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<110> REG Life Sciences, LLC

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<170> PatentIn versión 3.5

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<213> *Marinobacter aquaeolei*

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Leu Glu Asp Ile Asp Val Ser Asn Pro Phe Leu Tyr Arg Gln Gly Gln
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Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
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 ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcgaat 2340
 cgtcagatga tgacttgctg cagtcgtgca tgcggtgac gtctggcgct gcgcctctaa 2400

<210> 8

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 8

Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
1 5 10 15

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

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
50 55 60

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
 100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
 115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Val Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
 180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
 705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
 740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
 755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
 770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
 785 790 795

<210> 9

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido
 Sintético

<400> 9

atgccaacac tgcccagaac atttgacgac attcagtccc gactgattaa cgccacctcc	60
aggggtggtgc cgatgcagag gcaaattcag ggactgaaat tcttaatgag cgccaagagg	120
aagaccttcg gccacgccc accgatgccc gaattcggtg aaacacccat cccggacgtt	180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag	240
tgggacgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc	300
cctttcggcc ccttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcggtg accctccgga ggggctgtcg	420
gtggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgac acgcaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaag	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggt gcagcatcgg ccaccggcgg ggagtttgcc	720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccg gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggcaacgat acgacgcgca actcgatgag tgggtggcctg	960
gtggccatga acgaattccc cagggaattt gaaaaattga aggcaaaacc ggagttgatt	1020
ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaagcagg atgtcgaact gggcggccag accatcaaga aggggtgatcg agttgtcatg	1140
tggtagcgt cggttaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt	1200

gatcgcaagg acgcacgaaa ccacatgtcg ttcggctatg gggttcaccg ttgcatgggc 1260
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aacatcgaag tcgtcgaaga gcccagacgg gtgcagtcca acttcgtgcg gggctattcc 1380
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ggcgctccgg atgctccgta gtacgaaatc gccgtgact tagatccgga aagccgtggg 1680
ggaagccgct atattcatga acagctggaa gttggaagtc cgctgcgtat gcgtggccca 1740
cgcaaccatt tcgccctgga tccgggtgcg gaacattacg tgtttggtgc cgggggtatc 1800
ggcatcacgc cggtgctggc aatggcggat catgcccgtg cgcgtggttg gtcgtacgaa 1860
ctgcattatt gtggtcgtaa tcgtagcggg atggcttacc tggaacgcgt cgcgggacat 1920
ggtgaccgcg ctgccttgca cgtatctgaa gaaggcacc gcattgatct ggcggcatta 1980
cttgctgaac cggcgccggg cgtgcaaata tacgcctgcg gtccgggccg tttattagcg 2040
ggtcttgaag acgcgtctcg taattggccg gatggcgcgc ttcattgtga gcatttact 2100
tcgagtttag ccgctttgga tccggatgta gaacatgcct ttgatttgga gctgcgtgac 2160
tctggcctta ccgttcgcgt cgagccaact cagaccgttt tagacgcttt gcgtgcgaac 2220
aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt 2280
ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcaat 2340
cgtcagatga tgacttgctg cagtcgtgca tgcggtgatc gtctggcgct gcgcctctaa 2400

<210> 10

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 10

Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
1 5 10 15

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

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
 35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
 50 55 60

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

Trp Asp Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
 85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
 100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
 115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Val Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
 180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
785 790 795

<210> 11

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido Sintético

<400> 11

atgccaacac tgcccagaac atttgacgac attcagtccc gactgattaa cgccacctcc	60
aggggtggtgc cgatgcagag gcaaattcag ggactgaaat tcttaatgag cgccaagagg	120
aagaccttcg gccacgccg accgatgccc gaattcggtg aaacacccat cccggacgtt	180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag	240
tggcgcgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc	300
cctttcggcc ctttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcgggtg accctccgga ggggctgtcg	420
atcgaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgatc acgcaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaag	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggt gcagcatcgg ccaccggcgg ggagtttgcc	720

gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccg gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggcaacgat acgacgcgca actcgatgag tgggtggcctg	960
gtggccatga acgaattccc cagggaattt gaaaaattga aggcaaaacc ggagttgatt	1020
ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaagcagg atgtcgaact gggcggccag accatcaaga agggatgatcg agttgtcatg	1140
tgggtacgct cgggtaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt	1200
gatcgcaagg acgcacgaaa ccacatgtcg ttcggctatg gggttcaccg ttgcatgggc	1260
aaccgtctgg ctgaactgca actgcgcata ctctgggaag aaataactca gcgttttgac	1320
aacatcgaag tcgtcgaaga gcccagcgg gtgcagtcca acttcgtgcg gggctattcc	1380
aggttgatgg tcaaactgac accgaacagt gtactccatc gtcataacc tgtcaccatc	1440
ggcgagccgg ccgctcgtgc tgtgagccgc acggtgaccg ttgagcgtct tgatcgcatt	1500
gccgacgatg tccttcgcct ggtccttcgc gatgctggag gtaaaaccct cccgacgtgg	1560
acgcctggcg ctacatcga cctggatctg ggtgctctga gccgtcagta ttcgctctgc	1620
ggcgctccgg atgtccgtc gtacgaaatc gccgtgcact tagatccgga aagccgtggt	1680
ggaagccgct atattcatga acagctggaa gttggaagtc cgctgcgtat gcgtggccca	1740
cgcaaccatt tcgccctgga tccgggtgcg gaacattacg tgtttgttgc cgggggtatc	1800
ggcatcacgc cgggtgctggc aatggcggat catgcccgtg cgcgtggttg gtcgtacgaa	1860
ctgcattatt gtggtcgtaa tcgtagcggg atggcttacc tggaacgcgt cgcgggacat	1920
ggtgaccgcg ctgccttgca cgtatctgaa gaaggcaccg gcattgatct ggcggcatta	1980
cttgctgaac cggcgccggg cgtgcaaata tacgcctgcg gtccggggccg tttattagcg	2040
ggtcttgaag acgcgtctcg taattggccg gatggcgcgc ttcattgtga gcatttcact	2100
tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga gctgcgtgac	2160
tctggcctta ccgttcgcgt cgagccaact cagaccgttt tagacgcttt gcgtgcgaac	2220
aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt	2280
ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgcgcgaat	2340
cgtcagatga tgacttgctg cagtcgtgca tgcggtgatc gtctggcgct gcgcctctaa	2400

<210> 12

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 12

Met	Pro	Thr	Leu	Pro	Arg	Thr	Phe	Asp	Asp	Ile	Gln	Ser	Arg	Leu	Ile
1				5					10					15	

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

Lys	Phe	Leu	Met	Ser	Ala	Lys	Arg	Lys	Thr	Phe	Gly	Pro	Arg	Arg	Pro
		35					40					45			

Met	Pro	Glu	Phe	Val	Glu	Thr	Pro	Ile	Pro	Asp	Val	Asn	Thr	Leu	Ala
	50					55					60				

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

Trp	Arg	Ala	Tyr	Phe	Lys	Arg	Leu	Arg	Asp	Glu	Ala	Pro	Val	His	Tyr
				85					90					95	

Gln	Lys	Asn	Ser	Pro	Phe	Gly	Pro	Phe	Trp	Ser	Val	Thr	Arg	Phe	Glu
			100					105					110		

Asp	Ile	Leu	Phe	Val	Asp	Lys	Ser	His	Asp	Leu	Phe	Ser	Ala	Glu	Pro
		115					120					125			

Gln	Ile	Ile	Leu	Gly	Asp	Pro	Pro	Glu	Gly	Leu	Ser	Ile	Glu	Met	Phe
	130					135					140				

Ile	Ala	Met	Asp	Pro	Pro	Lys	His	Asp	Val	Gln	Arg	Ser	Ser	Val	Gln
145						150				155					160

Gly	Val	Val	Ala	Pro	Lys	Asn	Leu	Lys	Glu	Met	Glu	Gly	Leu	Ile	Arg
				165					170					175	

Ser	Arg	Thr	Gly	Asp	Val	Leu	Asp	Ser	Leu	Pro	Thr	Asp	Lys	Pro	Phe
			180					185					190		

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
785 790 795

<210> 13

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido Sintético

<400> 13

atgccaacac tgcccagaac atttgacgac attcagtccc gactgattaa cgccacctcc 60

aggggtggtgc cgatgcagag gcaaattcag ggactgaaat tcttaatgag cgccaagagg 120

aagaccttcg gccacgccg accgatgccc gaattcggtg aaacacccat cccggacgtt 180

aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag 240

tggcgcgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc	300
ccttttcggcc ccttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
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caggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgac acgcaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaag	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggc gcagcatcgg ccaccggcgg ggagtttgcc	720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
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ctgcattatt gtggctgtaa tcgtagcgg atggcttacc tggaacgcgt cgcgggacat	1920
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 ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcgaat 2340
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<210> 14

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 14

Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
 1 5 10 15

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

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
 35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
 50 55 60

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
 85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
 100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
 115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Gln Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
 180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
785 790 795

