aaccaactg tataacgagc tcaacctggg acgcagggaa	1260
gagtatgacg ttttggaaca gcgcagagga cgggaccctg agatgggtgg caaaccaaga	1320
cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc	1380
tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac	1440
cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca	1500
cctagggcc aagaagtgg cagcggggag ggccggggat ctctccttac atgtggggac	1560
gtggaagaaa atccggggcc tatgggtgcc ggcgccacgg gaagggtat ggatggccc	1620
cgactgcttc tcctgctgtt gttgggcgtg tctctcggag gcgctaagga ggcctgtcca	1680
acgggcctct acactcactc cggatgaatgt tgcaaagcct gtaaccttgg cgagggcgtc	1740
gcacaacctt gtggtgctaa ccagacagtc tgtgaaccat gcctggattc agtgacattc	1800
agcgatgttg tctcagccac cgagccttgc aagccttgta ccgaatgtgt gggccttcag	1860

tccatgtccg cccctgtgt cgaagccgat gatgcagtgt gcagatgtgc ctatggatat	1920
taccaggacg aaactaccgg gcggtgtgag gcctgccggg tgtgtgaagc cggctctggc	1980
ctcgtgttca gttgccagga taagcaaac acagtatgtg aggagtgtcc agacggaacc	2040
tacagcgacg aggcgaacca cgtcgaccct tgcttgccgt gcaccgtctg cgaggatacc	2100
gaacgccagc tgagagagtg tacgcgctgg gcagacgctg agtgcgagga gatccctggg	2160
agatgggatca cccggagcac acctcctgag ggatcagaca gtacagcccc gagtacccaa	2220
gaaccggagg cccctccaga gcaggacctg atcgcttcta cagttgctgg cgtgggtgacg	2280
acagtcatgg gatcctcaca accagtcgtg acgcggggca caaccgacaa tctgattcct	2340
gtctactgta gcatcttggc agccgtggtc gtgggcctgg tagcctacat cgcctttaag	2400
agatgaccta ggtaa	2415

<210> 24

<211> 801

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 24

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
			20					25					30		

Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
		35					40					45			

Thr	Phe	Ser	Thr	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln
	50					55					60				

Arg	Leu	Glu	Trp	Met	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Gly	Asn	Thr	Asp
65					70					75					80

Phe	Asn	Glu	Lys	Phe	Gln	Gly	Arg	Val	Thr	Phe	Thr	Ala	Asp	Thr	Ser
				85					90					95	

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

Ala Val Tyr Tyr Cys Thr Arg Trp Gly Tyr Tyr Gly Thr Arg Gly Tyr
115 120 125

Phe Asn Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
145 150 155 160

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
165 170 175

Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe
180 185 190

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ser Thr Ser
195 200 205

Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
210 215 220

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
225 230 235 240

Val Tyr Tyr Cys Gln Gln Arg Arg Ser Phe Pro Tyr Thr Phe Gly Gln
245 250 255

Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Phe Val Pro Val Phe Leu
260 265 270

Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
275 280 285

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
290 295 300

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
305 310 315 320

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
325 330 335

Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys
340 345 350

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
355 360 365

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
370 375 380

Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
385 390 395 400

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
405 410 415

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
420 425 430

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
435 440 445

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
450 455 460

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
465 470 475 480

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
485 490 495

Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly Arg
500 505 510

Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met
515 520 525

Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu Leu
530 535 540

Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro
545 550 555 560

Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu
565 570 575

Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu
580 585 590

Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu
595 600 605

Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala
610 615 620

Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr
625 630 635 640

Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu
645 650 655

Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val
660 665 670

Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val
675 680 685

Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu
690 695 700

Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly
705 710 715 720

Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala
725 730 735

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

Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro
755 760 765

Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys Ser
770 775 780

Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe Lys
785 790 795 800

Arg

<210> 25

<211> 2433

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 25

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ccgcaggtgc agctggtgca gagcggagcc gaggtgaaga agcccggagc cagcgtgaag 120

gtgagctgca aagccagcgg ctacaccttc tccacctact ggatcgagtg ggtgagacag 180

gccccggac agaggctgga atggatggga gagatcctgc ccggcagcgg caacaccgac 240

ttcaacgaga agttccaggg cagagtgacc ttcaccgccg ataccagcag cgacaccgcc 300

tacatggaac tgagcagcct gagaagcgag gataccgccg tctactactg caccagatgg 360

ggctactacg gcaccagggg ctatttcaac gtgtggggcc aggggaaccct cgtgaccgtg 420

agcagcggag gcggaggatc tggtggcggt gggttctggcg gcggaggctc cgagattgtg 480

ctgaccagca gccctgctac actgagcctg agccccggcg agagagccac actgagctgc 540

agagccagca gcagcgtgag ctacatgcac tggttccagc aaaagcccgg ccaggcccct 600

aggctgctga tctacagcac atccaacctg gccagcggca tccctgccag attcagcggc 660

tctggctccg gcaccgacta caccctgacc atctccagcc tggagcccga ggactttgcc 720

gtgtattact gccagcagag gaggagcttc ccctacacat tcggccaggg caccaaactg	780
gagatcaagg ccgctgcctt cgtgcctggt tttctgcccg cgaaaccac aactaccccc	840
gcccctcggc ccccaactcc tgcaccaact atcgcttccc aaccctgtc tctgagacct	900
gaggcatgcc gccccgcggc aggcggcgcc gtgcacacta gaggcctgga cttgcctgc	960
gatatttata tctgggcccc ctttgccggg acatgcgggg tactgtctgt gtctctggtg	1020
attaccctct actgcaacca cagaaaccgc ttttccgtcg ttaagcgggg gagaaaaaag	1080
ctgctgtaca ttttcaaaca gccgtttatg aggcgggtcc aaacgactca ggaagaggac	1140
ggctgctcct gccgctttcc tgaggaggag gagggcgggt gcgaactgag ggtgaagttt	1200
tccagatctg cagatgcacc agcgtatcag cagggccaga accaactgta taacgagctc	1260
aacctgggac gcagggaaga gtatgacgtt ttggacaagc gcagaggacg ggaccctgag	1320
atgggtggca aaccaagacg aaaaaacccc caggagggtc tctataatga gctgcagaag	1380
gataagatgg ctgaagccta ttctgaaata ggcatgaaag gagagcggag aaggggaaaa	1440
gggcacgacg gtttgtacca gggactcagc actgctacga aggatactta tgacgtctc	1500
cacatgcaag ccctgccacc tagggccaag agaagtggca gcggggaggg ccggggatct	1560
ctccttacat gtggggacgt ggaagaaaat ccggggccta tgggtgccgg cgccacggga	1620
agggttatgg atggcccgcg actgcttctc ctgctgttgt tgggcgtgtc tctcggaggc	1680
gctaaggagg cctgtccaac gggcctctac actcactccg gtgaatgttg caaagcctgt	1740
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gaatgtgtgg gccttcagtc catgtccgcc ccctgtgtcg aagccgatga tgcagtgtgc	1920
agatgtgcct atggatatta ccaggacgaa actaccgggc ggtgtgaggc ctgccgggtg	1980
tgtgaagccg gctctggcct cgtgttcagt tgccaggata agcaaaacac agtatgtgag	2040
gagtgtccag acggaaccta cagcgacgag gcgaaccacg tcgacccttg cttgccgtgc	2100
accgtctgcg aggataccga acgccagctg agagagtgtg cgcgctgggc agacgctgag	2160
tgcgaggaga tccctgggag atggatcacc cggagcacac ctctgaggg atcagacagt	2220
acagccccga gtaccaaga accggaggcc cctccagagc aggacctgat cgcttctaca	2280
gttgctggcg tggtgacgac agtcatggga tcctcacaac cagtcgtgac gcggggcaca	2340

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gcctacatcg cctttaagag atgacctagg taa 2433

<210> 26
<211> 807
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 26
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Ser Thr Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Arg Leu Glu Trp Met Gly Glu Ile Leu Pro Gly Ser Gly Asn Thr Asp
65 70 75 80

Phe Asn Glu Lys Phe Gln Gly Arg Val Thr Phe Thr Ala Asp Thr Ser
85 90 95

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

Ala Val Tyr Tyr Cys Thr Arg Trp Gly Tyr Tyr Gly Thr Arg Gly Tyr
115 120 125

Phe Asn Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
145 150 155 160

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
165 170 175

Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe
180 185 190

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ser Thr Ser
195 200 205

Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
210 215 220

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
225 230 235 240

Val Tyr Tyr Cys Gln Gln Arg Arg Ser Phe Pro Tyr Thr Phe Gly Gln
245 250 255

Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Phe Val Pro Val Phe Leu
260 265 270

Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
275 280 285

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
290 295 300

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
305 310 315 320

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
325 330 335

Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Phe Ser
340 345 350

Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
355 360 365

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys

370

375

380

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
 385 390 395 400

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
 405 410 415

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 420 425 430

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 435 440 445

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 450 455 460

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 465 470 475 480

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 485 490 495

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser
 500 505 510

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
 515 520 525

Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp
 530 535 540

Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly
 545 550 555 560

Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys
 565 570 575

Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala
 580 585 590

Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp
595 600 605

Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly
610 615 620

Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys
625 630 635 640

Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
645 650 655

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
660 665 670

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
675 680 685

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
690 695 700

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
705 710 715 720

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
725 730 735

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
740 745 750

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
755 760 765

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu
770 775 780

Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val
785 790 795 800

Ala Tyr Ile Ala Phe Lys Arg

<210> 27
 <211> 2493
 <212> ADN
 <213> Secuencia artificial

<220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 27
 atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
 ccggagattc agctggtgca gagcggcgcc gaggtgaaaa agcccggagc caccgtgaag 120
 atcagctgca aggccagcgg ctacacattc accaactacg gcatgaactg ggtgcaacag 180
 gccccggcc agggactgga gtggatgggc tggatgaaca catacaccgg cgagcccacc 240
 tacgccgaca agttccaggg cagggtgaca ttcacactcg ataccagcgc cagaaccgtg 300
 tatatggaac tgagcagcct gaggagcag gacaccgctg tgtacttctg cgcaagggct 360
 ggaggccagc tgagacctgg cgctatggac tactggggcc agggcaccat ggtgaccgtg 420
 agctccggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgacatcgtg 480
 ctgaccaga cacctctctc cctgtccgtg acccccggac agcctgcctc catttcctgt 540
 aaggcctccc agagcgtgga ctatgacggc gacagcttca tgaactggta cctgcagaag 600
 cccggacaac cccccagct gctgatctac gtggccagca acctggagtc cggcgtgcct 660
 gacaggtttt ccggctccgg cagcggcacc gacttcaccc tgaagatcag cagggtggaa 720
 gccgaggacg tgggcgtgta ctactgccag cagagcaacg aggagcccc taccttcgga 780
 cagggcacca agctggagat caaggccgct gcccttgata atgaaaagtc aaacggaaca 840
 atcattcacg tgaagggcaa gcacctctgt ccgtcaccct tgttccctgg tccatccaag 900
 ccattctggg tgttggctgt agtgggtgga gtcctcgctt gttactctct gtcgtcacc 960
 gtggctttta taatcttctg ggtagatcc aaaagaagcc gcctgctcca tagcgattac 1020
 atgaatatga ctccacgccg ccctggcccc acaaggaaac actaccagcc ttacgcacca 1080
 cctagagatt tcgctgccta tcggagccgc ttttccgtcg ttaagcgggg gagaaaaaag 1140
 ctgctgtaca ttttcaaaca gccgtttatg aggccgttcc aaacgactca ggaagaggac 1200
 ggctgctcct gccgctttcc tgaggaggag gagggcgggt gcgaactgag ggtgaagttt 1260

tccagatctg cagatgcacc agcgtatcag cagggccaga accaactgta taacgagctc	1320
aacctgggac gcaggggaaga gtatgacgtt ttggacaagc gcagaggacg ggaccctgag	1380
atgggtggca aaccaagacg aaaaaacccc caggagggtc tctataatga gctgcagaag	1440
gataagatgg ctgaagccta ttctgaaata ggcatgaaag gagagcggag aaggggaaaa	1500
gggcacgacg gtttgtacca gggactcagc actgctacga aggatactta tgacgctctc	1560
cacatgcaag ccctgccacc tagggccaag agaagtggca gcggggaggg ccggggatct	1620
ctccttacat gtggggacgt ggaagaaaat ccggggccta tgggtgccgg cgccacggga	1680
agggctatgg atggcccgcg actgcttctc ctgctgttgt tgggcgtgtc tctcggaggc	1740
gctaaggagg cctgtccaac gggcctctac actcactccg gtgaatgttg caaagcctgt	1800
aaccttggcg agggcgtcgc acaaccttgt ggtgctaacc agacagtctg tgaaccatgc	1860
ctggattcag tgacattcag cgatgttgtc tcagccaccg agccttgcaa gccttgtacc	1920
gaatgtgtgg gccttcagtc catgtccgcc ccctgtgtcg aagccgatga tgcagtgtgc	1980
agatgtgcct atggatatta ccaggacgaa actaccgggc ggtgtgaggc ctgccgggtg	2040
tgtgaagccg gctctggcct cgtgttcagt tgccaggata agcaaaacac agtatgtgag	2100
gagtgtccag acggaaccta cagcgacgag gcgaaccacg tcgacccttg cttgccgtgc	2160
accgtctgcg aggataccga acgccagctg agagagtgtg cgcgctgggc agacgctgag	2220
tgcgaggaga tccctgggag atggatcacc cggagcacac ctctgaggg atcagacagt	2280
acagccccga gtaccaaga accggaggcc cctccagagc aggacctgat cgcttctaca	2340
gttgctggcg tggtgacgac agtcatggga tcctcacaac cagtcgtgac gcggggcaca	2400
accgacaatc tgattcctgt ctactgtagc atcttggcag ccgtggtcgt gggcctggta	2460
gcctacatcg cctttaagag atgacctagg taa	2493

<210> 28

<211> 827

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 28

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Lys Lys Pro Gly Ala Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Gln Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Trp Met Asn Thr Tyr Thr Gly Glu Pro Thr
65 70 75 80

Tyr Ala Asp Lys Phe Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser
85 90 95

Ala Arg Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Phe Cys Ala Arg Ala Gly Gly Gln Leu Arg Pro Gly Ala
115 120 125

Met Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145 150 155 160

Leu Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala
165 170 175

Ser Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser
180 185 190

Phe Met Asn Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro Gln Leu Leu
195 200 205

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

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

Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Ser Asn Glu Glu Pro
245 250 255

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Leu
260 265 270

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

Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val
290 295 300

Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
305 310 315 320

Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu
325 330 335

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
340 345 350

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
355 360 365

Ser Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
370 375 380

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
385 390 395 400

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
405 410 415

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
420 425 430

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
435 440 445

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
450 455 460

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
465 470 475 480

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
485 490 495

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
500 505 510

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
515 520 525

Ala Lys Arg Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys
530 535 540

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly
545 550 555 560

Arg Ala Met Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu Leu Gly Val
565 570 575

Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His
580 585 590

Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln
595 600 605

Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val
610 615 620

Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr
625 630 635 640

Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp
645 650 655

Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr
660 665 670

Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val
675 680 685

Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp
690 695 700

Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys
705 710 715 720

Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp
725 730 735

Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser
740 745 750

Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro
755 760 765

Glu Ala Pro Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val
770 775 780

Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr
785 790 795 800

Thr Asp Asn Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val
805 810 815

Val Gly Leu Val Ala Tyr Ile Ala Phe Lys Arg
820 825

<210> 29

<211> 2352

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 29

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atcagctgca aggccagcgg ctacacattc accaactacg gcatgaactg ggtgcaacag	180
gccccggcc agggactgga gtggatgggc tggatgaaca catacaccgg cgagcccacc	240
tacgccgaca agttccaggg cagggtgaca ttcacactcg ataccagcgc cagaaccgtg	300
tatatggaac tgagcagcct gaggagcgag gacaccgctg tgtacttctg cgcaagggct	360
ggaggccagc tgagacctgg cgctatggac tactggggcc agggcaccat ggtgaccgtg	420
agctccggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgacatcgtg	480
ctgaccaga cacctctctc cctgtccgtg acccccggac agcctgcctc catttcctgt	540
aaggcctccc agagcgtgga ctatgacggc gacagcttca tgaactggta cctgcagaag	600
cccggacaac cccccagct gctgatctac gtggccagca acctggagtc cggcgtgcct	660
gacaggtttt ccggctccgg cagcggcacc gacttcaccc tgaagatcag cagggtggaa	720
gccgaggacg tgggcgtgta ctactgccag cagagcaacg aggagcccc taccttcgga	780
cagggcacca agctggagat caaggccgct gcccttgata atgaaaagtc aaacggaaca	840
atcattcacg tgaagggcaa gcacctctgt ccgtcacctt tgttccctgg tccatccaag	900
ccattctggg tgttggctgt agtgggtgga gtcctcgctt gttactctct gctcgtcacc	960
gtggctttta taatcttctg ggtagatcc aaaagaagcc gcctgctcca tagcgattac	1020
atgaatatga ctccacgccg ccctggcccc acaaggaaac actaccagcc ttacgcacca	1080
cctagagatt tcgctgccta tcggagcagg gtgaagtttt ccagatctgc agatgcacca	1140
gcgtatcagc agggccagaa ccaactgtat aacgagctca acctgggacg cagggaagag	1200
tatgacgttt tggacaagcg cagaggacgg gaccctgaga tgggtggcaa accaagacga	1260
aaaaaccccc aggaggtct ctataatgag ctgcagaagg ataagatggc tgaagcctat	1320
tctgaaatag gcatgaaagg agagcggaga aggggaaaag ggcacgacgg tttgtaccag	1380
ggactcagca ctgctacgaa ggatacttat gacgctctcc acatgcaagc cctgccacct	1440
aggccaaga gaagtggcag cggggagggc cggggatctc tccttacatg tggggacgtg	1500
gaagaaaatc cggggcctat gggtgccggc gccacgggaa gggctatgga tggcccgca	1560

ctgcttctcc tgctgttggt gggcgtgtct ctcgaggcg ctaaggaggc ctgtccaacg	1620
ggcctctaca ctactccgg tgaatgttgc aaagcctgta accttggcga gggcgtcgca	1680
caaccttggtg gtgctaacca gacagtctgt gaaccatgcc tggattcagt gacattcagc	1740
gatgttgtct cagccaccga gccttgcaag ccttgtaccg aatgtgtggg ccttcagtcc	1800
atgtccgccc cctgtgtcga agccgatgat gcagtgtgca gatgtgccta tggatattac	1860
caggacgaaa ctaccgggcg gtgtgaggcc tgccgggtgt gtgaagccgg ctctggcctc	1920
gtgttcagtt gccaggataa gcaaaacaca gtatgtgagg agtgtccaga cggaacctac	1980
agcgacgagg cgaaccacgt cgacccttgc ttgccgtgca ccgtctgcga ggataccgaa	2040
cgccagctga gagagtgtac gcgctgggca gacgtgagt gcgaggagat ccctgggaga	2100
tggatcaccg ggagcacacc tcctgaggga tcagacagta cagccccgag tacccaagaa	2160
ccggaggccc ctccagagca ggacctgac gcttctacag ttgttggcgt ggtgacgaca	2220
gtcatgggat cctcacaacc agtcgtgacg cggggcacia cgcacaatct gattcctgtc	2280
tactgtagca tcttggcagc cgtggtcgtg ggcctggtag cctacatcgc cttaagaga	2340
tgacctaggt aa	2352