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido Sintético

<400> 15

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aagaccttcg gcccacgccg accgatgccc gaattcggtg aaacacccat cccggacgtt	180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcaggggtcag	240
tggcgcgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc	300
cctttcggcc ctttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcgggtg accctccgga ggggctgtcg	420
ggggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgatc acgcaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaag	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggt gcagcatcgg ccaccggcgg ggagtttgcc	720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gagggagccc gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggcaacgat acgacgcgca actcgatgag tgggtggcctg	960
gtggccatga acgaattccc cagggaattt gaaaaattga aggcaaaacc ggagttgatt	1020
ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaagcagg atgtcgaact gggcggccag accatcaaga aggggtgatcg agttgtcatg	1140
tggtagcgct cgggtaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt	1200
gatcgcaagg acgcacgaaa ccacatgtcg ttcggctatg gggttcaccg ttgcatgggc	1260
aaccgtctgg ctgaactgca actgcgcata ctctgggaag aaataactca gcgttttgac	1320
aacatcgaag tcgtcgaaga gcccagcgg gtgcagtcca acttcgtgcg gggctattcc	1380
aggttgatgg tcaaactgac accgaacagt gtactccatc gtcatacaacc tgtcaccatc	1440

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ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcgaat 2340
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<210> 16

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido
Sintético

<400> 16

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Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
1           5           10           15

```

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

```

```

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
          35           40           45

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```

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
          50           55           60

```

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Gly Glu Met Phe
130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
 705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
 740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
 755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
 770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
 785 790 795

<210> 17

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido
 Sintético

<400> 17

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aagaccttcg gccacgccc accgatgccc gaattcggtt aaacacccat cccggacgtt	180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag	240
tggcgcgctt atttcaaacg gttgcgtgat gaggcgccc tccattacca gaagaacagc	300
cctttcggcc ctttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcggtg accctccgga ggggctgtcg	420
atggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgac acgcaccggc	540
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gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggt gcagcatcgg ccaccggcgg ggagtttgcc	720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagccc gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggcaacgat acgacgcgca actcgatgag tgggtggcctg	960

gtggccatga acgaattccc caggggaattt gaaaaattga aggcaaaacc ggagttgatt	1020
ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaaagcagg atgtcgaact gggcggccag accatcaaga agggatgatcg agttgtcatg	1140
tggtagcgt cggttaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt	1200
gatcgcaagg acgcacgaaa ccacatgtcg ttcggctatg gggttcaccg ttgcatgggc	1260
aaccgtcttg ctgaactgca actgcgcata ctctgggaag aaataactca gcgttttgac	1320
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acgcctggcg ctcacatcga cctggatctg ggtgctctga gccgtcagta ttcgctctgc	1620
ggcgtcccg atgctccgtc gtacgaaatc gccgtgact tagatccgga aagccgtggt	1680
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cgcaaccatt tcgccctgga tccgggtgcg gaacattacg tgtttgttgc cgggggtatc	1800
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ctgcattatt gtggtcgtaa tcgtagcgg atggcttacc tggaacgcgt cgcgggacat	1920
ggtgaccgcg ctgccttgca cgtatctgaa gaaggcacc gcattgatct ggcggcatta	1980
cttgctgaac cggcgccgg cgtgcaaata tacgcctgcg gtccggggccg tttattagcg	2040
ggtcttgaag acgcgtctcg taattggccg gatggcgcg ttcattgtga gcatttcact	2100
tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga gctgcgtgac	2160
tctggcctta ccgttcgcgt cgagccaact cagaccgttt tagacgcttt gcgtgcgaac	2220
aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt	2280
ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cggcggaat	2340
cgtcagatga tgacttgctg cagtcgtgca tgcggtgatc gtctggcgct gcgcctctaa	2400

<210> 18

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 18

Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
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Asn Ala Thr Ser Arg Val Val Pro Met Gln Arg Gln Ile Gln Gly Leu
 20 25 30

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
 35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
 50 55 60

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
 85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
 100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
 115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Met Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
 180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
785 790 795

<210> 19
<211> 2400
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de Secuencia Artificial: Polinucleótido Sintético

<400> 19
atgccaacac tgcccagaac atttgacgac attcagtccc gactgattaa cgccacctcc 60
agggtggtgc cgatgcagag gcaaattcag ggactgaaat tcttaatgag cgccaagagg 120
aagaccttcg gccacgccg accgatgcc gaattcggtg aaacacccat cccggacgtt 180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag 240
tggcgcgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc 300
cctttcggcc ccttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt 360
cacgacctgt tttccgccga gccgcaaadc attctcggtg accctccgga ggggctgtcg 420
ctggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgcag ctcggtgcag 480

ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgac acgcaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaag	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggt gcagcatcgg ccaccggcgg ggagtttgcc	720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccg gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggcaacgat acgacgcgca actcgatgag tggtagcctg	960
gtggccatga acgaattccc caggggaattt gaaaaattga aggcaaaacc ggagttgatt	1020
ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaagcagg atgtcgaact gggcggccag accatcaaga agggtagatc agttgtcatg	1140
tggtagcgt cggttaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt	1200
gatcgcaagg acgcacgaaa ccacatgtcg ttccggtatg gggttcaccg ttgcatgggc	1260
aaccgtctgg ctgaactgca actgcgcac cttctgggaag aaataactca gcgttttgac	1320
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ggtgaccgcg ctgccttgca cgtatctgaa gaaggcacc gcattgatct ggcggcatta	1980
cttgctgaac cggcgccggg cgtgcaaatc tacgcctgcg gtccggggccg tttattagcg	2040
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tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga gctgcgtgac	2160
tctggcctta ccgttcgcgt cgagccaact cagaccgttt tagacgcttt gcgtgcgaac	2220

aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt 2280
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 cgtcagatga tgacttgctg cagtcgtgca tgcggtgatc gtctggcgct ggcctctaa 2400

<210> 20

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido
 Sintético

<400> 20

Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
 1 5 10 15

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

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
 35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
 50 55 60

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
 85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
 100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
 115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Leu Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
 180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
 705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
 740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
 755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
 770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
 785 790 795

<210> 21

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido Sintético

<400> 21
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agggtggtgc cgatgcagag gcaaattcag ggactgaaat tcttaatgag cgccaagagg 120
aagaccttcg gccacgccg accgatgccc gaattcggtg aaacacccat cccggacgtt 180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag 240
tggcgcgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc 300
cctttcggcc ccttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt 360
cacgacctgt tttccgccga gccgcaaadc attctcgggtg accctccgga ggggctgtcg 420
acggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag 480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgatc acgcaccggc 540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaag 600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag 660
ctggttgagt ggtcggacag aatggcaggt gcagcatcgg ccaccggcgg ggagtttgcc 720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg 780
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccg gtttcgattt gatcagcctg 840
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gccaagcagg atgtcgaact gggcggccag accatcaaga aggggtgatcg agttgtcatg 1140
tggtagcgtg cgggtaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt 1200
gatcgcaagg acgcacgaaa ccacatgtcg ttcggctatg gggttcaccg ttgcatgggc 1260
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ggcgctccgg atgctccgtc gtacgaaatc gccgtgcact tagatccgga aagccgtggg 1680

ggaagccgct atattcatga acagctggaa gttggaagtc cgctgcgtat gcgtggccca 1740
 cgcaaccatt tcgccctgga tccgggtgcg gaacattacg tgtttgttgc cgggggtatc 1800
 ggcacacgc cggtgctggc aatggcggat catgcccgtg cgcgtggttg gtcgtacgaa 1860
 ctgcattatt gtggtcgtaa tcgtagcggc atggcttacc tggaacgcgt cgcgggacat 1920
 ggtgaccgcg ctgccttgca cgtatctgaa gaaggcaccg gcattgatct ggcggcatta 1980
 cttgctgaac cggcgccggg cgtgcaaata tacgcctgcg gtccgggccc tttattagcg 2040
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 tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga gctgcgtgac 2160
 tctggcctta ccgttcgcgt cgagccaact cagaccgttt tagacgcttt gcgtgcgaac 2220
 aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt 2280
 ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcaat 2340
 cgtcagatga tgacttgctg cagtcgtgca tgcggtgata gtctggcgct gcgcctctaa 2400

<210> 22

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 22

Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
 1 5 10 15

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

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
 35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
 50 55 60

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
 85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
 100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
 115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Thr Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
 180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
 705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
 740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
 755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
 770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
 785 790 795

<210> 23

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido
 Sintético

<400> 23

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aagaccttcg gccacgccc accgatgccc gaattcggtg aaacacccat cccggacgtt	180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag	240
tggcgcgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc	300
cctttcggcc ccttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcggtg accctccgga ggggctgtcg	420
gtggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgac aaacaccggc	540
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gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
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gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccg gtttcgattt gatcagcctg	840
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 ctgcattatt gtggctgtaa tcgtagcggg atggcttacc tggaacgcgt cgcgggacat 1920
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 cttgctgaac cggcgccggg cgtgcaaatc tacgcctgcg gtccgggccg tttattagcg 2040
 ggtcttgaag acgcgtctcg taattggccg gatggcgcgc ttcattgtgga gcatttact 2100
 tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga gctgcgtgac 2160
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 aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt 2280
 ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcgaat 2340
 cgtcagatga tgacttgctg cagtcgtgca tgcggtgatc gtctggcgct gcgcctctaa 2400

<210> 24

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 24

Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
 1 5 10 15

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

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
 35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
 50 55 60

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
 85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
 100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
 115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Val Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

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

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
785 790 795

<210> 25

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido
Sintético

<400> 25

atgccaacac tgcccagaac atttgacgac attcagtccc gactgattaa cgccacctcc	60
aggggtggtgc cgatgcagag gcaaattcag ggactgaaat tcttaatgag cgccaagagg	120
aagaccttcg gccacgccg accgatgccc gaattcggtg aaacacccat cccggacgtt	180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag	240
tggcgcgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc	300
cctttcggcc ctttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcgggtg accctccgga ggggctgtcg	420
gtggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgatc acgcaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact ggggtacctgc tgtttccaag	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggt gcagcatcgg ccaccggcgg ggagtttgcc	720

gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccc gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggccgggat acgacgcgca actcgatgag tgggtggcctg	960
gtggccatga acgaattccc cagggaattt gaaaaattga aggcaaaacc ggagttgatt	1020
ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaagcagg atgtcgaact gggcggccag accatcaaga agggatgatcg agttgtcatg	1140
tgggtacgct cgggtaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt	1200
gatcgcaagg acgcacgaaa ccacatgtcg ttcggctatg gggttcaccg ttgcatgggc	1260
aaccgtctgg ctgaactgca actgcgcata ctctgggaag aaataactca gcgttttgac	1320
aacatcgaag tcgtcgaaga gcccagcgg gtgcagtcca acttcgtgcg gggctattcc	1380
aggttgatgg tcaaactgac accgaacagt gtactccatc gtcatacaacc tgtcaccatc	1440
ggcgagccgg ccgctcgtgc tgtgagccgc acggtgaccg ttgagcgtct tgatcgcatt	1500
gccgacgatg tccttcgcct ggtccttcgc gatgctggag gtaaaaccct cccgacgtgg	1560
acgcctggcg ctacatcga cctggatctg ggtgctctga gccgtcagta ttcgctctgc	1620
ggcgctccgg atgtccgtc gtacgaaatc gccgtgcact tagatccgga aagccgtggt	1680
ggaagccgct atattcatga acagctggaa gttggaagtc cgctgcgtat gcgtggccca	1740
cgcaaccatt tcgccctgga tccgggtgcg gaacattacg tgtttgttgc cgggggtatc	1800
ggcatcacgc cgggtgctggc aatggcggat catgcccgtg cgcgtggttg gtcgtacgaa	1860
ctgcattatt gtggctgtaa tcgtagcggg atggcttacc tggaacgcgt cgcgggacat	1920
ggtgaccgcg ctgccttgca cgtatctgaa gaaggcaccg gcattgatct ggcggcatta	1980
cttgctgaac cggcgccggg cgtgcaaata tacgcctgcg gtccggggccg tttattagcg	2040
ggtcttgaag acgcgtctcg taattggccg gatggcgcgc ttcattgtga gcatttcact	2100
tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga gctgcgtgac	2160
tctggcctta ccgttcgcgt cgagccaact cagaccgttt tagacgcttt gcgtgcgaac	2220
aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt	2280
ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgcgcgaat	2340
cgtcagatga tgacttgctg cagtcgtgca tgcggtgatc gtctggcgct gcgcctctaa	2400

<210> 26

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido
Sintético

<400> 26

Met	Pro	Thr	Leu	Pro	Arg	Thr	Phe	Asp	Asp	Ile	Gln	Ser	Arg	Leu	Ile
1				5					10					15	

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

Lys	Phe	Leu	Met	Ser	Ala	Lys	Arg	Lys	Thr	Phe	Gly	Pro	Arg	Arg	Pro
		35					40					45			

Met	Pro	Glu	Phe	Val	Glu	Thr	Pro	Ile	Pro	Asp	Val	Asn	Thr	Leu	Ala
	50					55					60				

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

Trp	Arg	Ala	Tyr	Phe	Lys	Arg	Leu	Arg	Asp	Glu	Ala	Pro	Val	His	Tyr
				85					90					95	

Gln	Lys	Asn	Ser	Pro	Phe	Gly	Pro	Phe	Trp	Ser	Val	Thr	Arg	Phe	Glu
			100					105					110		

Asp	Ile	Leu	Phe	Val	Asp	Lys	Ser	His	Asp	Leu	Phe	Ser	Ala	Glu	Pro
		115					120					125			