<210> 30

<211> 780

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 30

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1			5				10					15			

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

Lys	Lys	Pro	Gly	Ala	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
		35					40					45			

Thr	Phe	Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Gln	Gln	Ala	Pro	Gly	Gln
	50					55				60					

Gly Leu Glu Trp Met Gly Trp Met Asn Thr Tyr Thr Gly Glu Pro Thr
65 70 75 80

Tyr Ala Asp Lys Phe Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser
85 90 95

Ala Arg Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Phe Cys Ala Arg Ala Gly Gly Gln Leu Arg Pro Gly Ala
115 120 125

Met Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145 150 155 160

Leu Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala
165 170 175

Ser Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser
180 185 190

Phe Met Asn Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro Gln Leu Leu
195 200 205

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

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

Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Ser Asn Glu Glu Pro
245 250 255

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Leu
260 265 270

Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His

275

280

285

Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val
 290 295 300

Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
 305 310 315 320

Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu
 325 330 335

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
 340 345 350

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
 355 360 365

Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
 370 375 380

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 385 390 395 400

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
 405 410 415

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
 420 425 430

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
 435 440 445

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
 450 455 460

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
 465 470 475 480

Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
 485 490 495

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr
500 505 510

Gly Arg Ala Met Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly
515 520 525

Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr
530 535 540

His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala
545 550 555 560

Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser
565 570 575

Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys
580 585 590

Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala
595 600 605

Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr
610 615 620

Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu
625 630 635 640

Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro
645 650 655

Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro
660 665 670

Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg
675 680 685

Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg
690 695 700

Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu

705		710		715		720									
Pro	Glu	Ala	Pro	Pro	Glu	Gln	Asp	Leu	Ile	Ala	Ser	Thr	Val	Ala	Gly
			725						730					735	
Val	Val	Thr	Thr	Val	Met	Gly	Ser	Ser	Gln	Pro	Val	Val	Thr	Arg	Gly
		740					745						750		
Thr	Thr	Asp	Asn	Leu	Ile	Pro	Val	Tyr	Cys	Ser	Ile	Leu	Ala	Ala	Val
		755					760					765			
Val	Val	Gly	Leu	Val	Ala	Tyr	Ile	Ala	Phe	Lys	Arg				
	770					775					780				

<210> 31
 <211> 2370
 <212> ADN
 <213> Secuencia artificial

<220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 31	
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ccggagattc agctggtgca gagcggcgcc gaggtgaaaa agcccggagc caccgtgaag	120
atcagctgca aggccagcgg ctacacattc accaactacg gcatgaactg ggtgcaacag	180
gccccggcc agggactgga gtggatgggc tggatgaaca catacaccgg cgagcccacc	240
tacgccgaca agttccaggg cagggtgaca ttcacactcg ataccagcgc cagaaccgtg	300
tatatggaac tgagcagcct gaggagcgag gacaccgctg tgtacttctg cgcaagggtc	360
ggaggccagc tgagacctgg cgctatggac tactggggcc agggcaccat ggtgaccgtg	420
agctccggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgacatcgtg	480
ctgaccaga cacctctctc cctgtccgtg acccccggac agcctgcctc catttcctgt	540
aaggcctccc agagcgtgga ctatgacggc gacagcttca tgaactggta cctgcagaag	600
cccggacaac cccccagct gctgatctac gtggccagca acctggagtc cggcgtgcct	660
gacaggtttt ccggctccgg cagcggcacc gacttcaccc tgaagatcag cagggtggaa	720
gccgaggacg tgggcgtgta ctactgccag cagagcaacg aggagcccc taccttcgga	780

cagggcacca agctggagat caaggccgct gcccttgata atgaaaagtc aaacggaaca	840
atcattcacg tgaagggcaa gcacctctgt ccgtcacctt tgttccctgg tccatccaag	900
ccattctggg tgttggtcgt agtgggtgga gtcctcgctt gttactctct gctcgtcacc	960
gtggctttta taatcttctg ggttcgcttt tccgtcgtta agcgggggag aaaaaagctg	1020
ctgtacattt tcaaacagcc gtttatgagg ccggtccaaa cgactcagga agaggacggc	1080
tgctcctgcc gctttcctga ggaggaggag ggcgggtgcg aactgagggt gaagttttcc	1140
agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac	1200
ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg	1260
ggtggcaaac caagacgaaa aaacccccag gagggctctt ataatgagct gcagaaggat	1320
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gctatggatg gcccgcgact gcttctcctg ctgttggttg gcgtgtctct cggaggcgct	1620
aaggaggcct gtccaacggg cctctacact cactccggtg aatgttgcaa agcctgtaac	1680
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gattcagtga cattcagcga tgttgtctca gccaccgagc cttgcaagcc ttgtaccgaa	1800
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gtctgcgagg ataccgaacg ccagctgaga gagtgtacgc gctgggcaga cgctgagtgc	2100
gaggagatcc ctgggagatg gatcaccgag agcacacctc ctgagggatc agacagtaca	2160
gccccgagta cccaagaacc ggaggcccct ccagagcagg acctgatcgc ttctacagtt	2220
gctggcgtgg tgacgacagt catgggatcc tcacaaccag tcgtgacgcg gggcacaacc	2280
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<210> 32
 <211> 786
 <212> PRT
 <213> Secuencia artificial

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 32
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His Ala Ala Arg Pro Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Pro Gly Ala Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Gln Gln Ala Pro Gly Gln
 50 55 60

Gly Leu Glu Trp Met Gly Trp Met Asn Thr Tyr Thr Gly Glu Pro Thr
 65 70 75 80

Tyr Ala Asp Lys Phe Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser
 85 90 95

Ala Arg Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 100 105 110

Ala Val Tyr Phe Cys Ala Arg Ala Gly Gly Gln Leu Arg Pro Gly Ala
 115 120 125

Met Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
 130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
 145 150 155 160

Leu Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala
 165 170 175

Ser Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser
180 185 190

Phe Met Asn Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro Gln Leu Leu
195 200 205

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

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

Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Ser Asn Glu Glu Pro
245 250 255

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Leu
260 265 270

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

Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val
290 295 300

Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
305 310 315 320

Val Ala Phe Ile Ile Phe Trp Val Arg Phe Ser Val Val Lys Arg Gly
325 330 335

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
340 345 350

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
355 360 365

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
370 375 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385 390 395 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
405 410 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
420 425 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

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

Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly
485 490 495

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

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
515 520 525

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
530 535 540

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
545 550 555 560

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
565 570 575

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
580 585 590

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
595 600 605

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
610 615 620

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
625 630 635 640

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
645 650 655

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
660 665 670

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
675 680 685

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
690 695 700

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
705 710 715 720

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
725 730 735

Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln
740 745 750

Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys
755 760 765

Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe
770 775 780

Lys Arg
785

<210> 33

<211> 2430

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 33

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atcagctgca aggccagcgg ctacacattc accaactacg gcatgaactg ggtgcaacag	180
gccccgggcc agggactgga gtggatgggc tggatgaaca catacaccgg cgagcccacc	240
tacgccgaca agttccaggg cagggtgaca ttcacactcg ataccagcgc cagaaccgtg	300
tatatggaac tgagcagcct gaggagcgag gacaccgctg tgtacttctg cgcaagggtc	360
ggaggccagc tgagacctgg cgctatggac tactggggcc agggcaccat ggtgaccgtg	420
agctccggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgacatcgtg	480
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aaggcctccc agagcgtgga ctatgacggc gacagcttca tgaactggta cctgcagaag	600
cccggacaac cccccagct gctgatctac gtggccagca acctggagtc cggcgtgcct	660
gacaggtttt ccggctccgg cagcggcacc gacttcaccc tgaagatcag cagggtggaa	720
gccgaggacg tgggcgtgta ctactgccag cagagcaacg aggagcccc taccttcgga	780
cagggcacca agctggagat caaggccgct gccttcgtgc ctgtttttct gcccgcgaaa	840
cccacaacta cccccgccc tcggcccca actcctgcac caactatcgc ttccaaccc	900
ctgtctctga gacctgaggc atgccgcccc gcggcaggcg gcgccgtgca cactagaggc	960
ctggacttcg cctgcgatat ttatatctgg gcccccttg ccgggacatg cggggtactg	1020
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ctgtccata gcgattacat gaatatgact ccacgccgcc ctggccccac aaggaaacac	1140
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atgcaagccc tgccacctag ggccaagaga agtggcagcg gggagggccg gggatctctc	1560
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tgtgcctatg gatattacca ggacgaaact accgggcggt gtgaggcctg ccgggtgtgt	1980
gaagccggct ctggcctcgt gttcagttgc caggataagc aaaacacagt atgtgaggag	2040
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gaggagatcc ctgggagatg gatcaccgag agcacacctc ctgagggatc agacagtaca	2220
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gctggcgtgg tgacgacagt catgggatcc tcacaaccag tcgtgacgcg gggcacaacc	2340
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tacatcgctt ttaagagatg acctaggtaa	2430

<210> 34

<211> 806

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 34

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

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

Lys	Lys	Pro	Gly	Ala	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Gln Gln Ala Pro Gly Gln
 50 55 60

Gly Leu Glu Trp Met Gly Trp Met Asn Thr Tyr Thr Gly Glu Pro Thr
 65 70 75 80

Tyr Ala Asp Lys Phe Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser
 85 90 95

Ala Arg Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 100 105 110

Ala Val Tyr Phe Cys Ala Arg Ala Gly Gly Gln Leu Arg Pro Gly Ala
 115 120 125

Met Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
 130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
 145 150 155 160

Leu Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala
 165 170 175

Ser Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser
 180 185 190

Phe Met Asn Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro Gln Leu Leu
 195 200 205

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

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

Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Ser Asn Glu Glu Pro
 245 250 255

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Phe
260 265 270

Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
275 280 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
290 295 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305 310 315 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
325 330 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
340 345 350

Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
355 360 365

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
370 375 380

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser
385 390 395 400

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
405 410 415

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
420 425 430

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
435 440 445

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
450 455 460

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly

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

Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp
690 695 700

Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys
705 710 715 720

Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly
725 730 735

Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu
740 745 750

Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met
755 760 765

Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile
770 775 780

Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala
785 790 795 800

Tyr Ile Ala Phe Lys Arg
805

<210> 35

<211> 2448

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

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atcagctgca aggccagcgg ctacacattc accaactacg gcatgaactg ggtgcaacag 180

gccccgggcc agggactgga gtggatgggc tggatgaaca catacaccgg cgagcccacc 240

tacgccgaca agttccaggg cagggtgaca ttcacactcg ataccagcgc cagaaccgtg 300

tatatggaac tgagcagcct gaggagcgag gacaccgctg tgtacttctg cgcaagggct 360

ggaggccagc tgagacctgg cgctatggac tactggggcc agggcaccat ggtgaccgtg	420
agctccggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgacatcgtg	480
ctgaccaga cacctctctc cctgtccgtg acccccggac agcctgcctc catttcctgt	540
aaggcctccc agagcgtgga ctatgacggc gacagcttca tgaactggta cctgcagaag	600
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gccgaggacg tgggcgtgta ctactgccag cagagcaacg aggagcccc taccttcgga	780
cagggcacca agctggagat caaggccgct gccttcgtgc ctgtttttct gcccgcgaaa	840
cccacaacta cccccgccc tcggcccca actcctgcac caactatcgc ttcccaaccc	900
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ctggacttcg cctgcgatat ttatatctgg gcccccttg ccgggacatg cggggtactg	1020
ctgctgtctc tggtgattac cctctactgc aaccacagaa accgcttttc cgtcgttaag	1080
cgggggagaa aaaagctgct gtacattttc aaacagccgt ttatgaggcc ggtccaaacg	1140
actcaggaag aggacggctg ctctgccgc tttcctgagg aggaggaggg cgggtgcgaa	1200
ctgagggtga agttttccag atctgcagat gcaccagcgt atcagcaggg ccagaaccaa	1260
ctgtataacg agctcaacct gggacgcagg gaagagtatg acgttttgga caagcgaga	1320
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aatgagctgc agaaggataa gatggctgaa gcctattctg aaataggcat gaaaggagag	1440
cggagaaggg gaaaagggca cgacggtttg taccagggac tcagcactgc tacgaaggat	1500
acttatgacg ctctccacat gcaagccctg ccacctaggg ccaagagaag tggcagcggg	1560
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gccggcgcca cgggaagggc tatggatggc ccgcgactgc ttctcctgct gttgttgggc	1680
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gtctgtgaac catgcctgga ttcagtgaca ttcagcgatg ttgtctcagc caccgagcct	1860
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gatgatgcag tgtgcagatg tgcctatgga tattaccagg acgaaactac cgggcggtgt	1980

gaggcctgcc ggggtgtgtga agccggctct ggcctcgtgt tcagttgcca ggataagcaa	2040
aacacagtat gtgaggagtg tccagacgga acctacagcg acgaggcgaa ccacgtcgac	2100
ccttgcttgc cgtgcaccgt ctgcgaggat accgaacgcc agctgagaga gtgtacgcgc	2160
tgggcagacg ctgagtgcga ggagatccct gggagatgga tcacccggag cacacctcct	2220
gagggatcag acagtacagc cccgagtacc caagaaccgg agggccctcc agagcaggac	2280
ctgatcgctt ctacagttgc tggcgtgggtg acgacagtca tgggatcctc acaaccagtc	2340
gtgacgcggg gcacaaccga caatctgatt cctgtctact gtagcatctt ggcagccgtg	2400
gtcgtgggcc tggtagccta catcgccttt aagagatgac ctaggtaa	2448

<210> 36

<211> 812

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 36

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

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

Lys	Lys	Pro	Gly	Ala	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
		35					40					45			

Thr	Phe	Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Gln	Gln	Ala	Pro	Gly	Gln
	50					55					60				

Gly	Leu	Glu	Trp	Met	Gly	Trp	Met	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr
65					70					75				80	

Tyr	Ala	Asp	Lys	Phe	Gln	Gly	Arg	Val	Thr	Phe	Thr	Leu	Asp	Thr	Ser
			85						90					95	

Ala	Arg	Thr	Val	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr
			100					105					110		

Ala Val Tyr Phe Cys Ala Arg Ala Gly Gly Gln Leu Arg Pro Gly Ala
115 120 125

Met Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145 150 155 160

Leu Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala
165 170 175

Ser Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser
180 185 190

Phe Met Asn Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro Gln Leu Leu
195 200 205

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

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

Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Ser Asn Glu Glu Pro
245 250 255

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Phe
260 265 270

Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
275 280 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
290 295 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305 310 315 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
325 330 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
340 345 350

Arg Asn Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr
355 360 365

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
370 375 380

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
385 390 395 400

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
405 410 415

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
420 425 430

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
435 440 445

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
450 455 460

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
465 470 475 480

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
485 490 495

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
500 505 510

Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
515 520 525

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr
530 535 540

Gly Arg Ala Met Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly
545 550 555 560

Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr
565 570 575

His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala
580 585 590

Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser
595 600 605

Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys
610 615 620

Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala
625 630 635 640

Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr
645 650 655

Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu
660 665 670

Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro
675 680 685

Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro
690 695 700

Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg
705 710 715 720

Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg
725 730 735

Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu
740 745 750

Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly
755 760 765

Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly
770 775 780

Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val
785 790 795 800

Val Val Gly Leu Val Ala Tyr Ile Ala Phe Lys Arg
805 810

<210> 37

<211> 2481

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 37

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ccgcaggtgc agctggtgca gtccggcgcc gaagtgaaga agcccggagc cagcgtgaag	120
gtgagctgca aggcctccgg ctacaccttc accacctact ggatgcactg ggtcagacag	180
gctcccggac agggcctgga atggatgggc gaaatcaacc cctcctccgg caggaccaac	240
tacaacgaga agttcaagac cagggtgacc atgaccaggg acaccagcac cagcaccgtg	300
tacatggagc tgtccagcct gaggagcgag gacaccgccg tgtactactg tgccaagctg	360
ggacccggcc cccagtacta tgccatggac tactggggcc aaggcaccat ggtgaccgtg	420
agcagcggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgacatccag	480
atgaccaga gccctccag cctgtccgct agcgtgggcg acagggtcac cattacctgc	540
cacgccagcc agaacatcaa cgtgtggctg agctgggtatc agcagaaacc cggcaaggct	600
cccaagctgc tgatctacaa ggccagcaag ctgcacaccg gcgtgcccag caggttttagc	660
ggttctggct ccggcaccga cttcacctc accatcagca gcctgcagcc cgaagacttc	720
gctacctact actgccagca gggacaaagc taccctgga ccttcggcca gggaaccaag	780
ctggaaatca aggccgtgc cttgataat gaaaagtcaa acggaacaat cattcacgtg	840

aagggaagc acctctgtcc gtcacccttg ttccctggtc catccaagcc attctgggtg	900
ttggtcgtag tgggtggagt cctcgcttgt tactctctgc tcgtcaccgt ggcttttata	960
atcttctggg ttagatccaa aagaagccgc ctgctccata gcgattacat gaatatgact	1020
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gctgcctatc ggagccgctt ttccgtcgtt aagcggggga gaaaaaagct gctgtacatt	1140
ttcaaacagc cgtttatgag gccgggtccaa acgactcagg aagaggacgg ctgctcctgc	1200
cgctttcctg aggaggagga gggcgggtgc gaactgaggg tgaagttttc cagatctgca	1260
gatgcaccag cgtatcagca gggccagaac caactgtata acgagctcaa cctgggacgc	1320
aggggaagagt atgacgtttt ggacaagcgc agaggacggg accctgagat ggggtggcaaa	1380
ccaagacgaa aaaaccccc aagggggtctc tataatgagc tgcagaagga taagatggct	1440
gaagcctatt ctgaaatagg catgaaagga gagcggagaa ggggaaaagg gcacgacggt	1500
ttgtaccagg gactcagcac tgctacgaag gatacttatg acgctctcca catgcaagcc	1560
ctgccaccta gggccaagag aagtggcagc ggggagggcc ggggatctct cttacatgt	1620
ggggacgtgg aagaaaatcc ggggcctatg ggtgccggcg ccacgggaag ggctatggat	1680
ggcccgcgac tgcttctcct gctgttgttg ggcgtgtctc tcggaggcgc taaggaggcc	1740
tgtccaacgg gcctctacac tcactccggt gaatgttgca aagcctgtaa ccttggcgag	1800
ggcgtcgcac aaccttgttg tgctaaccag acagtctgtg aaccatgcct ggattcagtg	1860
acattcagcg atgttgtctc agccaccgag ctttgcaagc cttgtaccga atgtgtgggc	1920
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ggatattacc aggacgaaac taccgggcgg tgtgaggcct gccgggtgtg tgaagccggc	2040
tctggcctcg tgttcagttg ccaggataag caaaacacag tatgtgagga gtgtccagac	2100
ggaacctaca gcgacgaggc gaaccacgtc gacccttgct tgccgtgcac cgtctgcgag	2160
gataccgaac gccagctgag agagtgtacg cgctgggcag acgctgagtg cgaggagatc	2220
cctgggagat ggatcaccgc gagcacacct cctgagggat cagacagtac agccccgagt	2280
acccaagaac cggaggcccc tccagagcag gacctgatcg cttctacagt tgctggcgtg	2340
gtgacgacag tcatgggatc ctcaacaacca gtcgtgacgc ggggcacaac cgacaatctg	2400
attcctgtct actgtagcat cttggcagcc gtggctcgtg gcctggtagc ctacatcgcc	2460

tttaagagat gacctaggta a

2481

<210> 38

<211> 823

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 38

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Thr Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Glu Ile Asn Pro Ser Ser Gly Arg Thr Asn
65 70 75 80

Tyr Asn Glu Lys Phe Lys Thr Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Lys Leu Gly Pro Gly Pro Gln Tyr Tyr Ala
115 120 125

Met Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
145 150 155 160

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val

165

170

175

Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser Trp
 180 185 190

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala
 195 200 205

Ser Lys Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
 210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
 225 230 235 240

Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Trp Thr Phe Gly
 245 250 255

Gln Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Leu Asp Asn Glu Lys
 260 265 270

Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser
 275 280 285

Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
 290 295 300

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
 305 310 315 320

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
 325 330 335

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
 340 345 350

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Phe Ser
 355 360 365

Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
 370 375 380

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
385 390 395 400

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
405 410 415

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
420 425 430

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
435 440 445

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
450 455 460

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
465 470 475 480

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
485 490 495

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
500 505 510

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser
515 520 525

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
530 535 540

Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp
545 550 555 560

Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly
565 570 575

Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys
580 585 590

Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala

595

600

605

Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp
 610 615 620

Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly
 625 630 635 640

Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys
 645 650 655

Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
 660 665 670

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
 675 680 685

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
 690 695 700

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
 705 710 715 720

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
 725 730 735

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
 740 745 750

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
 755 760 765

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
 770 775 780

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu
 785 790 795 800

Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val
 805 810 815

Ala Tyr Ile Ala Phe Lys Arg
820

<210> 39

<211> 2340

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 39

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gtgagctgca aggcctccgg ctacaccttc accacctact ggatgcactg ggtcagacag	180
gctcccggac agggcctgga atggatgggc gaaatcaacc cctcctccgg caggaccaac	240
tacaacgaga agttcaagac cagggtgacc atgaccaggg acaccagcac cagcaccgtg	300
tacatggagc tgtccagcct gaggagcgag gacaccgccg tgtactactg tgccaagctg	360
ggacccggcc cccagtacta tgccatggac tactggggcc aaggcaccat ggtgaccgtg	420
agcagcggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgacatccag	480
atgaccaga gccctccag cctgtccgct agcgtggggc acagggtcac cattacctgc	540
cacgccagcc agaacatcaa cgtgtggctg agctggtatc agcagaaacc cggcaaggct	600
ccaagctgc tgatctacaa ggccagcaag ctgcacaccg gcgtgcccag caggtttagc	660
ggttctggct ccggcaccga cttcacctc accatcagca gcctgcagcc cgaagacttc	720
gctacctact actgccagca gggacaaagc tacccttgga ccttcggcca gggaaccaag	780
ctggaaatca aggccgctgc cttgataat gaaaagtcaa acggaacaat cattcacgtg	840
aagggaagc acctctgtcc gtcacccttg ttccctgggtc catccaagcc attctgggtg	900
ttggtcgtag tgggtggagt cctcgcttgt tactctctgc tcgtcaccgt ggcttttata	960
atcttctggg ttagatccaa aagaagccgc ctgctccata gcgattacat gaatatgact	1020
ccacgccgcc ctggccccac aaggaaacac taccagcctt acgcaccacc tagagatttc	1080
gctgcctatc ggagcagggt gaagttttcc agatctgcag atgcaccagc gtatcagcag	1140
ggccagaacc aactgtataa cgagctcaac ctgggacgca gggaagagta tgacgttttg	1200

gacaagcgca gaggacggga ccctgagatg ggtggcaaac caagacgaaa aaacccccag	1260
gaggggtctct ataatgagct gcagaaggat aagatggctg aagcctattc tgaaataggc	1320
atgaaaggag agcggagaag gggaaaaggg cacgacgggt tgtaccaggg actcagcact	1380
gctacgaagg atacttatga cgctctccac atgcaagccc tgccacctag ggccaagaga	1440
agtggcagcg gggagggccg gggatctctc cttacatgtg gggacgtgga agaaaatccg	1500
gggcctatgg gtgccggcgc cacgggaagg gctatggatg gcccgcgact gcttctcctg	1560
ctgttggttg gcgtgtctct cggaggcgct aaggaggcct gtccaacggg cctctacact	1620
cactccggtg aatgttgcaa agcctgtaac cttggcgagg gcgtcgaca accttggtgt	1680
gctaaccaga cagtctgtga accatgcctg gattcagtga cattcagcga tgttgtctca	1740
gccaccgagc cttgcaagcc ttgtaccgaa tgtgtgggcc ttcagtccat gtccgcccc	1800
tgtgtcgaag ccgatgatgc agtgtgcaga tgtgcctatg gatattacca ggacgaaact	1860
accgggcggt gtgaggcctg ccgggtgtgt gaagccggct ctggcctcgt gttcagttgc	1920
caggataagc aaaacacagt atgtgaggag tgtccagacg gaacctacag cgacgaggcg	1980
aaccacgtcg acccttgctt gccgtgcacc gtctgcgagg ataccgaacg ccagctgaga	2040
gagtgtacgc gctgggcaga cgctgagtgc gaggagatcc ctgggagatg gatcaccggg	2100
agcacacctc ctgagggatc agacagtaca gccccgagta cccaagaacc ggaggcccct	2160
ccagagcagg acctgatcgc ttctacagtt gctggcgtgg tgacgacagt catgggatcc	2220
tcacaaccag tcgtgacgcg gggcacaacc gacaatctga ttcctgtcta ctgtagcatc	2280
ttggcagccg tggtcgtggg cctggtagcc tacatgcct ttaagagatg acctaggtaa	2340

<210> 40

<211> 776

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 40

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

1

5

10

15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Thr Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Glu Ile Asn Pro Ser Ser Gly Arg Thr Asn
65 70 75 80

Tyr Asn Glu Lys Phe Lys Thr Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Lys Leu Gly Pro Gly Pro Gln Tyr Tyr Ala
115 120 125

Met Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln
145 150 155 160

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

Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala
195 200 205

Ser Lys Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
225 230 235 240

Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Trp Thr Phe Gly
245 250 255

Gln Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Leu Asp Asn Glu Lys
260 265 270

Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser
275 280 285

Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
290 295 300

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
305 310 315 320

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
325 330 335

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
340 345 350

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
355 360 365

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
370 375 380

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
385 390 395 400

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
405 410 415

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
420 425 430

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
435 440 445

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
450 455 460

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg
465 470 475 480

Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
485 490 495

Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met
500 505 510

Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly
515 520 525

Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu
530 535 540

Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly
545 550 555 560

Ala Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser
565 570 575

Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val
580 585 590

Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val
595 600 605

Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys
610 615 620

Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys
625 630 635 640

Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr
645 650 655

Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys
660 665 670

Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala
675 680 685

Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro
690 695 700

Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro
705 710 715 720

Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr
725 730 735

Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
740 745 750

Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu
755 760 765

Val Ala Tyr Ile Ala Phe Lys Arg
770 775

<210> 41

<211> 2358

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 41

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gtgagctgca aggcctccgg ctacaccttc accacctact ggatgcactg ggtcagacag 180

gctcccggac agggcctgga atggatgggc gaaatcaacc cctcctccgg caggaccaac 240

tacaacgaga agttcaagac cagggtgacc atgaccaggg acaccagcac cagcaccgtg 300

tacatggagc tgtccagcct gaggagcgag gacaccgccg tgtactactg tgccaagctg 360

ggacccggcc cccagtacta tgccatggac tactggggcc aaggcaccat ggtgaccgtg 420

agcagcggag gcgaggatc tgggtggcgg	ggttctggcg gcggaggctc cgacatccag	480
atgaccaga gccctccag cctgtccgct	agcgtgggcg acagggtcac cattacctgc	540
cacgccagcc agaacatcaa cgtgtggctg	agctgggtatc agcagaaacc cggcaaggct	600
ccaagctgc tgatctacaa ggccagcaag	ctgcacaccg gcgtgcccag caggttttagc	660
ggttctggct ccggcaccga cttcacctc	accatcagca gcctgcagcc cgaagacttc	720
gctacctact actgccagca gggacaaagc	tacccttgga cttcggcca gggaaccaag	780
ctggaaatca aggccgctgc cttgataat	gaaaagtcaa acggaacaat cattcacgtg	840
aagggaagc acctctgtcc gtcacccttg	ttccctggtc catccaagcc attctgggtg	900
ttggtcgtag tgggtggagt cctcgcttgt	tactctctgc tcgtcaccgt ggcttttata	960
atcttctggg ttcgcttttc cgtcgtttaag	cgggggagaa aaaagctgct gtacattttc	1020
aaacagccgt ttatgaggcc ggtccaaacg	actcaggaag aggacggctg ctcctgccgc	1080
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gcaccagcgt atcagcaggg ccagaaccaa	ctgtataacg agctcaacct gggacgcagg	1200
gaagagtatg acgttttgga caagcgcaga	ggacgggacc ctgagatggg tggcaaacca	1260
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taccagggac tcagcactgc tacgaaggat	acttatgacg ctctccacat gcaagccctg	1440
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gacgtggaag aaaatccggg gcctatgggt	gccggcgcca cgggaagggc tatggatggc	1560
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tattaccagg acgaaactac cgggcggtgt	gaggcctgcc ggggtgtgtga agccggctct	1920
ggcctcgtgt tcagttgcca ggataagcaa	aacacagtat gtgaggagtg tccagacgga	1980
acctacagcg acgaggcgaa ccacgtcgac	ccttgcttgc cgtgcaccgt ctgcaggat	2040

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accgaacgcc agctgagaga gtgtacgcgc tgggcagacg ctgagtgcga ggagatccct      2100
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caagaaccgg aggcccctcc agagcaggac ctgatcgctt ctacagttgc tggcgtgggtg      2220
acgacagtca tgggatactc acaaccagtc gtgacgcggg gcacaaccga caatctgatt      2280
cctgtctact gtagcatctt ggcagccgtg gtcgtggggc tggtagccta catcgccttt      2340
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<210> 42

<211> 782

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 42

```

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1           5           10           15

```

```

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
          20           25           30

```

```

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35           40           45

```

```

Thr Phe Thr Thr Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln
50           55           60

```

```

Gly Leu Glu Trp Met Gly Glu Ile Asn Pro Ser Ser Gly Arg Thr Asn
65           70           75           80

```

```

Tyr Asn Glu Lys Phe Lys Thr Arg Val Thr Met Thr Arg Asp Thr Ser
85           90           95

```

```

Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100          105          110

```

```

Ala Val Tyr Tyr Cys Ala Lys Leu Gly Pro Gly Pro Gln Tyr Tyr Ala
115          120          125

```

Met Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
145 150 155 160

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

Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala
195 200 205

Ser Lys Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
225 230 235 240

Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Trp Thr Phe Gly
245 250 255

Gln Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Leu Asp Asn Glu Lys
260 265 270

Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser
275 280 285

Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
290 295 300

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
305 310 315 320

Ile Phe Trp Val Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu
325 330 335

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln

340

345

350

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
 355 360 365

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
 370 375 380

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
 385 390 395 400

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
 405 410 415

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
 420 425 430

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
 435 440 445

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
 450 455 460

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
 465 470 475 480

Pro Pro Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu
 485 490 495

Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ala Gly
 500 505 510

Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu
 515 520 525

Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu
 530 535 540

Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly
 545 550 555 560

Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu
565 570 575

Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys
580 585 590

Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val
595 600 605

Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp
610 615 620

Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser
625 630 635 640

Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu
645 650 655

Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys
660 665 670

Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys
675 680 685

Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile
690 695 700

Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr
705 710 715 720

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

Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr
740 745 750

Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala
755 760 765

Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe Lys Arg

770

775

780

<210> 43

<211> 2418

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 43

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gtgagctgca aggcctccgg ctacaccttc accacctact ggatgcactg ggtcagacag	180
gctcccggac agggcctgga atggatgggc gaaatcaacc cctcctccgg caggaccaac	240
tacaacgaga agttcaagac cagggtgacc atgaccaggg acaccagcac cagcaccgtg	300
tacatggagc tgtccagcct gaggagcgag gacaccgccg tgtactactg tgccaagctg	360
ggacccggcc cccagtacta tgccatggac tactggggcc aaggcaccat ggtgaccgtg	420
agcagcggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgacatccag	480
atgaccaga gccctccag cctgtccgct agcgtgggcg acagggtcac cattacctgc	540
cacgccagcc agaacatcaa cgtgtggctg agctggatatc agcagaaacc cggcaaggct	600
cccaagctgc tgatctacaa ggccagcaag ctgcacaccg gcgtgcccag caggtttagc	660
ggttctggct ccggcaccga cttcaccttc accatcagca gcctgcagcc cgaagacttc	720
gctacctact actgccagca gggacaaagc taccctgga ctttcggcca gggaaccaag	780
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tgcgatattt atatctgggc cccccttgcc gggacatgcg ggggtactgct gctgtctctg	1020
gtgattacc tctactgcaa ccacagaaac agatccaaaa gaagccgcct gctccatagc	1080
gattacatga atatgactcc acgccgccct ggccccacaa ggaaacacta ccagccttac	1140
gcaccaccta gagatttcgc tgcctatcgg agcagggtga agttttccag atctgcagat	1200
gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg	1260

gaagagtatg acgttttggg caagcgcaga ggacgggacc ctgagatggg tggcaaacca	1320
agacgaaaaa acccccagga gggctctctat aatgagctgc agaaggataa gatggctgaa	1380
gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg	1440
taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg	1500
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accgaacgcc agctgagaga gtgtacgcgc tgggcagacg ctgagtgcga ggagatccct	2160
gggagatgga tcacccggag cacacctcct gagggatcag acagtacagc cccgagtacc	2220
caagaaccgg aggcccctcc agagcaggac ctgatcgctt ctacagttgc tggcgtgggtg	2280
acgacagtca tgggatcctc acaaccagtc gtgacgcggg gcacaaccga caatctgatt	2340
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aagagatgac ctaggtaa	2418

<210> 44

<211> 802

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 44

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

1

5

10

15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Thr Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Glu Ile Asn Pro Ser Ser Gly Arg Thr Asn
65 70 75 80

Tyr Asn Glu Lys Phe Lys Thr Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Lys Leu Gly Pro Gly Pro Gln Tyr Tyr Ala
115 120 125

Met Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln
145 150 155 160

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

Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala
195 200 205

Ser Lys Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
225 230 235 240

Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Trp Thr Phe Gly
245 250 255

Gln Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Phe Val Pro Val Phe
260 265 270

Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
275 280 285

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
290 295 300

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
305 310 315 320

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
325 330 335

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser
340 345 350

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
355 360 365

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
370 375 380

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
385 390 395 400

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
405 410 415

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
420 425 430

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
435 440 445

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
450 455 460

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
465 470 475 480

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
485 490 495

Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly
500 505 510

Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
515 520 525

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
530 535 540

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
545 550 555 560

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
565 570 575

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
580 585 590

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
595 600 605

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
610 615 620

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
625 630 635 640

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
645 650 655

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
660 665 670

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
675 680 685

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
690 695 700

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
705 710 715 720

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
725 730 735

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

Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln
755 760 765

Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys
770 775 780

Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe
785 790 795 800

Lys Arg

<210> 45

<211> 2436

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 45

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ccgcaggtgc agctggtgca gtccggcgcc gaagtgaaga agcccgagc cagcgtgaag 120

gtgagctgca aggcctccgg ctacaccttc accacctact ggatgcactg ggtcagacag	180
gctcccggac agggcctgga atggatgggc gaaatcaacc cctcctccgg caggaccaac	240
tacaacgaga agttcaagac cagggtgacc atgaccaggg acaccagcac cagcaccgtg	300
tacatggagc tgtccagcct gaggagcgag gacaccgccg tgtactactg tgccaagctg	360
ggacccggcc cccagtacta tgccatggac tactggggcc aaggcaccat ggtgaccgtg	420
agcagcggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgacatccag	480
atgaccaga gccctccag cctgtccgct agcgtgggcg acagggtcac cattacctgc	540
cacgccagcc agaacatcaa cgtgtggctg agctgggtatc agcagaaacc cggcaaggct	600
cccaagctgc tgatctacaa ggccagcaag ctgcacaccg gcgtgcccag caggttttagc	660
ggttctggct ccggcaccga cttcacctc accatcagca gcctgcagcc cgaagacttc	720
gctacctact actgccagca gggacaaagc tacccttgga cttcggcca gggaaccaag	780
ctggaaatca aggccgtgc cttcgtgcct gtttttctgc ccgcgaaacc cacaactacc	840
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cctgaggcat gccgccccgc ggcaggcggc gccgtgcaca ctagaggcct ggacttcgcc	960
tgcgatattt atatctgggc ccccttgcc gggacatgcg ggggtactgct gctgtctctg	1020
gtgattacc tctactgcaa ccacagaaac cgcttttccg tcgttaagcg ggggagaaaa	1080
aagctgctgt acattttcaa acagccgttt atgaggccgg tccaaacgac tcaggaagag	1140
gacggctgct cctgccgctt tcctgaggag gaggaggcg ggtgcgaact gaggggtgaag	1200
ttttccagat ctgcagatgc accagcgtat cagcagggcc agaaccaact gtataacgag	1260
ctcaacctgg gacgcaggga agagtatgac gttttggaca agcgcagagg acgggaccct	1320
gagatgggtg gcaaaccaag acgaaaaaac ccccaggagg gtctctataa tgagctgcag	1380
aaggataaga tggctgaagc ctattctgaa ataggcatga aaggagagcg gagaagggga	1440
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ctccacatgc aagccctgcc acctagggcc aagagaagtg gcagcgggga gggccgggga	1560
tctctcctta catgtgggga cgtggaagaa aatccggggc ctatgggtgc cggcgccacg	1620
ggaagggtc tggatggccc gcgactgctt ctctgtgtg tgttgggcgt gtctctcgga	1680
ggcgctaagg aggcctgtcc aacgggcctc tacactcact ccggtgaatg ttgcaaagcc	1740

tgtaaccttg gcgagggcgt cgcacaacct tgtggtgcta accagacagt ctgtgaacca	1800
tgcctggatt cagtgacatt cagcgatggt gtctcagcca ccgagccttg caagccttgt	1860
accgaatgtg tgggccttca gtccatgtcc gccccctgtg tcgaagccga tgatgcagtg	1920
tgcagatgtg cctatggata ttaccaggac gaaactaccg ggcggtgtga ggcctgccgg	1980
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gaggagtgtc cagacggaac ctacagcgac gaggcgaacc acgtcgaccc ttgcttgccg	2100
tgcaccgtct gcgaggatac cgaacgccag ctgagagagt gtacgcgctg ggcagacgct	2160
gagtgcgagg agatccctgg gagatggatc acccgagca cacctcctga gggatcagac	2220
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acagttgctg gcgtggtgac gacagtcatt ggatcctcac aaccagtcgt gacgcggggc	2340
acaaccgaca atctgattcc tgtctactgt agcatcttgg cagccgtggt cgtgggcctg	2400
gtagcctaca tcgcctttaa gagatgacct aggtaa	2436

<210> 46

<211> 808

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 46

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
			20					25					30		

Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
		35					40					45			

Thr	Phe	Thr	Thr	Tyr	Trp	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln
	50					55					60				

Gly	Leu	Glu	Trp	Met	Gly	Glu	Ile	Asn	Pro	Ser	Ser	Gly	Arg	Thr	Asn
65					70					75					80

Tyr Asn Glu Lys Phe Lys Thr Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Lys Leu Gly Pro Gly Pro Gln Tyr Tyr Ala
115 120 125

Met Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
145 150 155 160

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

Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala
195 200 205

Ser Lys Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
225 230 235 240

Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Trp Thr Phe Gly
245 250 255

Gln Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Phe Val Pro Val Phe
260 265 270

Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
275 280 285

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys

290

295

300

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
 305 310 315 320

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
 325 330 335

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Phe
 340 345 350

Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
 355 360 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
 370 375 380

Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
 385 390 395 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
 405 410 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
 420 425 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
 435 440 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
 450 455 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
 465 470 475 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 485 490 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg
 500 505 510

Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
515 520 525

Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met
530 535 540

Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly
545 550 555 560

Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu
565 570 575

Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly
580 585 590

Ala Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser
595 600 605

Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val
610 615 620

Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val
625 630 635 640

Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys
645 650 655

Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys
660 665 670

Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr
675 680 685

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

Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala
705 710 715 720

Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro

725

730

735

Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro
 740 745 750

Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr
 755 760 765

Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
 770 775 780

Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu
 785 790 795 800

Val Ala Tyr Ile Ala Phe Lys Arg
 805

<210> 47

<211> 2481

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 47

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
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gtgtcctgca aggcttctgg atacagcttc accagttatg atatcaactg ggtgcgacag	180
gccactggac aagggttga gtggatgggg tggatgaacc cgaacagtgg taacacaggc	240
tatgcacaga agttccaggg cagagtcacc atgaccaggg acacctccat aagcacagcc	300
tacatggaac tgagcagcct gagatctgag gacacggccg tgtattactg tgggagagcc	360
ggttactact actacttcgg tatggacgtc tggggccaag ggaccacggc caccgtatcc	420
tcaggaggcg gcggttcagg cggaggtggc tctggcggcg gcggaagtga aattgtgttg	480
acgcagtctc caggcaccct gtctttgtct ccaggggaaa gagccaccct ctctgcagg	540
gccggtcaga gtgttaccag cagctccttt gcttggtacc aacagaaacc tggccaggct	600
cccaggctcc tcatctatca gacatccacc agggccactg gcatcccaga caggttcagt	660

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gcagtgtatt	actgtcagca	gtatggtggc	tcacggctgt	tcggccaagg	gaccaaggtg	780
gaactcaaac	gagccgctgc	ccttgataat	gaaaagtcaa	acggaacaat	cattcacgtg	840
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cttcagtcca	tgtccgcccc	ctgtgtcgaa	gccgatgatg	cagtgtgcag	atgtgcctat	1980
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cctgggagat	ggatcaccgc	gagcacacct	cctgagggat	cagacagtac	agccccgagt	2280

acccaagaac cggaggcccc tccagagcag gacctgatcg cttctacagt tgctggcgtg 2340
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 tttaagagat gacctaggta a 2481

<210> 48

<211> 823

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 48

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

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

Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly
 65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
 85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Gly Arg Ala Gly Tyr Tyr Tyr Tyr Phe Gly Met
 115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
145 150 155 160

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
165 170 175

Leu Ser Cys Arg Ala Gly Gln Ser Val Thr Ser Ser Ser Phe Ala Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gln Thr
195 200 205

Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
225 230 235 240

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Arg Ser Phe Gly Gln
245 250 255

Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys
260 265 270

Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser
275 280 285

Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
290 295 300

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
305 310 315 320

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
325 330 335

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
340 345 350

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Phe Ser
355 360 365

Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
370 375 380

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
385 390 395 400

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
405 410 415

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
420 425 430

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
435 440 445

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
450 455 460

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
465 470 475 480

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
485 490 495

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
500 505 510

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser
515 520 525

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
530 535 540

Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp
545 550 555 560

Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly
565 570 575

Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys
580 585 590

Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala
595 600 605

Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp
610 615 620

Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly
625 630 635 640

Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys
645 650 655

Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
660 665 670

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
675 680 685

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
690 695 700

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
705 710 715 720

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
725 730 735

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
740 745 750

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
755 760 765

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
770 775 780

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu
785 790 795 800

Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val
805 810 815

Ala Tyr Ile Ala Phe Lys Arg
820

<210> 49
<211> 2340
<212> ADN
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 49
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gtgtcctgca aggcttctgg atacagcttc accagttatg atatcaactg ggtgcgacag 180
gccactggac aagggcttga gtggatgggg tggatgaacc cgaacagtgg taacacaggc 240
tatgcacaga agttccaggg cagagtcacc atgaccaggg acacctccat aagcacagcc 300
tacatggaac tgagcagcct gagatctgag gacacggccg tgtattactg tgggagagcc 360
ggttactact actacttcgg tatggacgtc tggggccaag ggaccacggt caccgtatcc 420
tcaggaggcg gcggttcagg cggaggtggc tctggcgggtg gcggaagtga aattgtgttg 480
acgcagtctc caggcaccct gtctttgtct ccaggggaaa gagccaccct ctcttcgagg 540
gccggtcaga gtgttaccag cagctccttt gcttggtacc aacagaaacc tggccaggct 600
cccaggctcc tcatttatca gacatccacc agggccactg gcatcccaga caggttcagt 660
ggcagtgggt ctgggacaga tttcactctc accatcagca gactggagcc tgaagatttt 720
gcagtgtatt actgtcagca gtatggtggc tcacggtcgt tcggccaagg gaccaagggtg 780
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atcttctggg ttagatccaa aagaagccgc ctgctccata gcgattacat gaatatgact	1020
ccacgccgcc ctggcccccac aaggaaacac taccagcctt acgcaccacc tagagatttc	1080
gctgcctatc ggagcagggt gaagttttcc agatctgcag atgcaccagc gtatcagcag	1140
ggccagaacc aactgtataa cgagctcaac ctgggacgca gggaagagta tgacgttttg	1200
gacaagcgca gaggacggga ccctgagatg ggtggcaaac caagacgaaa aaacccccag	1260
gagggctctct ataatgagct gcagaaggat aagatggctg aagcctattc tgaaataggc	1320
atgaaaggag agcggagaag gggaaaaggg cacgacgggt tgtaccaggg actcagcact	1380
gctacgaagg atacttatga cgctctccac atgcaagccc tgccacctag ggccaagaga	1440
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gctaaccaga cagtctgtga accatgcctg gattcagtga cattcagcga tgttgtctca	1740
gccaccgagc cttgcaagcc ttgtaccgaa tgtgtgggcc ttcagtccat gtccgcccc	1800
tgtgtcgaag ccgatgatgc agtgtgcaga tgtgcctatg gatattacca ggacgaaact	1860
accgggcggt gtgaggcctg ccgggtgtgt gaagccggct ctggcctcgt gttcagttgc	1920
caggataagc aaaacacagt atgtgaggag tgtccagacg gaacctacag cgacgaggcg	1980
aaccacgtcg acccttgctt gccgtgcacc gtctgcgagg ataccgaaacg ccagctgaga	2040
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agcacacctc ctgagggatc agacagtaca gccccagta cccaagaacc ggaggcccct	2160
ccagagcagg acctgatcgc ttctacagtt gctggcgtgg tgacgacagt catgggatcc	2220
tcacaaccag tcgtgacgcg gggcacaacc gacaatctga ttcctgtcta ctgtagcatc	2280
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<210> 50

<211> 776

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 50

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

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

Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Gly Arg Ala Gly Tyr Tyr Tyr Tyr Phe Gly Met
115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
145 150 155 160

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
165 170 175

Leu Ser Cys Arg Ala Gly Gln Ser Val Thr Ser Ser Ser Phe Ala Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gln Thr
195 200 205

Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
225 230 235 240

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Arg Ser Phe Gly Gln
245 250 255

Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys
260 265 270

Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser
275 280 285

Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
290 295 300

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
305 310 315 320

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
325 330 335

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
340 345 350

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
355 360 365

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
370 375 380

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
385 390 395 400

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
405 410 415

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met

420

425

430

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
 435 440 445

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 450 455 460

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg
 465 470 475 480

Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
 485 490 495

Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met
 500 505 510

Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly
 515 520 525

Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu
 530 535 540

Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly
 545 550 555 560

Ala Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser
 565 570 575

Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val
 580 585 590

Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val
 595 600 605

Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys
 610 615 620

Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys
 625 630 635 640

Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr
645 650 655

Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys
660 665 670

Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala
675 680 685

Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro
690 695 700

Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro
705 710 715 720

Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr
725 730 735

Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
740 745 750

Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu
755 760 765

Val Ala Tyr Ile Ala Phe Lys Arg
770 775

<210> 51

<211> 2358

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 51

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gtgtcctgca aggcttctgg atacagcttc accagttatg atatcaactg ggtgacgacag 180

gccactggac aagggttga gtggatgggg tggatgaacc cgaacagtgg taacacaggc 240

tatgcacaga agttccaggg cagagtcacc atgaccaggg acacctccat aagcacagcc	300
tacatggaac tgagcagcct gagatctgag gacacggccg tgtattactg tgggagagcc	360
ggttactact actacttcgg tatggacgtc tggggccaag ggaccacggc caccgtatcc	420
tcaggaggcg gcggttcagg cggaggtggc tctggcggcg gcggaagtga aattgtgttg	480
acgcagtctc caggcacccct gtctttgtct ccaggggaaa gagccaccct ctcctgcagg	540
gccggtcaga gtgttaccag cagctccttt gcttggtacc aacagaaacc tggccaggct	600
cccaggctcc tcatttatca gacatccacc agggccactg gcatcccaga caggttcagt	660
ggcagtgggc ctgggacaga tttcactctc accatcagca gactggagcc tgaagatttt	720
gcagtgtatt actgtcagca gtatggtggc tcacggctgt tcggccaagg gaccaaggcg	780
gaactcaaac gagccgtgc ccttgataat gaaaagtcaa acggaacaat cattcacgtg	840
aagggaagc acctctgtcc gtcacccttg ttccctggcg catccaagcc attctgggtg	900
ttggtcgtag tgggtggagt cctcgcttgt tactctctgc tcgtcaccgt ggcttttata	960
atcttctggg ttcgcttttc cgtcgttaag cgggggagaa aaaagctgct gtacattttc	1020
aaacagccgt ttatgaggcc ggtccaaacg actcaggaag aggacggctg ctcctgccgc	1080
tttcctgagg aggaggagg cgggtgcgaa ctgagggtga agttttccag atctgcagat	1140
gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg	1200
gaagagtatg acgttttggc caagcgcaga ggacgggacc ctgagatggg tggcaaacca	1260
agacgaaaaa acccccagga gggctcttat aatgagctgc agaaggataa gatggctgaa	1320
gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg	1380
taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg	1440
ccacctaggg ccaagagaag tggcagcggg gagggccggg gatctctcct tacatgtggg	1500
gacgtggaag aaaatccggg gcctatgggt gccggcgcca cgggaagggc tatggatggc	1560
ccgcgactgc ttctcctgct gttgttgggc gtgtctctcg gaggcgctaa ggaggcctgt	1620
ccaacgggcc tctacactca ctccggtgaa tgttgcaaag cctgtaacct tggcgagggc	1680
gtcgcacaa cttgtgtgct taaccagaca gtctgtgaac catgcctgga ttcagtgaca	1740
ttcagcgatg ttgtctcagc caccgagcct tgcaagcctt gtaccgaatg tgtgggcctt	1800
cagtccatgt ccgccccctg tgtcgaagcc gatgatgcag tgtgcagatg tgcctatgga	1860

tattaccagg acgaaactac cgggcggtgt gaggcctgcc ggggtgtgtga agccggctct	1920
ggcctcgtgt tcagttgccca ggataagcaa aacacagtat gtgaggagtg tccagacgga	1980
acctacagcg acgaggcgaa ccacgtcgac ccttgcttgc cgtgcaccgt ctgagaggat	2040
accgaacgcc agctgagaga gtgtacgcgc tgggcagacg ctgagtgcga ggagatccct	2100
gggagatgga tcacccggag cacacctcct gagggatcag acagtacagc cccgagtacc	2160
caagaaccgg agggccctcc agagcaggac ctgatcgctt ctacagttgc tggcgtgggtg	2220
acgacagtca tgggatacctc acaaccagtc gtgacgcggg gcacaaccga caatctgatt	2280
cctgtctact gtagcatctt ggcagccgtg gtcgtgggcc tggtagccta catcgctttt	2340
aagagatgac ctaggtaa	2358

<210> 52

<211> 782

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 52

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
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His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
			20					25					30		

Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
		35					40					45			

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

Gly	Leu	Glu	Trp	Met	Gly	Trp	Met	Asn	Pro	Asn	Ser	Gly	Asn	Thr	Gly
65					70				75						80

Tyr	Ala	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser
			85						90					95	

Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Gly Arg Ala Gly Tyr Tyr Tyr Tyr Phe Gly Met
115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
145 150 155 160

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
165 170 175

Leu Ser Cys Arg Ala Gly Gln Ser Val Thr Ser Ser Ser Phe Ala Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gln Thr
195 200 205

Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
225 230 235 240

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Arg Ser Phe Gly Gln
245 250 255

Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys
260 265 270

Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser
275 280 285

Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
290 295 300

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
305 310 315 320

Ile Phe Trp Val Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu
325 330 335