Gln	Ile	Ile	Leu	Gly	Asp	Pro	Pro	Glu	Gly	Leu	Ser	Val	Glu	Met	Phe
	130					135					140				

Ile	Ala	Met	Asp	Pro	Pro	Lys	His	Asp	Val	Gln	Arg	Ser	Ser	Val	Gln
145					150					155					160

Gly	Val	Val	Ala	Pro	Lys	Asn	Leu	Lys	Glu	Met	Glu	Gly	Leu	Ile	Arg
				165					170					175	

Ser	Arg	Thr	Gly	Asp	Val	Leu	Asp	Ser	Leu	Pro	Thr	Asp	Lys	Pro	Phe
			180					185					190		

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Arg Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
785 790 795

<210> 27

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido
Sintético

<400> 27

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aggggtggtgc cgatgcagag gcaaattcag ggactgaaat tcttaatgag cgccaagagg 120

aagaccttcg gccacgccg accgatgccc gaattcggtg aaacacccat cccggacgtt 180

aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag 240

tggcgcgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc	300
ccttttcggcc ccttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcggtg accctccgga ggggctgtcg	420
gtggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgac acgcaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaag	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggt gcggcatcgg ccaccggcgg ggagtttgcc	720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccc gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggcaacgat acgacgcgca actcgatgag tggtagcctg	960
gtggccatga acgaattccc cagggaattt gaaaaattga aggcaaaacc ggagttgatt	1020
ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaaagcagg atgtcgaact gggcggccag accatcaaga agggtagatc agttgtcatg	1140
tggtagcgt cggttaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt	1200
gatcgcaagg acgcacgaaa ccacatgtcg ttcggctatg gggttcaccg ttgcatgggc	1260
aaccgtctgg ctgaactgca actgcgcac cttctgggaag aaataactca gcgttttgac	1320
aacatcgaag tcgtcgaaga gcccagcgg gtgcagtcca acttcgtgcg gggctattcc	1380
aggttgatgg tcaaactgac accgaacagt gtactccatc gtcacaaacc tgtcaccatc	1440
ggcagagccgg ccgctcgtgc tgtgagccgc acggtgaccg ttgagcgtct tgatcgcat	1500
gccgacgatg tccttcgcct ggtccttcgc gatgctggag gtaaaaccct cccgacgtgg	1560
acgcctggcg ctcacatcga cctggatctg ggtgctctga gccgtcagta ttcgctctgc	1620
ggcgtcccg atgtccgtc gtacgaaatc gccgtgcact tagatccgga aagccgtggt	1680
ggaagccgct atattcatga acagctggaa gttggaagtc cgctgcgtat gcgtggccca	1740
cgcaaccatt tcgccctgga tccgggtgcg gaacattacg tgtttgttg cgggggtatc	1800
ggcatcacgc cgggtgctggc aatggcggat catgccctg cgcgtggttg gtcgtacgaa	1860
ctgcattatt gtggctgtaa tcgtagcgg atggcttacc tggaacgcgt cgcgggacat	1920
ggtgaccgcg ctgccttgca cgtatctgaa gaaggcacc gcattgatct ggcggcatta	1980

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cttgctgaac cggcgccggg cgtgcaaatac tacgcctgcg gtccggggccg tttattagcg      2040
ggctcttgaag acgcgtctcg taattggccg gatggcgcgcg ttcattgtgga gcatttcact      2100
tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga gctgcgtgac      2160
tctggcctta ccgttcgctg cgagccaact cagaccgttt tagacgcttt gcgtgcgaac      2220
aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt      2280
ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcgaat      2340
cgtcagatga tgacttgctg cagtcgtgca tgcggtgatc gtctggcgct gcgcctctaa      2400

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<210> 28

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 28

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Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
1           5           10           15

```

```

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

```

```

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
          35           40           45

```

```

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
          50           55           60

```

```

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

```

```

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
          85           90           95

```

```

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
          100          105          110

```