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
340 345 350

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
355 360 365

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
370 375 380

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
385 390 395 400

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
405 410 415

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
420 425 430

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
435 440 445

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
450 455 460

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
465 470 475 480

Pro Pro Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu
485 490 495

Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ala Gly
500 505 510

Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu Leu Leu Leu
515 520 525

Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu
530 535 540

Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly
545 550 555 560

Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu
565 570 575

Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys
580 585 590

Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val
595 600 605

Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp
610 615 620

Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser
625 630 635 640

Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu
645 650 655

Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys
660 665 670

Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys
675 680 685

Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile
690 695 700

Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr
705 710 715 720

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

Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr
740 745 750

Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala
755 760 765

Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe Lys Arg
770 775 780

<210> 53

<211> 2418

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 53

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctggggc ctcaagtgaag	120
gtgtcctgca aggcttctgg atacagcttc accagttatg atatcaactg ggtgcgacag	180
gccactggac aagggcttga gtggatgggg tggatgaacc cgaacagtgg taacacaggc	240
tatgcacaga agttccaggg cagagtcacc atgaccaggg acacctccat aagcacagcc	300
tacatggaac tgagcagcct gagatctgag gacacggccg tgtattactg tgggagagcc	360
ggttactact actacttcgg tatggacgtc tggggccaag ggaccacggt caccgtatcc	420
tcaggaggcg gcggttcagg cggaggtggc tctggcgggt gcggaagtga aattgtgttg	480
acgcagtctc caggcacctt gtctttgtct ccaggggaaa gagccaccct ctcttcgagg	540
gccggtcaga gtgttaccag cagctccttt gcttgggtacc aacagaaacc tggccaggct	600
cccaggctcc tcatttatca gacatccacc agggccactg gcatcccaga caggttcagt	660
ggcagtgggt ctgggacaga ttctactctc accatcagca gactggagcc tgaagatctt	720
gcagtgtatt actgtcagca gtatggtggc tcacggctcg tcggccaagg gaccaagggtg	780
gaactcaaac gagccgctgc cttcgtgcct gtttttctgc ccgcgaaacc cacaactacc	840
cccgcccctc ggcccccaac tcctgcacca actatcgctt cccaaccctt gtctctgaga	900
cctgaggcat gccgccccgc ggcaggcggc gccgtgcaca ctagaggcct ggacttcgcc	960
tgcgatattt atatctgggc ccccttgcc gggacatgcg ggggtactgct gctgtctctg	1020

gtgattaccc tctactgcaa ccacagaaac agatccaaaa gaagccgcct gctccatagc	1080
gattacatga atatgactcc acgccgcctt ggccccacaa ggaaacacta ccagccttac	1140
gcaccaccta gagatttcgc tgcctatcgg agcaggggtga agttttccag atctgcagat	1200
gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg	1260
gaagagtatg acgtttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca	1320
agacgaaaaa acccccagga gggctctctat aatgagctgc agaaggataa gatggctgaa	1380
gcctatttctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg	1440
taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg	1500
ccacctaggg ccaagagaag tggcagcggg gagggccggg gatctctcct tacatgtggg	1560
gacgtggaag aaaatccggg gcctatgggt gccggcgcca cgggaagggc tatggatggc	1620
ccgcgactgc ttctcctgct gttgttgggc gtgtctctcg gaggcgctaa ggaggcctgt	1680
ccaacgggcc tctacactca ctccggtgaa tgttgcaaag cctgtaacct tggcgagggc	1740
gtcgcacaa cttgtggtgc taaccagaca gtctgtgaac catgcctgga ttcagtgaca	1800
ttcagcgatg ttgtctcagc caccgagcct tgcaagcctt gtaccgaatg tgtgggcctt	1860
cagtccatgt ccgccccctg tgtcgaagcc gatgatgcag tgtgcagatg tgcctatgga	1920
tattaccagg acgaaactac cgggcggtgt gaggcctgcc ggggtgtgtga agccggctct	1980
ggcctcgtgt tcagttgcca ggataagcaa aacacagtat gtgaggagtg tccagacgga	2040
acctacagcg acgaggcgaa ccacgtcgac ccttgcttgc cgtgcaccgt ctgcgaggat	2100
accgaacgcc agctgagaga gtgtacgcgc tgggcagacg ctgagtgcga ggagatccct	2160
gggagatgga tcacccggag cacacctcct gagggatcag acagtacagc cccgagtacc	2220
caagaaccgg agggccctcc agagcaggac ctgatcgctt ctacagttgc tggcgtggtg	2280
acgacagtca tgggatcctc acaaccagtc gtgacgcggg gcacaaccga caatctgatt	2340
cctgtctact gtagcatctt ggcagccgtg gtcgtgggcc tggtagccta catcgctttt	2400
aagagatgac ctaggtaa	2418

<210> 54

<211> 802

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 54

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

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

Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Gly Arg Ala Gly Tyr Tyr Tyr Tyr Phe Gly Met
115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
145 150 155 160

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
165 170 175

Leu Ser Cys Arg Ala Gly Gln Ser Val Thr Ser Ser Ser Phe Ala Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gln Thr

195

200

205

Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
 210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
 225 230 235 240

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Arg Ser Phe Gly Gln
 245 250 255

Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Phe Val Pro Val Phe
 260 265 270

Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
 275 280 285

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
 290 295 300

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
 305 310 315 320

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
 325 330 335

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser
 340 345 350

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
 355 360 365

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
 370 375 380

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
 385 390 395 400

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
 405 410 415

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
420 425 430

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
435 440 445

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
450 455 460

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
465 470 475 480

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
485 490 495

Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly
500 505 510

Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
515 520 525

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
530 535 540

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
545 550 555 560

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
565 570 575

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
580 585 590

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
595 600 605

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
610 615 620

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly

625		630		635		640									
Tyr	Tyr	Gln	Asp	Glu	Thr	Thr	Gly	Arg	Cys	Glu	Ala	Cys	Arg	Val	Cys
				645					650					655	
Glu	Ala	Gly	Ser	Gly	Leu	Val	Phe	Ser	Cys	Gln	Asp	Lys	Gln	Asn	Thr
			660					665					670		
Val	Cys	Glu	Glu	Cys	Pro	Asp	Gly	Thr	Tyr	Ser	Asp	Glu	Ala	Asn	His
		675					680					685			
Val	Asp	Pro	Cys	Leu	Pro	Cys	Thr	Val	Cys	Glu	Asp	Thr	Glu	Arg	Gln
	690					695					700				
Leu	Arg	Glu	Cys	Thr	Arg	Trp	Ala	Asp	Ala	Glu	Cys	Glu	Glu	Ile	Pro
705					710					715					720
Gly	Arg	Trp	Ile	Thr	Arg	Ser	Thr	Pro	Pro	Glu	Gly	Ser	Asp	Ser	Thr
				725					730					735	
Ala	Pro	Ser	Thr	Gln	Glu	Pro	Glu	Ala	Pro	Pro	Glu	Gln	Asp	Leu	Ile
			740					745					750		
Ala	Ser	Thr	Val	Ala	Gly	Val	Val	Thr	Thr	Val	Met	Gly	Ser	Ser	Gln
		755					760					765			
Pro	Val	Val	Thr	Arg	Gly	Thr	Thr	Asp	Asn	Leu	Ile	Pro	Val	Tyr	Cys
	770					775					780				
Ser	Ile	Leu	Ala	Ala	Val	Val	Val	Gly	Leu	Val	Ala	Tyr	Ile	Ala	Phe
785					790					795					800

Lys Arg

<210> 55

<211> 2436

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 55

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctggggc ctcagtgaag	120
gtgtcctgca aggcttctgg atacagcttc accagttatg atatcaactg ggtgcgacag	180
gccactggac aagggttga gtggatgggg tggatgaacc cgaacagtgg taacacaggc	240
tatgcacaga agttccaggg cagagtcacc atgaccaggg acacctccat aagcacagcc	300
tacatggaac tgagcagcct gagatctgag gacacggccg tgtattactg tgggagagcc	360
ggttactact actacttcgg tatggacgtc tggggccaag ggaccacggt caccgtatcc	420
tcaggaggcg gcggttcagg cggaggtggc tctggcgggt gcggaagtga aattgtgttg	480
acgcagtctc caggcacctt gtctttgtct ccaggggaaa gagccaccct ctctgcagg	540
gccggtcaga gtgttaccag cagctccttt gcttggtacc aacagaaacc tggccaggct	600
cccaggctcc tcatctatca gacatccacc agggccactg gcatcccaga caggttcagt	660
ggcagtgggt ctgggacaga tttcactctc accatcagca gactggagcc tgaagatfff	720
gcagtgtatt actgtcagca gtatggtggc tcacggctgt tcggccaagg gaccaagggtg	780
gaactcaaac gagccgtgc cttcgtgcct gtttttctgc ccgcgaaacc cacaactacc	840
cccgccctc ggcccccaac tcctgcacca actatcgctt cccaacccct gtctctgaga	900
cctgaggcat gccgccccgc ggcaggcggc gccgtgcaca ctagaggcct ggacttcgcc	960
tgcgatattt atatctgggc cccccttgcc gggacatgcg ggggtactgct gctgtctctg	1020
gtgattacc tctactgcaa ccacagaaac cgcttttccg tcgttaagcg ggggagaaaa	1080
aagctgctgt acattttcaa acagccgttt atgaggccgg tccaaacgac tcaggaagag	1140
gacggctgct cctgccgctt tcctgaggag gaggaggcg ggtgcgaact gaggggtgaag	1200
ttttccagat ctgcagatgc accagcgtat cagcagggcc agaaccaact gtataacgag	1260
ctcaacctgg gacgcaggga agagtatgac gttttggaca agcgcagagg acgggaccct	1320
gagatgggtg gcaaaccaag acgaaaaaac cccaggagg gtctctataa tgagctgcag	1380
aaggataaga tggctgaagc ctattctgaa ataggcatga aaggagagcg gagaagggga	1440
aaagggcacg acggtttgta ccagggactc agcactgcta cgaaggatac ttatgacgct	1500
ctccacatgc aagccctgcc acctagggcc aagagaagtg gcagcgggga gggccgggga	1560

tctctcctta catgtgggga cgtggaagaa aatccggggc ctatgggtgc cggcgccacg	1620
ggaagggcta tggatggccc gcgactgctt ctctgtctgt tgttgggcgt gtctctcgga	1680
ggcgctaagg aggccctgtcc aacgggcctc tacactcact ccggtgaatg ttgcaaagcc	1740
tgtaaccttg gcgagggcgt cgcacaacct tgtggtgcta accagacagt ctgtgaacca	1800
tgcctggatt cagtgcatt cagcgatggt gtctcagcca ccgagccttg caagccttgt	1860
accgaatgtg tgggccttca gtccatgtcc gccccctgtg tcgaagccga tgatgcagt	1920
tgcagatgtg cctatggata ttaccaggac gaaactaccg ggcggtgtga ggcttgccgg	1980
gtgtgtgaag ccggctctgg cctcgtgttc agttgccagg ataagcaaaa cacagtatgt	2040
gaggagtgtc cagacggaac ctacagcgac gaggcgaacc acgtcgaccc ttgcttgccg	2100
tgcaccgtct gcgaggatac cgaacgccag ctgagagagt gtacgcgctg ggagacgct	2160
gagtgcgagg agatccctgg gagatggatc acccgagca cacctcctga gggatcagac	2220
agtacagccc cgagtaccca agaaccggag gcccctccag agcaggacct gatcgcttct	2280
acagttgctg gcgtgggtgac gacagtcatt ggatcctcac aaccagtcgt gacgcggggc	2340
acaaccgaca atctgattcc tgtctactgt agcatcttgg cagccgtgggt cgtgggcctg	2400
gtagcctaca tcgcctttaa gagatgacct aggtaa	2436

<210> 56

<211> 808

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 56

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
			20					25					30		

Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
		35					40					45			

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

Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Gly Arg Ala Gly Tyr Tyr Tyr Tyr Phe Gly Met
115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
145 150 155 160

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
165 170 175

Leu Ser Cys Arg Ala Gly Gln Ser Val Thr Ser Ser Ser Phe Ala Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gln Thr
195 200 205

Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
225 230 235 240

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Arg Ser Phe Gly Gln
245 250 255

Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Phe Val Pro Val Phe
260 265 270

Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
275 280 285

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
290 295 300

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
305 310 315 320

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
325 330 335

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Phe
340 345 350

Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
355 360 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
370 375 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385 390 395 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
405 410 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
420 425 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
435 440 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
450 455 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465 470 475 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
485 490 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg
500 505 510

Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
515 520 525

Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met
530 535 540

Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly
545 550 555 560

Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu
565 570 575

Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly
580 585 590

Ala Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser
595 600 605

Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val
610 615 620

Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val
625 630 635 640

Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys
645 650 655

Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys
660 665 670

Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr
675 680 685

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

Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala
705 710 715 720

Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro
725 730 735

Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro
740 745 750

Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr
755 760 765

Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
770 775 780

Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu
785 790 795 800

Val Ala Tyr Ile Ala Phe Lys Arg
805

<210> 57

<211> 2481

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 57

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctggggc ctcagtgaag 120

gtgtcctgca aggcttctgg atacagcttc accagttatg atatcaactg ggtgacgacag 180

gccactggac aagggttga gtggatgggg tggatgaacc cgaacagtgg taacacaggc 240

tatgcacaga agttccaggg cagagtcacc atgaccaggg acacctccat aagcacagcc 300

tacatggaac tgagcagcct gagatctgag gacacggccg tgtattactg tgggagagcc 360

ggttactact actacttcgg tatggacgtc tggggccaag ggaccacggt caccgtatcc 420

tcaggaggcg gcggttcagg cggagggtggc tctggcgggtg gcggaagtga aattgtgttg	480
acgcagtctc caggcaccct gtctttgtct ccaggggaaa gagccaccct ctcttcagg	540
gccggtcaga gtgttaccag cagctcctta gcttgggtacc agcagaaacc tggccaggct	600
cccaggctcc tcatctatca gacatccacc agggccactg gcatcccaga caggttcagt	660
ggcagtgggt ctgggacaga tttcactctc accatcagca gactggagcc tgaagatttt	720
gcagtgtatt actgtcagca gtatgggtggc tcacgggcgt tcggccaagg gaccaagggtg	780
gaactcaaac gagccgctgc ccttgataat gaaaagtcaa acggaacaat cattcacgtg	840
aagggaagc acctctgtcc gtcacccttg ttccctgggtc catccaagcc attctgggtg	900
ttggtcgtag tgggtggagt cctcgcttgt tactctctgc tcgtcaccgt ggcttttata	960
atcttctggg ttagatccaa aagaagccgc ctgctccata gcgattacat gaatatgact	1020
ccacgccgcc ctggccccac aaggaaacac taccagcctt acgcaccacc tagagatttc	1080
gctgcctatc ggagccgctt ttccgtcggt aagcggggga gaaaaaagct gctgtacatt	1140
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cgctttcctg aggaggagga gggcgggtgc gaactgaggg tgaagttttc cagatctgca	1260
gatgcaccag cgtatcagca gggccagaac caactgtata acgagctcaa cctgggacgc	1320
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tctggcctcg tgttcagttg ccaggataag caaaacacag tatgtgagga gtgtccagac	2100
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<210> 58

<211> 823

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 58

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
			20					25					30		

Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
		35					40					45			

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

Gly	Leu	Glu	Trp	Met	Gly	Trp	Met	Asn	Pro	Asn	Ser	Gly	Asn	Thr	Gly
65					70				75					80	

Tyr	Ala	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser
			85						90					95	

Ile	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr
			100					105					110		

Ala Val Tyr Tyr Cys Gly Arg Ala Gly Tyr Tyr Tyr Tyr Phe Gly Met
115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
145 150 155 160

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
165 170 175

Leu Ser Cys Arg Ala Gly Gln Ser Val Thr Ser Ser Ser Leu Ala Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gln Thr
195 200 205

Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
225 230 235 240

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Arg Ala Phe Gly Gln
245 250 255

Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys
260 265 270

Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser
275 280 285

Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
290 295 300

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
305 310 315 320

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr

325

330

335

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
 340 345 350

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Phe Ser
 355 360 365

Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
 370 375 380

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
 385 390 395 400

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
 405 410 415

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
 420 425 430

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 435 440 445

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 450 455 460

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 465 470 475 480

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 485 490 495

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 500 505 510

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser
 515 520 525

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
 530 535 540

Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp
545 550 555 560

Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly
565 570 575

Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys
580 585 590

Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala
595 600 605

Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp
610 615 620

Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly
625 630 635 640

Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys
645 650 655

Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
660 665 670

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
675 680 685

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
690 695 700

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
705 710 715 720

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
725 730 735

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
740 745 750

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro

755

760

765

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
 770 775 780

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu
 785 790 795 800

Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val
 805 810 815

Ala Tyr Ile Ala Phe Lys Arg
 820

<210> 59

<211> 2340

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 59

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ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctggggc ctcagtgaag 120

gtgtcctgca aggcttctgg atacagcttc accagttatg atatcaactg ggtgcgacag 180

gccactggac aagggcttga gtggatgggg tggatgaacc cgaacagtgg taacacaggc 240

tatgcacaga agttccaggg cagagtcacc atgaccaggg acacctccat aagcacagcc 300

tacatggaac tgagcagcct gagatctgag gacacggccg tgtattactg tgggagagcc 360

ggttactact actacttcgg tatggacgtc tggggccaag ggaccacggt caccgtatcc 420

tcaggaggcg gcggttcagg cggaggtggc tctggcggtg gcggaagtga aattgtgttg 480

acgcagtctc caggcaccct gtctttgtct ccaggggaaa gagccaccct ctctgcagg 540

gccggtcaga gtgttaccag cagctcctta gcttgggtacc agcagaaacc tggccaggct 600

cccaggctcc tcatctatca gacatccacc agggccactg gcatcccaga caggttcagt 660

ggcagtgggt ctgggacaga tttcactctc accatcagca gactggagcc tgaagatttt 720

gcagtgtatt actgtcagca gtatggtggc tcacgggcgt tcggccaagg gaccaagggtg 780

gaactcaaac gagccgctgc ccttgataat gaaaagtcaa acggaacaat cattcacgtg	840
aagggcaagc acctctgtcc gtcacccttg ttccctgggtc catccaagcc attctgggtg	900
ttggctcgtag tgggtggagt cctcgcttgt tactctctgc tcgtcaccgt ggcttttata	960
atcttctggg ttagatccaa aagaagccgc ctgctccata gcgattacat gaatatgact	1020
ccacgccgcc ctggccccac aaggaaacac taccagcctt acgcaccacc tagagatttc	1080
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gacaagcgca gaggacggga ccctgagatg ggtggcaaac caagacgaaa aaacccccag	1260
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tcacaaccag tcgtgacgcg gggcacaacc gacaatctga ttctgtctta ctgtagcatc	2280
ttggcagccg tggtcgtggg cctggtagcc tacatgcct ttaagagatg acctaggtaa	2340

<210> 60
 <211> 776
 <212> PRT
 <213> Secuencia artificial

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 60
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

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

Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly
 65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
 85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Gly Arg Ala Gly Tyr Tyr Tyr Tyr Phe Gly Met
 115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
 145 150 155 160

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
 165 170 175

Leu Ser Cys Arg Ala Gly Gln Ser Val Thr Ser Ser Ser Leu Ala Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gln Thr
195 200 205

Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
225 230 235 240

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Arg Ala Phe Gly Gln
245 250 255

Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys
260 265 270

Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser
275 280 285

Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
290 295 300

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
305 310 315 320

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
325 330 335

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
340 345 350

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
355 360 365

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
370 375 380

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
385 390 395 400

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
405 410 415

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
420 425 430

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
435 440 445

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
450 455 460

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg
465 470 475 480

Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
485 490 495

Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met
500 505 510

Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly
515 520 525

Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu
530 535 540

Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly
545 550 555 560

Ala Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser
565 570 575

Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val
580 585 590

Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val
595 600 605

Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys
610 615 620

Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys
625 630 635 640

Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr
645 650 655

Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys
660 665 670

Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala
675 680 685

Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro
690 695 700

Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro
705 710 715 720

Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr
725 730 735

Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
740 745 750

Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu
755 760 765

Val Ala Tyr Ile Ala Phe Lys Arg
770 775

<210> 61

<211> 2358

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 61

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gtgtcctgca aggcttctgg atacagcttc accagttatg atatcaactg ggtgcgacag	180
gccactggac aagggcttga gtggatgggg tggatgaacc cgaacagtgg taacacaggc	240
tatgcacaga agttccaggg cagagtcacc atgaccaggg acacctccat aagcacagcc	300
tacatggaac tgagcagcct gagatctgag gacacggccg tgtattactg tgggagagcc	360
ggttactact actacttcgg tatggacgtc tggggccaag ggaccacggt caccgtatcc	420
tcaggaggcg gcggttcagg cggaggtggc tctggcgggtg gcggaagtga aattgtgttg	480
acgcagtctc caggcacctt gtctttgtct ccaggggaaa gagccaccct ctctgcagg	540
gccggtcaga gtgttaccag cagctcctta gcttgggtacc agcagaaaacc tggccaggct	600
cccaggctcc tcatctatca gacatccacc agggccactg gcatcccaga caggttcagt	660
ggcagtgggt ctgggacaga tttcactctc accatcagca gactggagcc tgaagatttt	720
gcagtgtatt actgtcagca gtatggtggc tcacgggcgt tcggccaagg gaccaaggtg	780
gaactcaaac gagccgctgc ccttgataat gaaaagtcaa acggaacaat cattcacgtg	840
aagggaagc acctctgtcc gtcacccttg ttccctgggtc catccaagcc attctgggtg	900
ttggtcgtag tgggtggagt cctcgcttgt tactctctgc tcgtcaccgt ggcttttata	960
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aaacagccgt ttatgaggcc ggtccaaacg actcaggaag aggacggctg ctctgcccgc	1080
tttctgagg aggaggagg cgggtgcgaa ctgagggtga agttttccag atctgcagat	1140
gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg	1200
gaagagtatg acgtttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca	1260
agacgaaaaa acccccagga gggctcttat aatgagctgc agaaggataa gatggctgaa	1320
gcctattctg aaatagcat gaaaggagag cggagaaggg gaaaaggga cgacggtttg	1380
taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg	1440
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gacgtggaag aaaatccggg gcctatgggt gccggcgcca cgggaagggc tatggatggc	1560
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ccaacgggcc tctacactca ctccggtgaa tgttgcaaag cctgtaacct tggcgagggc	1680
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ttcagcgatg ttgtctcagc caccgagcct tgcaagcctt gtaccgaatg tgtgggcctt	1800
cagtccatgt ccgccccctg tgtcgaagcc gatgatgcag tgtgcagatg tgcctatgga	1860
tattaccagg acgaaactac cgggcggtgt gaggcctgcc ggggtgtgtga agccggctct	1920
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acctacagcg acgaggcgaa ccacgtcgac ccttgcttgc cgtgcaccgt ctgcgaggat	2040
accgaacgcc agctgagaga gtgtacgcgc tgggcagacg ctgagtgcga ggagatccct	2100
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caagaaccgg aggcccctcc agagcaggac ctgatcgctt ctacagttgc tggcgtggtg	2220
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aagagatgac ctaggtaa	2358

<210> 62

<211> 782

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 62

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
			20				25						30		

Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
		35					40					45			

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

Gly	Leu	Glu	Trp	Met	Gly	Trp	Met	Asn	Pro	Asn	Ser	Gly	Asn	Thr	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
290 295 300

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
305 310 315 320

Ile Phe Trp Val Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu
325 330 335

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
340 345 350

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
355 360 365

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
370 375 380

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
385 390 395 400

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
405 410 415

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
420 425 430

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
435 440 445

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
450 455 460

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
465 470 475 480

Pro Pro Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu
485 490 495

Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ala Gly

500

505

510

Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu
 515 520 525

Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu
 530 535 540

Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly
 545 550 555 560

Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu
 565 570 575

Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys
 580 585 590

Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val
 595 600 605

Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp
 610 615 620

Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser
 625 630 635 640

Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu
 645 650 655

Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys
 660 665 670

Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys
 675 680 685

Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile
 690 695 700

Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr
 705 710 715 720

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

Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr
740 745 750

Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala
755 760 765

Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe Lys Arg
770 775 780

<210> 63

<211> 2418

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 63

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gtgtcctgca aggcttctgg atacagcttc accagttatg atatcaactg ggtgcgacag 180

gccactggac aagggcttga gtggatgggg tggatgaacc cgaacagtgg taacacaggc 240

tatgcacaga agttccaggg cagagtcacc atgaccaggg acacctccat aagcacagcc 300

tacatggaac tgagcagcct gagatctgag gacacggccg tgtattactg tgggagagcc 360

ggttactact actacttcgg tatggacgtc tggggccaag ggaccacggt caccgtatcc 420

tcaggaggcg gcggttcagg cggaggtggc tctggcggtg gcggaagtga aattgtgttg 480

acgcagtctc caggcacctt gtctttgtct ccaggggaaa gagccaccct ctctgcagg 540

gccggtcaga gtgttaccag cagctcctta gcttggtacc agcagaaacc tggccaggct 600

cccaggctcc tcatctatca gacatccacc agggccactg gcatcccaga caggttcagt 660

ggcagtgggt ctgggacaga tttcactctc accatcagca gactggagcc tgaagatttt 720

gcagtgtatt actgtcagca gtatggtggc tcacgggcgt tcggccaagg gaccaagggtg 780

gaactcaaac gagccgtgc cttcgtgcct gtttttctgc ccgcgaaacc cacaactacc 840

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tgcgatattt atatctgggc cccccttgcc gggacatgcg ggggtactgct gctgtctctg	1020
gtgattacc tctactgcaa ccacagaaac agatccaaaa gaagccgcct gctccatagc	1080
gattacatga atatgactcc acgccgcctt ggccccacaa ggaaacacta ccagccttac	1140
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gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg	1260
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aagagatgac ctaggtaa	2418

<210> 64
 <211> 802
 <212> PRT
 <213> Secuencia artificial

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

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His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
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Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

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

Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly
 65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
 85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Gly Arg Ala Gly Tyr Tyr Tyr Tyr Phe Gly Met
 115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
 145 150 155 160

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
 165 170 175

Leu Ser Cys Arg Ala Gly Gln Ser Val Thr Ser Ser Ser Leu Ala Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gln Thr
195 200 205

Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
225 230 235 240

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Arg Ala Phe Gly Gln
245 250 255

Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Phe Val Pro Val Phe
260 265 270

Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
275 280 285

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
290 295 300

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
305 310 315 320

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
325 330 335

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser
340 345 350

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
355 360 365

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
370 375 380

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
385 390 395 400

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
405 410 415

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
420 425 430

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
435 440 445

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
450 455 460

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
465 470 475 480

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
485 490 495

Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly
500 505 510

Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
515 520 525

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
530 535 540

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
545 550 555 560

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
565 570 575

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
580 585 590

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
595 600 605

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
610 615 620

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
625 630 635 640

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
645 650 655

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
660 665 670

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
675 680 685

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
690 695 700

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
705 710 715 720

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
725 730 735

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

Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln
755 760 765

Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys
770 775 780

Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe
785 790 795 800

Lys Arg

<210> 65
 <211> 2436
 <212> ADN
 <213> Secuencia artificial

<220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

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gtgtcctgca aggcttctgg atacagcttc accagttatg atatcaactg ggtgcgacag	180
gccactggac aagggttga gtggatgggg tggatgaacc cgaacagtgg taacacaggc	240
tatgcacaga agttccaggg cagagtcacc atgaccaggg acacctccat aagcacagcc	300
tacatggaac tgagcagcct gagatctgag gacacggccg tgtattactg tgggagagcc	360
ggttactact actacttcgg tatggacgtc tggggccaag ggaccacggt caccgtatcc	420
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gccggtcaga gtgttaccag cagctcctta gcttgggtacc agcagaaacc tggccaggct	600
cccaggctcc tcatttatca gacatccacc agggccactg gcatcccaga caggttcagt	660
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gaactcaaac gagccgtgc cttcgtgcct gtttttctgc ccgcgaaacc cacaactacc	840
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<210> 66

<211> 808

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 66

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
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His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20

25

30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

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

Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly
 65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
 85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Gly Arg Ala Gly Tyr Tyr Tyr Tyr Phe Gly Met
 115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
 145 150 155 160

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
 165 170 175

Leu Ser Cys Arg Ala Gly Gln Ser Val Thr Ser Ser Ser Leu Ala Trp
 180 185 190

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gln Thr
 195 200 205

Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
 210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
 225 230 235 240

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Arg Ala Phe Gly Gln
245 250 255

Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Phe Val Pro Val Phe
260 265 270

Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
275 280 285

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
290 295 300

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
305 310 315 320

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
325 330 335

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Phe
340 345 350

Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
355 360 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
370 375 380

Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385 390 395 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
405 410 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
420 425 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
435 440 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met

450

455

460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
 465 470 475 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 485 490 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg
 500 505 510

Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
 515 520 525

Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met
 530 535 540

Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly
 545 550 555 560

Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu
 565 570 575

Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly
 580 585 590

Ala Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser
 595 600 605

Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val
 610 615 620

Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val
 625 630 635 640

Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys
 645 650 655

Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys
 660 665 670

Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr
675 680 685

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

Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala
705 710 715 720

Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro
725 730 735

Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro
740 745 750

Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr
755 760 765

Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
770 775 780

Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu
785 790 795 800

Val Ala Tyr Ile Ala Phe Lys Arg
805

<210> 67

<211> 2496

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

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gtgtcctgca aggcttctgg atacaccttc accggctact atatgcactg ggtgacgacag 180

gcccctggac aagggttga gtggatggga tggatcaacc ctaatagtgg tggcacaac 240

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tacatggagc tgaacaggct gagatctgac gacacggccg tttattactg tgcgagagga	360
tggctacaga cgtactactt tgacaactgg ggccagggaa ccctggtcac cgtatcctca	420
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tgcctggatt cagtgcatt cagcgatgtt gtctcagcca ccgagccttg caagccttgt	1920
accgaatgtg tgggccttca gtccatgtcc gccccctgtg tcgaagccga tgatgcagtg	1980
tgcagatgtg cctatggata ttaccaggac gaaactaccg ggcgggtgtga ggcctgccgg	2040
gtgtgtgaag ccggctctgg cctcgtgttc agttgccagg ataagcaaaa cacagtatgt	2100
gaggagtgtc cagacggaac ctacagcgac gaggcgaacc acgtcgaccc ttgcttgccg	2160
tgcaccgtct gcgaggatac cgaacgccag ctgagagagt gtacgcgctg ggcagacgct	2220
gagtgcgagg agatccctgg gagatggatc acccgagca cacctcctga gggatcagac	2280
agtacagccc cgagtaccca agaaccggag gcccctccag agcaggacct gatcgcttct	2340
acagttgctg gcgtggtgac gacagtcatg ggatcctcac aaccagtcgt gacgcggggc	2400
acaaccgaca atctgattcc tgtctactgt agcatcttgg cagccgtggt cgtgggcctg	2460
gtagcctaca tcgcctttaa gagatgacct aggtaa	2496

<210> 68

<211> 828

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 68

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
			20					25					30		

Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
		35					40					45			

Thr	Phe	Thr	Gly	Tyr	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln
	50					55					60				

Gly	Leu	Glu	Trp	Met	Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn
65					70				75						80

Ser Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Asn Arg Leu Arg Ser Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Gly Trp Leu Gln Thr Tyr Tyr Phe Asp
115 120 125

Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
145 150 155 160

Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile
165 170 175

Tyr Cys Lys Ser Ser Gln Thr Val Leu Thr Ser Ser Asn Asn Lys Asn
180 185 190

Phe Leu Ala Trp Tyr Gln Gln Lys Leu Gly Gln Pro Pro Lys Leu Leu
195 200 205

Ile Ser Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser
210 215 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
225 230 235 240

Ala Glu Asp Val Ala Ile Tyr Tyr Cys Gln His Tyr Tyr Thr Ser Pro
245 250 255

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala
260 265 270

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

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
290 295 300

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
305 310 315 320

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
325 330 335

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
340 345 350

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
355 360 365

Arg Ser Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr
370 375 380

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
385 390 395 400

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
405 410 415

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
420 425 430

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
435 440 445

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
450 455 460

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
465 470 475 480

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
485 490 495

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
500 505 510

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
515 520 525

Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
530 535 540

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr
545 550 555 560

Gly Arg Ala Met Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu Gly
565 570 575

Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr
580 585 590

His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala
595 600 605

Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser
610 615 620

Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys
625 630 635 640

Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala
645 650 655

Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr
660 665 670

Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu
675 680 685

Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro
690 695 700

Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro
705 710 715 720

Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg
725 730 735

Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg
740 745 750

Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu
755 760 765

Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly
770 775 780

Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly
785 790 795 800

Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val
805 810 815

Val Val Gly Leu Val Ala Tyr Ile Ala Phe Lys Arg
820 825

<210> 69

<211> 2355

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 69

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ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctggggc ctgagtgaag 120

gtgtcctgca aggcttctgg atacaccttc accggctact atatgcactg ggtgcgacag 180

gcccctggac aagggttga gtggatggga tggatcaacc ctaatagtgg tggcacaac 240

tctgcacaga agtttcaggg cagggtcacc atgaccaggg acacgtccat cagtacagcc 300

tacatggagc tgaacaggct gagatctgac gacacggccg tttattactg tgcgagagga 360

tggctacaga cgtactactt tgacaactgg ggccagggaa ccctggtcac cgtatcctca 420

ggaggcggcg gttcaggcgg aggtggctct ggcggtggcg gaagtgacat cgtgatgacc 480

cagtctccag actccctggc tgtgtctctg ggcgagaggg ccaccatcta ctgcaagtcc 540

agccagactg	ttttgaccag	ctccaacaat	aagaacttct	tagcttggtgta	ccaacagaaa	600
ctaggacagc	ctcctaagct	gttcattttcc	tgggcctcta	cccgggaatc	cggggtccct	660
gaccgattca	gtggcagcgg	gtctgggaca	gatttcactc	tcaccatcag	cagcctgcag	720
gctgaagatg	tggcaattta	ttactgtcag	cactattata	ctagtccact	cactttcggc	780
ggcgggacca	aggtggagat	caaacgagcc	gctgcccttg	ataatgaaaa	gtcaaacgga	840
acaatcattc	acgtgaaggg	caagcacctc	tgtccgtcac	ccttgttccc	tgggtccatcc	900
aagccattct	gggtgttggt	cgtagtgggt	ggagtccctcg	cttgttactc	tctgctcgtc	960
accgtggctt	ttataatctt	ctgggttaga	tccaaaagaa	gccgcctgct	ccatagcgat	1020
tacatgaata	tgactccacg	ccgccctggc	cccacaagga	aacactacca	gccttacgca	1080
ccacctagag	atttcgctgc	ctatcggagc	agggtgaagt	tttccagatc	tgcagatgca	1140
ccagcgtatc	agcagggcca	gaaccaactg	tataacgagc	tcaacctggg	acgcagggaa	1200
gagtatgacg	ttttggacaa	gcgcagagga	cgggaccctg	agatgggtgg	caaaccaaga	1260
cgaaaaaacc	cccaggaggg	tctctataat	gagctgcaga	aggataagat	ggctgaagcc	1320
tattctgaaa	taggcatgaa	aggagagcgg	agaaggggaa	aagggcacga	cggtttgtac	1380
cagggactca	gcactgctac	gaaggatact	tatgacgctc	tccacatgca	agccctgcca	1440
cctagggcca	agagaagtgg	cagcggggag	ggccggggat	ctctccttac	atgtggggac	1500
gtggaagaaa	atccggggcc	tatgggtgcc	ggcgccacgg	gaagggttat	ggatggccc	1560
cgactgcttc	tcctgctgtt	gttgggcgtg	tctctcggag	gcgctaagga	ggcctgtcca	1620
acgggcctct	acactcactc	cggtgaatgt	tgcaaagcct	gtaaccttgg	cgagggcgctc	1680
gcacaacctt	gtggtgctaa	ccagacagtc	tgtgaaccat	gcctggattc	agtgcattc	1740
agcgatgttg	tctcagccac	cgagccttgc	aagccttgta	ccgaatgtgt	gggccttcag	1800
tccatgtccg	ccccctgtgt	cgaagccgat	gatgcagtgt	gcagatgtgc	ctatggatat	1860
taccaggacg	aaactaccgg	gcggtgtgag	gcctgccggg	tgtgtgaagc	cggctctggc	1920
ctcgtgttca	gttgccagga	taagcaaaac	acagtatgtg	aggagtgtcc	agacggaacc	1980
tacagcgacg	aggcgaacca	cgtcgaccct	tgcttgccgt	gcaccgtctg	cgaggatacc	2040
gaacgccagc	tgagagagtg	tacgcgctgg	gcagacgctg	agtgcgagga	gatccctggg	2100
agatggatca	cccggagcac	acctcctgag	ggatcagaca	gtacagcccc	gagtacccaa	2160

gaaccggagg cccctccaga gcaggacctg atcgcttcta cagttgctgg cgtggtgacg 2220
acagtcatgg gaccttcaca accagtcgtg acgcggggca caaccgacaa tctgattcct 2280
gtctactgta gcatcttggc agccgtggtc gtgggcctgg tagcctacat cgcctttaag 2340
agatgaccta ggtaa 2355