```

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
          115          120          125

```

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Val Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
 180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
 705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
 740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
 755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
 770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
 785 790 795

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido Sintético

<400> 29

atgccaacac tgcccagaac atttgacgac attcagtccc gactgattaa cgccacctcc	60
aggggtggtgc cgatgcagag gcaaattcag ggactgaaat tcttaatgag cgccaagagg	120
aagaccttcg gccacgccg accgatgccc gaattcggtg aaacacccat cccggacgtt	180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcaggggtcag	240
tggcgcgcct atttcaaacg gttgcgtgat gaggcgccg tccattacca gaagaacagc	300
cctttcggcc ctttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcggtg accctccgga ggggctgtcg	420
gtggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgac acgcaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaag	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggt gcagcatcgg ccaccggcgg ggagtttgcc	720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccc gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggcaacgat acgacgcgca actcgatgag tgggtggcctg	960
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ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaagcagg atgtcgaact gggcggccag accatcaaga aggggtgatcg agttgtcatg	1140
tggtagcgt cggttaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt	1200
gatcgcaagg acgcacgaaa ccacatgtcg ttcggctatg ggcgtcaccg ttgcatgggc	1260
aaccgtctgg ctgaactgca actgcgcac ctcctgggaag aaataactca gcgttttgac	1320
aacatcgaag tcgtcgaaga gcccgagcgg gtgcagtcca acttcgtgcg gggctattcc	1380
aggttgatgg tcaaactgac accgaacagt gtactccatc gtcacatcaacc tgtcaccatc	1440

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ggcgagccgg ccgctcgtgc tgtgagccgc acggtgaccg ttgagcgtct tgatcgcatt      1500
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acgcctggcg ctacacatcga cctggatctg ggtgctctga gccgtcagta ttcgctctgc      1620
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tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga gctgcgtgac      2160
tctggcctta ccgttcgcgt cgagccaact cagaccgttt tagacgcttt gcgtgcgaac      2220
aatatcgacg tcccgtcggg ttgcgaagag gggctgtgtg gttcttgca agtagccgtt      2280
ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcgaat      2340
cgtcagatga tgacttgctg cagtcgtgca tgcggtgatc gtctggcgct gcgcctctaa      2400

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<210> 30

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido
Sintético

<400> 30

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Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
1           5           10          15

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