<210> 70

<211> 781

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 70

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80

Ser Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Asn Arg Leu Arg Ser Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Gly Trp Leu Gln Thr Tyr Tyr Phe Asp
115 120 125

Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
145 150 155 160

Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile
165 170 175

Tyr Cys Lys Ser Ser Gln Thr Val Leu Thr Ser Ser Asn Asn Lys Asn
180 185 190

Phe Leu Ala Trp Tyr Gln Gln Lys Leu Gly Gln Pro Pro Lys Leu Leu
195 200 205

Ile Ser Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser
210 215 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
225 230 235 240

Ala Glu Asp Val Ala Ile Tyr Tyr Cys Gln His Tyr Tyr Thr Ser Pro
245 250 255

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala
260 265 270

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

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
290 295 300

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
305 310 315 320

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
325 330 335

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
340 345 350

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr

355

360

365

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
 370 375 380

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
 385 390 395 400

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
 405 410 415

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
 420 425 430

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
 435 440 445

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
 450 455 460

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
 465 470 475 480

Pro Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
 485 490 495

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala
 500 505 510

Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu
 515 520 525

Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr
 530 535 540

Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val
 545 550 555 560

Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu Asp
 565 570 575

Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro
580 585 590

Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu
595 600 605

Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu
610 615 620

Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly
625 630 635 640

Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys
645 650 655

Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu
660 665 670

Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr
675 680 685

Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr
690 695 700

Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln
705 710 715 720

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

Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr Arg
740 745 750

Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala
755 760 765

Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe Lys Arg
770 775 780

<210> 71

<211> 2373
 <212> ADN
 <213> Secuencia artificial

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

 <400> 71
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 gtgtcctgca aggcttctgg atacaccttc accggctact atatgcactg ggtgcgacag 180
 gcccctggac aagggcttga gtggatggga tggatcaacc ctaatagtgg tggcacaaac 240
 tctgcacaga agtttcaggg cagggtcacc atgaccaggg acacgtccat cagtacagcc 300
 tacatggagc tgaacaggct gagatctgac gacacggccg tttattactg tgcgagagga 360
 tggctacaga cgtactactt tgacaactgg ggccaggga ccctgggtcac cgtatcctca 420
 ggaggcggcg gttcaggcgg aggtggctct ggcggtggcg gaagtgacat cgtgatgacc 480
 cagtctccag actccctggc tgtgtctctg ggcgagaggg ccaccatcta ctgcaagtcc 540
 agccagactg ttttgaccag ctccaacaat aagaacttct tagcttggta ccaacagaaa 600
 ctaggacagc ctcctaagct gtcattttcc tgggcctcta cccgggaatc cggggtcctt 660
 gaccgattca gtggcagcgg gtctgggaca gatttcactc tcaccatcag cagcctgcag 720
 gctgaagatg tggcaattta ttactgtcag cactattata ctagtccact cactttcggc 780
 ggcgggacca aggtggagat caaacgagcc gctgcccttg ataataaaaa gtcaaacgga 840
 acaatcattc acgtgaaggg caagcacctc tgtccgtcac cttgtttccc tgggtccatcc 900
 aagccattct ggggtgttggc cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960
 accgtggctt ttataatctt ctgggttcgc ttttccgtcg ttaagcgggg gagaaaaaag 1020
 ctgctgtaca ttttcaaaca gccgtttatg aggccggtcc aaacgactca ggaagaggac 1080
 ggctgctcct gccgctttcc tgaggaggag gagggcgggt gcgaactgag ggtgaagttt 1140
 tccagatctg cagatgcacc agcgtatcag cagggccaga accaactgta taacgagctc 1200
 aacctgggac gcagggaaga gtatgacgtt ttggacaagc gcagaggacg ggaccctgag 1260
 atgggtggca aaccaagacg aaaaaacccc caggagggtc tctataatga gctgcagaag 1320
 gataagatgg ctgaagccta ttctgaaata ggcatgaaag gagagcggag aaggggaaaa 1380

gggcacgacg gtttgtacca gggactcagc actgctacga aggatactta tgacgctctc	1440
cacatgcaag ccctgccacc tagggccaag agaagtggca gcggggaggg ccgggggatct	1500
ctccttacat gtggggacgt ggaagaaaat ccggggccta tgggtgccgg cgccacggga	1560
agggctatgg atggcccgcg actgcttctc ctgctgttgt tgggcgtgtc tctcggaggc	1620
gctaaggagg cctgtccaac gggcctctac actcactccg gtgaatgttg caaagcctgt	1680
aaccttggcg agggcgctgc acaaccttgt ggtgctaacc agacagtctg tgaacctatgc	1740
ctggattcag tgacattcag cgatgttgtc tcagccaccg agccttgcaa gccttgtacc	1800
gaatgtgtgg gccttcagtc catgtccgcc ccctgtgtcg aagccgatga tgcagtgtgc	1860
agatgtgcct atggatatta ccaggacgaa actaccgggc ggtgtgaggc ctgccgggtg	1920
tgtgaagccg gctctggcct cgtgttcagt tgccaggata agcaaaacac agtatgtgag	1980
gagtgtccag acggaaccta cagcgacgag gcgaaccacg tcgacccttg cttgccgtgc	2040
accgtctgcg aggataccga acgccagctg agagagtgtg cgcgctgggc agacgctgag	2100
tgcgaggaga tccctgggag atggatcacc cggagcacac ctcctgaggg atcagacagt	2160
acagccccga gtaccaaga accggaggcc cctccagagc aggacctgat cgcttctaca	2220
gttgctggcg tggtgacgac agtcatggga tcctcacaac cagtcgtgac gcggggcaca	2280
accgacaatc tgattcctgt ctactgtagc atcttggcag ccgtggtcgt gggcctggta	2340
gcctacatcg cctttaagag atgacctagg taa	2373

<210> 72

<211> 787

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 72

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
			20					25					30		

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80

Ser Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Asn Arg Leu Arg Ser Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Gly Trp Leu Gln Thr Tyr Tyr Phe Asp
115 120 125

Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
145 150 155 160

Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile
165 170 175

Tyr Cys Lys Ser Ser Gln Thr Val Leu Thr Ser Ser Asn Asn Lys Asn
180 185 190

Phe Leu Ala Trp Tyr Gln Gln Lys Leu Gly Gln Pro Pro Lys Leu Leu
195 200 205

Ile Ser Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser
210 215 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
225 230 235 240

Ala Glu Asp Val Ala Ile Tyr Tyr Cys Gln His Tyr Tyr Thr Ser Pro
245 250 255

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala
260 265 270

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

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
290 295 300

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
305 310 315 320

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Phe Ser Val Val Lys Arg
325 330 335

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
340 345 350

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
355 360 365

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
370 375 380

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
385 390 395 400

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
405 410 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
420 425 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
435 440 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
450 455 460

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

His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser Gly Ser Gly Glu
485 490 495

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

Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu
515 520 525

Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala
530 535 540

Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys
545 550 555 560

Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val
565 570 575

Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala
580 585 590

Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met
595 600 605

Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr
610 615 620

Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val
625 630 635 640

Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn
645 650 655

Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn
660 665 670

His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg
675 680 685

Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile
690 695 700

Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser
705 710 715 720

Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu
725 730 735

Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser
740 745 750

Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr
755 760 765

Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala
770 775 780

Phe Lys Arg
785

<210> 73

<211> 2433

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 73

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctggggc ctcagtgaag 120

gtgtcctgca aggcttctgg atacaccttc accggctact atatgcactg ggtgacgacag 180

gcccctggac aagggttga gtggatggga tggatcaacc ctaatagtgg tggcacaac 240

tctgcacaga agtttcaggg cagggtcacc atgaccaggg acacgtccat cagtacagcc 300

tacatggagc tgaacaggct gagatctgac gacacggccg tttattactg tgcgagagga 360

tggctacaga cgtactactt tgacaactgg ggccaggga ccctgggtcac cgtatcctca 420

ggaggcggcg gttcaggcgg aggtggctct ggcggtggcg gaagtgacat cgtgatgacc	480
cagtctccag actccctggc tgtgtctctg ggcgagaggg ccaccatcta ctgcaagtcc	540
agccagactg ttttgaccag ctccaacaat aagaacttct tagcttggtta ccaacagaaa	600
ctaggacagc ctcctaagct gctcatttcc tgggcctcta cccgggaatc cggggtcctt	660
gaccgattca gtggcagcgg gtctgggaca gatttcactc tcaccatcag cagcctgcag	720
gctgaagatg tggcaattta ttactgtcag cactattata ctagtccact cactttcggc	780
ggcgggacca aggtggagat caaacgagcc gctgccttcg tgcctgtttt tctgcccgcg	840
aaaccacaa ctacccccgc ccctcgggcc ccaactcctg caccaactat cgcttcccaa	900
cccctgtctc tgagacctga ggcatgccgc cccgcggcag gcggcgccgt gcacactaga	960
ggcctggact tcgcctgcga tatttatatc tgggcccccc ttgccgggac atgcggggta	1020
ctgctgctgt ctctggtgat taccctctac tgcaaccaca gaaacagatc caaaagaagc	1080
cgcttgctcc atagcgatta catgaatatg actccacgcc gccctggccc cacaaggaaa	1140
cactaccagc cttacgcacc acctagagat ttcgctgcct atcgagcag ggtgaagttt	1200
tccagatctg cagatgcacc agcgtatcag cagggccaga accaactgta taacgagctc	1260
aacctgggac gcagggaaga gtatgacgtt ttggacaagc gcagaggacg ggacctgag	1320
atgggtggca aaccaagacg aaaaaacccc caggagggtc tctataatga gctgcagaag	1380
gataagatgg ctgaagccta ttctgaaata ggcatgaaag gagagcggag aaggggaaaa	1440
gggcacgacg gtttgtacca gggactcagc actgctacga aggatactta tgacgctctc	1500
cacatgcaag ccctgccacc tagggccaag agaagtggca gcggggaggg ccggggatct	1560
ctccttacat gtggggacgt ggaagaaaat ccggggccta tgggtgccgg cgccacggga	1620
agggctatgg atggcccgcg actgcttctc ctgctgttgt tggcggtgc tctcggaggc	1680
gctaaggagg cctgtccaac gggcctctac actcactccg gtgaatgttg caaagcctgt	1740
aaccttggcg agggcgctgc acaaccttgt ggtgctaacc agacagtctg tgaacctatgc	1800
ctggattcag tgacattcag cgatgttgtc tcagccaccg agccttgcaa gccttgtaacc	1860
gaatgtgtgg gccttcagtc catgtccgcc ccctgtgtcg aagccgatga tgcagtgtgc	1920
agatgtgcct atggatatta ccaggacgaa actaccgggc ggtgtgaggc ctgccgggtg	1980
tgtgaagccg gctctggcct cgtgttcagt tgccaggata agcaaaacac agtatgtgag	2040

gagtgtccag acggaaccta cagcgacgag gcgaaccacg tcgacccttg cttgccgtgc 2100
accgtctgcg aggataccga acgccagctg agagagtgtg cgcgctgggc agacgctgag 2160
tgcgaggaga tccctgggag atggatcacc cggagcacac ctcctgaggg atcagacagt 2220
acagccccga gtaccaaga accggaggcc cctccagagc aggacctgat cgcttctaca 2280
gttgctggcg tggtgacgac agtcatggga tcctcacaac cagtcgtgac gcggggcaca 2340
accgacaatc tgattcctgt ctactgtagc atcttggcag ccgtggtcgt gggcctggta 2400
gcctacatcg cttttaagag atgacctagg taa 2433

<210> 74

<211> 807

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 74

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80

Ser Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Asn Arg Leu Arg Ser Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Gly Trp Leu Gln Thr Tyr Tyr Phe Asp

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

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
340 345 350

His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
355 360 365

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
370 375 380

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
385 390 395 400

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
405 410 415

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
420 425 430

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
435 440 445

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
450 455 460

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
465 470 475 480

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
485 490 495

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser
500 505 510

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
515 520 525

Glu Asn Pro Gly Pro Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp
530 535 540

Gly Pro Arg Leu Leu Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly

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

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu
770 775 780

Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val
785 790 795 800

Ala Tyr Ile Ala Phe Lys Arg
805

<210> 75

<211> 2451

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético

<400> 75

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ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctggggc ctcaagtgaag	120
gtgtcctgca aggcttctgg atacaccttc accggctact atatgcactg ggtgacgacag	180
gcccctggac aagggcttga gtggatggga tggatcaacc ctaatagtgg tggcacaaaac	240
tctgcacaga agtttcaggg caggggtcacc atgaccaggg acacgtccat cagtacagcc	300
tacatggagc tgaacaggct gagatctgac gacacggccg tttattactg tgcgagagga	360
tggctacaga cgtactactt tgacaactgg ggccagggaa ccctgggtcac cgtatcctca	420
ggaggcggcg gttcaggcgg aggtggctct ggcggtggcg gaagtgacat cgtgatgacc	480
cagtctccag actccctggc tgtgtctctg ggcgagaggg ccaccatcta ctgcaagtcc	540
agccagactg ttttgaccag ctccaacaat aagaacttct tagcttggta ccaacagaaa	600
ctaggacagc ctcctaagct gtcattttcc tgggcctcta cccgggaatc cggggtcctt	660
gaccgattca gtggcagcgg gtctgggaca gatttcactc tcaccatcag cagcctgcag	720
gctgaagatg tggcaattta ttactgtcag cactattata ctagtccact cactttcggc	780
ggcgggacca aggtggagat caaacgagcc gctgccttcg tgccgtgttt tctgcccgcg	840
aaaccacaaa ctacccccgc ccctcgcccc ccaactcctg caccaactat cgcttcccaa	900
cccctgtctc tgagacctga ggcatgccgc cccgcggcag gcggcgccgt gcacactaga	960

ggcctggact	tcgcctgcga	tatttatatc	tgggcccccc	ttgccgggac	atgcggggta	1020
ctgctgctgt	ctctgggtgat	taccctctac	tgcaaccaca	gaaaccgctt	ttccgtcgtt	1080
aagcggggga	gaaaaaagct	gctgtacatt	ttcaaacagc	cgtttatgag	gccgggtcaa	1140
acgactcagg	aagaggacgg	ctgctcctgc	cgctttcctg	aggaggagga	gggcgggtgc	1200
gaactgaggg	tgaagttttc	cagatctgca	gatgcaccag	cgtatcagca	gggccagaac	1260
caactgtata	acgagctcaa	cctgggacgc	agggaagagt	atgacgtttt	ggacaagcgc	1320
agaggacggg	accctgagat	gggtggcaaa	ccaagacgaa	aaaaccccca	ggagggtctc	1380
tataatgagc	tgcaagaagga	taagatggct	gaagcctatt	ctgaaatagg	catgaaagga	1440
gagcggagaa	ggggaaaagg	gcacgacggt	ttgtaccagg	gactcagcac	tgctacgaag	1500
gatacttatg	acgctctcca	catgcaagcc	ctgccaccta	gggccaagag	aagtggcagc	1560
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gaatgttgca	aagcctgtaa	ccttggcgag	ggcgtcgcac	aaccttgtgg	tgctaaccag	1800
acagtctgtg	aaccatgcct	ggattcagtg	acattcagcg	atgttgtctc	agccaccgag	1860
ccttgcaagc	cttgtaccga	atgtgtgggc	cttcagtcca	tgtccgcccc	ctgtgtcgaa	1920
gccgatgatg	cagtgtgcag	atgtgcctat	ggatattacc	aggacgaaac	taccgggcgg	1980
tgtgaggcct	gccgggtgtg	tgaagccggc	tctggcctcg	tgttcagttg	ccaggataag	2040
caaaacacag	tatgtgagga	gtgtccagac	ggaacctaca	gcgacgaggc	gaaccacgtc	2100
gacccttgct	tgccgtgcac	cgtctgcgag	gataccgaac	gccagctgag	agagtgtacg	2160
cgctgggcag	acgctgagtg	cgaggagatc	cctgggagat	ggatcacccg	gagcacacct	2220
cctgagggat	cagacagtac	agccccgagt	acccaagaac	cggaggcccc	tccagagcag	2280
gacctgatcg	cttctacagt	tgctggcgtg	gtgacgacag	tcatgggatc	ctcacaacca	2340
gtcgtgacgc	ggggcacaac	cgacaatctg	attcctgtct	actgtagcat	cttggcagcc	2400
gtggtcgtgg	gcctggtagc	ctacatcgcc	tttaagagat	gacctaggta	a	2451

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 76

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80

Ser Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Asn Arg Leu Arg Ser Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Gly Trp Leu Gln Thr Tyr Tyr Phe Asp
115 120 125

Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
145 150 155 160

Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile
165 170 175

Tyr Cys Lys Ser Ser Gln Thr Val Leu Thr Ser Ser Asn Asn Lys Asn
180 185 190

Phe Leu Ala Trp Tyr Gln Gln Lys Leu Gly Gln Pro Pro Lys Leu Leu
195 200 205

Ile Ser Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser
210 215 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
225 230 235 240

Ala Glu Asp Val Ala Ile Tyr Tyr Cys Gln His Tyr Tyr Thr Ser Pro
245 250 255

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala
260 265 270

Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro
275 280 285

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
290 295 300

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
305 310 315 320

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
325 330 335

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
340 345 350

His Arg Asn Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu
355 360 365

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
370 375 380

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
385 390 395 400

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
405 410 415

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
420 425 430

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
435 440 445

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
450 455 460

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

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
485 490 495

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
500 505 510

Pro Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
515 520 525

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ala Gly Ala
530 535 540

Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu Leu Leu Leu Leu
545 550 555 560

Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr
565 570 575

Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly Val
580 585 590

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

Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys Pro
610 615 620

Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu
625 630 635 640

Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu
645 650 655

Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly
660 665 670

Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys
675 680 685

Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu
690 695 700

Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr
705 710 715 720

Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr
725 730 735

Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln
740 745 750

Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala
755 760 765

Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr Arg
770 775 780

Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala
785 790 795 800

Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe Lys Arg
805 810

<210> 77

<211> 339

<212> PRT

<213> Homo sapiens

<400> 77

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met
1 5 10 15

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
20 25 30

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

Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
50 55 60

Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
65 70 75 80

Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
85 90 95

Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
100 105 110

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

Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly
130 135 140

Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
145 150 155 160

Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala
165 170 175

Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
180 185 190

Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
195 200 205

Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
210 215 220

Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
225 230 235 240

Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
245 250 255

Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe
260 265 270

Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro
275 280 285

Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe
290 295 300

Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile
305 310 315 320

Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys
325 330 335

Ser Gln Leu

<210> 78

<211> 63

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Oligonucleótido sintético"

<400> 78

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccg 63

<210> 79

<211> 21

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 79

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro
			20	

<210> 80

<211> 45

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Oligonucleótido sintético"

<400> 80

ggcgggtggag gctccggagg ggggggctct ggcggagggg gctcc 45

<210> 81

<211> 15

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 81

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

<210> 82

<211> 54

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Oligonucleótido sintético"

<400> 82

gggtctacat ccggctccgg gaagcccgga agtggcgaag gtagtacaaa gggg 54

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

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 83
 Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
 1 5 10 15

Lys Gly

<210> 84
 <211> 126
 <212> ADN
 <213> Desconocido

 <220>
 <221> fuente
 <223> /nota= "Descripción de lo desconocido: Secuencia de 4-1BB"

<400> 84
 aagcgcggca ggaagaagct cctctacatt tttaagcagc cttttatgag gcccgtacag 60
 acaacacagg aggaagatgg ctgtagctgc agatttcccg aggaggagga aggtgggtgc 120
 gagctg 126

<210> 85
 <211> 42
 <212> PRT
 <213> Desconocido

 <220>
 <221> fuente
 <223> /nota= "Descripción de lo desconocido: Secuencia de 4-1BB"

<400> 85
 Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 1 5 10 15

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

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 86
<211> 37
<212> PRT
<213> Desconocido

<220>
<221> fuente
<223> /nota= "Descripción de lo desconocido: Secuencia de 0X40"

<400> 86
Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
1 5 10 15

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
20 25 30

Thr Leu Ala Lys Ile
35

<210> 87
<211> 363
<212> ADN
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 87
caggttcagc tgcagcagtc tggagctgag atgatgaagc ctggggcctc agtgaagata 60
tcctgcaagg ctactggcta cacattcagc acctactgga tagagtgggt aaagcagagg 120
cctggacatg gccttgagtg gattggagag attttacctg gaagtggtaa tactgacttc 180
aatgagaagt tcaagggcaa ggccacattc actgcagata catcctccga cacagcctac 240
atgcatctca gcagcctgac atctgaggac tctgccgtct attactgtac aagatggggg 300
tactacggta ctagggggta cttcaatgtc tggggcgag ggtccacggg caccgtctcc 360
tca 363

<210> 88
<211> 121
<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 88

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Thr Tyr
20 25 30

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

Gly Glu Ile Leu Pro Gly Ser Gly Asn Thr Asp Phe Asn Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Phe Thr Ala Asp Thr Ser Ser Asp Thr Ala Tyr
65 70 75 80

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

Thr Arg Trp Gly Tyr Tyr Gly Thr Arg Gly Tyr Phe Asn Val Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 89

<211> 5

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 89

Thr Tyr Trp Ile Glu
1 5

<210> 90

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

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

 <400> 90
 Glu Ile Leu Pro Gly Ser Gly Asn Thr Asp Phe Asn Glu Lys Phe Gln
 1 5 10 15

Gly

<210> 91
 <211> 12
 <212> PRT
 <213> Secuencia artificial

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

 <400> 91
 Trp Gly Tyr Tyr Gly Thr Arg Gly Tyr Phe Asn Val
 1 5 10

<210> 92
 <211> 318
 <212> ADN
 <213> Secuencia artificial

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

 <400> 92
 caaattgttc tcaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
 ataacgtgca gtgccagctc aagtgttaagt tacatgcact ggttccagca gaagccaggc 120
 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctttac tctctcaca tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg cgtagtttcc cgtacacgtt cggagggggg 300
 accaagctgg aaattaaa 318

<210> 93
<211> 106
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

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

Ser Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

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

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 94
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 94
Arg Ala Ser Ser Ser Val Ser Tyr Met His
1 5 10

<210> 95
<211> 7

<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 95
Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 96
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 96
Gln Gln Arg Arg Ser Phe Pro Tyr Thr
1 5

<210> 97
<211> 363
<212> ADN
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 97
cagatccagt tgggtgcagtc tggacctgaa ctgaagaagc ctggagagac agtcaagatc 60
tcctgcaagg cttctggata taccttcaca aactatggaa tgaactgggt gaagcaggct 120
ccaggaaagg gtttacagtg gatgggctgg atgaacactt atactggaga gccaacatat 180
gctgatgact tcaagggacg gtttgccttc tctttggaaa cctctgccag aactgtctct 240
ttggacatca acgacctcaa aaatgaggac acggctacat atttctgtac aagagcaggg 300
ggacaactca ggcccggggc tatggactac tgggggtcaag gaacctcagt caccgtctcc 360
tca 363

<210> 98
<211> 119
<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 98

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

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

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

Met Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Lys Phe Gln Gly
50 55 60

Arg Val Thr Phe Thr Leu Asp Thr Ser Ala Arg Thr Val Tyr Met Glu
65 70 75 80

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg
85 90 95

Ala Gly Gly Gln Leu Arg Pro Gly Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser
115

<210> 99

<211> 5

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 99

Asn Tyr Gly Met Asn
1 5

<210> 100

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

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

 <400> 100
 Trp Met Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Lys Phe Gln
 1 5 10 15

Gly

<210> 101
 <211> 12
 <212> PRT
 <213> Secuencia artificial

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

 <400> 101
 Ala Gly Gly Gln Leu Arg Pro Gly Ala Met Asp Tyr
 1 5 10

<210> 102
 <211> 333
 <212> ADN
 <213> Secuencia artificial

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

 <400> 102
 gacattgtgc tgaccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
 atctcctgca aggccagcca aagtgttgat tatgatgggtg atagttttat gaactggtac 120
 caacagaaac caggacagcc acccaaactc ctcatctatg ttgcatccaa tctagaatct 180
 gggatcccag acaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
 cctgtggagg aggaggatgc tgcaacctat tattgtcagc aaagtaatga ggaacctccg 300
 acgttcggtg gaggcaccaa gctggaaatc aaa 333

<210> 103
 <211> 111
 <212> PRT
 <213> Secuencia artificial

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 103
 Asp Ile Val Leu Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Phe Met Asn Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Gln Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
 50 55 60

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

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

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

<210> 104
 <211> 15
 <212> PRT
 <213> Secuencia artificial

 <220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 104
 Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Phe Met Asn
 1 5 10 15

<210> 105
 <211> 7

<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 105
Val Ala Ser Asn Leu Glu Ser
1 5

<210> 106
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 106
Gln Gln Ser Asn Glu Glu Pro Pro Thr
1 5

<210> 107
<211> 360
<212> ADN
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 107
cagatacaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgtag cgtctggatt caccttcaag aactatggca tgactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atttggtatg atggaagtaa tgaatactat 180
ggagaccccg tgaagggccg attcaccatc tccagagaca actccaagaa catgttgat 240
ctgcaaatga acagcctgag agccgatgac acggctgtgt attactgtgc gaggtcggga 300
atagcagtgg ctggggcctt tgactactgg ggccaggga ccctggtcac cgtctcctca 360

<210> 108
<211> 121
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 108

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

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

Gly Glu Ile Asn Pro Ser Ser Gly Arg Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Thr Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

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

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 109
<211> 5
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 109

Thr Tyr Trp Met His
1 5

<210> 110
<211> 17
<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 110

Glu	Ile	Asn	Pro	Ser	Ser	Gly	Arg	Thr	Asn	Tyr	Asn	Glu	Lys	Phe	Lys
1				5				10					15		

Thr

<210> 111

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 111

Leu	Gly	Pro	Gly	Pro	Gln	Tyr	Tyr	Ala	Met	Asp	Tyr
1				5				10			

<210> 112

<211> 327

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 112

gaaattgtgt	tgacgcagtc	tccagacacc	ctgtctttgt	ctccagggga	aaaagccacc	60
ctctcctgca	gggccagtc	gagtgttagc	agcagcttct	tggcctggta	ccagcagaaa	120
cctggacagg	ctcccagtct	cctcatctat	gttgcattca	gaagggccgc	tggcatccct	180
gacaggttca	gtggcagtg	gtctgggaca	gacttcactc	tcaccatcag	cagactggag	240
cctgaagatt	ttggaatgtt	ttactgtcaa	cactatggta	ggacaccatt	cactttcggc	300
cctgggacca	aagtggatat	caaacga				327

<210> 113

<211> 107

<212> PRT
<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 113

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

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

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

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

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

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

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105		

<210> 114

<211> 11

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 114

His	Ala	Ser	Gln	Asn	Ile	Asn	Val	Trp	Leu	Ser
1				5				10		

<210> 115

<211> 7

<212> PRT

<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 115
Lys Ala Ser Lys Leu His Thr
1 5

<210> 116
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 116
Gln Gln Gly Gln Ser Tyr Pro Trp Thr
1 5

<210> 117
<211> 357
<212> ADN
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 117
caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc ggctactata tacactgggt gcgacaggcc 120
cctgaacaag ggcttgagtg gatgggatgg atcaacccta acagtgggtg cacaaactat 180
gcacagaagt ttcagggcag ggtcaccatg gccagggaca cgtccatcag cacagtttac 240
atggacctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagaatacgc 300
ggtggtaact cggtctttga ctactggggc caggaaccc tggtcaccgt ctctca 357

<210> 118
<211> 120
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 118

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

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

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Gly Arg Ala Gly Tyr Tyr Tyr Tyr Phe Gly Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 119

<211> 5

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 119

Ser Tyr Asp Ile Asn
1 5

<210> 120

<211> 17

<212> PRT

<213> Secuencia artificial

<220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 120
 Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 121
 <211> 11
 <212> PRT
 <213> Secuencia artificial

<220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 121
 Ala Gly Tyr Tyr Tyr Tyr Phe Gly Met Asp Val
 1 5 10

<210> 122
 <211> 342
 <212> ADN
 <213> Secuencia artificial

<220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 122
 gacatcgtga tgaccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
 atcaactgca agtccacca gagtatttta tacacctcca acaataagaa cttcttagct 120
 tgggtaccagc agaaaccagg gcagcctcct aaactgctca tttcctgggc atctatccgg 180
 gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cgctctcacc 240
 atcagcagcc tgcaggctga agatgtggca gtttattact gtcaacaata ttttagtact 300
 atgttcagtt ttggccaggg gaccaagctg gagatcaaac ga 342

<210> 123
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 123

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

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

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Arg
85 90 95

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

<210> 124

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 124

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

<210> 125

<211> 7

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 125
Gln Thr Ser Thr Arg Ala Thr
1 5

<210> 126
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 126
Gln Gln Tyr Gly Gly Ser Arg Ser
1 5

<210> 127
<211> 360
<212> ADN
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 127
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt agtggtgcat actactggac ttggatccgc 120
cagcaccag ggaagggcct ggagtggatt gggtagatcc attacagtgg gagcacctac 180
tccaaccgt ccctcaagag tcgaattacc atatcgtag acacgtctaa gaaccagttc 240
tccctgaagc tgaactctgt gactgccgag gacacggcag tgtattactg tgcgagacaa 300
gaggactacg gtggtttgtt tgactactgg ggccaggga ccctgggtcac cgtttcctca 360

<210> 128
<211> 120
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 128

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

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

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Gly Arg Ala Gly Tyr Tyr Tyr Tyr Phe Gly Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 129

<211> 5

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 129

Ser Tyr Asp Ile Asn
1 5

<210> 130

<211> 17

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 130

Trp	Met	Asn	Pro	Asn	Ser	Gly	Asn	Thr	Gly	Tyr	Ala	Gln	Lys	Phe	Gln
1				5				10					15		

Gly

<210> 131

<211> 11

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 131

Ala	Gly	Tyr	Tyr	Tyr	Tyr	Phe	Gly	Met	Asp	Val
1				5				10		

<210> 132

<211> 324

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 132

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ctctcctgca gggccagtca gagtgttacc accgacttag cctggtacca gcagatgcct 120

ggacaggctc cccggctcct catctatgat gcttccacca gggccactgg tttcccagcc 180

agattcagtg gcagtgggtc tgggacagac ttcacgctca ccatcagcag cctgcaggct 240

gaagattttg cagtttatta ctgtcaacat tataaaacct ggcctctcac tttcggcgga 300

gggactaagg tggagatcaa acga 324

<210> 133

<211> 108

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 133

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

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

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Arg
85 90 95

Ala Phe Gly Gln Gly Thr Lys Val Glu Leu Lys Arg
100 105

<210> 134

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 134

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

<210> 135

<211> 7

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 135
Gln Thr Ser Thr Arg Ala Thr
1 5

<210> 136
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 136
Gln Gln Tyr Gly Gly Ser Arg Ala
1 5

<210> 137
<211> 360
<212> ADN
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 137
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acctgcactg tctctggtgg ctccatcagt agtggtgcat actactggac ttggatccgc 120
cagcaccag ggaagggcct ggagtggatt gggatcatcc attacagtgg gagcacctac 180
tccaaccggt ccctcaagag tcgaattacc atatcgttag acacgtctaa gaaccagttc 240
tccctgaagc tgaactctgt gactgccgcg gacacggccg tgtattactg tgcgagacaa 300
gaggactacg gtggtttgtt tgactactgg ggccagggaa ccctgggtcac cgtttcctca 360

<210> 138
<211> 119
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 138
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

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

<210> 139
 <211> 5
 <212> PRT
 <213> Secuencia artificial

<220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 139
 Gly Tyr Tyr Met His
 1 5

<210> 140
 <211> 17
 <212> PRT
 <213> Secuencia artificial

<220>
 <221> fuente
 <223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 140

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

Gly

<210> 141

<211> 10

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 141

Gly Trp Leu Gln Thr Tyr Tyr Phe Asp Asn
1 5 10

<210> 142

<211> 324

<212> ADN

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 142

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ggacaggctc cccggctcct catctatgat gcttccacca gggccactgg tttcccagcc 180
agattcagtg gcagtgggtc tgggacagac ttcacgtca ccatcagcag cctgcaggct 240
gaagattttg cagtttatta ctgtcaacat tataaaacct ggcctctcac tttcggcgga 300
gggactaagg tggagatcaa acga 324

<210> 143

<211> 114

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Polipéptido sintético"

<400> 143

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

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

Ser Asn Asn Lys Asn Phe Leu Ala Trp Tyr Gln Gln Lys Leu Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Ser Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Ile Tyr Tyr Cys Gln His
85 90 95

Tyr Tyr Thr Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg

<210> 144

<211> 13

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente

<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 144

Thr Val Leu Thr Ser Ser Asn Asn Lys Asn Phe Leu Ala
1 5 10

<210> 145

<211> 7

<212> PRT

<213> Secuencia artificial

<220>

<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 145
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 146
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Péptido sintético"

<400> 146
Gln His Tyr Tyr Thr Ser Pro Leu Thr
1 5

<210> 147
<211> 6762
<212> ADN
<213> Secuencia artificial

<220>
<221> fuente
<223> /nota="Descripción de la Secuencia Artificial: Polinucleótido sintético"

<400> 147
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ccacgttcgc cggctttccc cgtcaagctc taaatcgggg gctcccttta gggttccgat 180
ttagtgcttt acggcacctc gacccccaaa aacttgatta gggatgatgtg tcacgtatgtg 240
ggccatcgcc ctgatagacg gtttttcgcc ctttgacgtt ggagtccacg ttctttaata 300
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ttaacgcgaa ttttaacaaa atattaacgc ttacaatttg ccattcgcca ttcaggctgc 480
gcaactgttg ggaagggcga tcggtgcggg cctcttcgct attacgccag ctggcgaaag 540
ggggatgtgc tgcaaggcga ttaagttggg taacgccagg gttttcccag tcacgacgtt 600
gtaaaacgac ggccagtga tttgtaatac actcactata gggcgacccg gggatggcgc 660

gccagtaatc aattacgggg tcattagttc atagcccata tatggagttc cgcgttacat	720
aacttacggt aaatggcccc cctggctgac cgcccaacga ccccgccca ttgacgtcaa	780
taatgacgta tgttcccata gtaacgcaa tagggacttt ccattgacgt caatgggtgg	840
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