```

```

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
          35          40          45

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Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
          50          55          60

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Val Glu Met Phe
130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Arg His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
 705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
 740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
 755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
 770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
 785 790 795

<210> 31

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido Sintético

<400> 31

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aagaccttcg gccacgccc accgatgccc gaattcggtt aaacacccat cccggacgtt	180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggctcag	240
tggcgcgctt atttcaaacg gttgcgtgat gaggcgccc tccattacca gaagaacagc	300
cctttcggcc ctttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcggtg accctccgga ggggctgtcg	420
atcgaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgac acgcaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaag	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggt acagcatcgg ccaccggcgg ggagtttgcc	720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagccc gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggcaacgat acgacgcgca actcgatgag tgggtggcctg	960

gtggccatga acgaattccc caggggaattt gaaaaattga aggcaaaacc ggagttgatt	1020
ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaaagcagg atgtcgaact gggcggccag accatcaaga agggatgatcg agttgtcatg	1140
tggtagcgt cggttaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt	1200
gatcgcaagg acgcacgaaa ccacatgtcg ttcggctatg gggttcaccg ttgcatgggc	1260
aaccgtcttg ctgaactgca actgcgcac cttctgggaag aaataactcaa gcgttttgac	1320
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gccgacgatg tccttcgcct ggtccttcgc gatgctggag gtaaaaccct cccgacgtgg	1560
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ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cggcggaat	2340
cgtcagatga tgacttgctg cagtcgtgca tgcgggtgatc gtctggcgct gcgcctctaa	2400

<210> 32

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 32

Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
 1 5 10 15

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

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
 35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
 50 55 60

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
 85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
 100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
 115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Ile Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
 180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Thr Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
 705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
 740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
 755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
 770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
 785 790 795

<210> 33
 <211> 2400
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de Secuencia Artificial: Polinucleótido Sintético

<400> 33
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 aagaccttcg gccacgccg accgatgccc gaattcgttg aaacacccat cccggacgtt 180
 aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag 240
 tgggacgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc 300
 cctttcggcc ccttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt 360
 cagacctgt tttccgccga gccgcaaatc attctcggtg accctccgga ggggctgtcg 420
 atggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag 480

ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgac	aaacaccggc	540	
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc	tgttccaag	600	
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga	acgccacaag	660	
ctggttgagt ggtcggacag aatggcaggt gcagcatcgg ccaccggcgg	ggagtttgcc	720	
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc	caggctttgg	780	
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccg gtttcgattt	gatcagcctg	840	
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt	tatcggtaat	900	
ttgacgctgc tcatagtcgc cggcgcggat acgacgcgca actcgatgag	tggtagcctg	960	
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ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat	gcgccgaatc	1080	
gccaagcagg atgtcgaact gggcggccag accatcaaga agggtagatc	gagttgcatg	1140	
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ctgcattatt gtggctgtaa tcgtagcgg	atggcttacc tggaacgcgt	cgcgggacat	1920
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cttgctgaac cggcgccggg cgtgcaaatc tacgcctgcg gtccggggccg	tttattagcg	2040	
ggtcttgaa acgcgtctcg taattggccg gatggcgcgc ttcattgtgga	gcatttcact	2100	
tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga	gctgcgtgac	2160	
tctggcctta ccgttcgcgt cgagccaact cagaccgttt tagacgcttt	gcgtgcgaac	2220	

aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt 2280
 ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcgaat 2340
 cgtcagatga tgacttgctg cagtcgtgca tgcggtgatc gtctggcgct ggcctctaa 2400

<210> 34

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido
 Sintético

<400> 34

Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
 1 5 10 15

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

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
 35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
 50 55 60

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

Trp Asp Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
 85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
 100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
 115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Met Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

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

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Ala Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
 705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
 740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
 755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
 770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
 785 790 795

<210> 35

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido Sintético

<400> 35
atgccaaacac tgcccagaac atttgacgac attcagtccc gactgattaa cgccacctcc 60
agggtggtgc cgatgcagag gcaaattcag ggactgaaat tcttaatgag cgccaagagg 120
aagaccttcg gccacgccc accgatgccc gaattcggtg aaacacccat cccggacgtt 180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag 240
tggcgcgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc 300
cctttcggcc ccttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt 360
cacgacctgt tttccgccga gccgcaaadc attctcgggtg accctccgga ggggctgtcg 420
gtggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctccggtgcag 480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgatc acgcaccggc 540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaag 600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag 660
ctggttgagt ggtcggacag aatggcaggc gcagcatcgg ccaccggcgg ggagtttgcc 720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg 780
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 aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt 2280
 ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcgaat 2340
 cgtcagatga tgacttgctg cagtcgtgca tgcggtgac gtctggcgct gcgcctctaa 2400

<210> 36

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 36

Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
 1 5 10 15

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

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
 35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
 50 55 60

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
 85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
 100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
 115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Val Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
 180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Ala Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
 705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
 740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
 755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
 770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Ala Leu Arg Leu
 785 790 795

<210> 37

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido
 Sintético

<400> 37

atgccaacac tgcccagaac atttgacgac attcagtccc gactgattaa cgccacctcc	60
aggggtggtgc cgatgcagag gcaaattcag ggactgaaat tcttaatgag cgccaagagg	120
aagaccttcg gccacgccc accgatgccc gaattcggtg aaacacccat cccggacgtt	180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag	240
tggcgcgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc	300
cctttcggcc ccttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcggtg accctccgga ggggctgtcg	420
gtggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgatc acgcaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaag	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggt gcagcatcgg ccaccggcgg ggagtttgcc	720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccg gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggcaacgat acgacgcgca actcgatgag tgggtggcctg	960
gtggccatga acgaattccc cagggaattt gaaaaattga aggcaaaacc ggagttgatt	1020
ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaagcagg atgtcgaact gggcggccag accatcaaga aggggtgatcg agttgtcatg	1140
tggtagcgt cggttaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt	1200

gatcgcaagg acgcacgaaa ccacatgtcg ttcggctatg gggttcaccg ttgcatgggc 1260
 aaccgtcttg ctgaactgca actgcgcata ctctgggaag aaataactcaa gcgttttgac 1320
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 ctgcattatt gtggtcgtaa tcgtagcggg atggcttacc tggaacgcgt cgcgggacat 1920
 ggtgaccgcg ctgccttgca cgtatctgaa gaaggcacc gcattgatct ggcggcatta 1980
 cttgctgaac cggcgccggg cgtgcaaata tacgcctgcg gtccgggccc tttattagcg 2040
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 tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga gctgcgtgac 2160
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 aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt 2280
 ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcaat 2340
 cgtcagatga tgacttgctg cagtcgtgca tgcggtgatc gtctggctct gcgcctctaa 2400

<210> 38

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 38

Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
 1 5 10 15

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

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
 35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
 50 55 60

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
 85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
 100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
 115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Val Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
 180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Val Leu Arg Leu
785 790 795

<210> 39

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido Sintético

<400> 39

atgccaacac tgcccagaac atttgacgac attcagtccc gactgattaa cgccacctcc	60
aggggtggtgc cgatgcagag gcaaattcag ggactgaaat tcttaatgag cgccaagagg	120
aagaccttcg gccacgccg accgatgccc gaattcggtg aaacacccat cccggacgtt	180
aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag	240
tggcgcgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc	300
cctttcggcc ctttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcgggtg accctccgga ggggctgtcg	420
gtggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgatc acgcaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaa	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggt gcagcatcgg ccaccggcgg ggagtttgcc	720

gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccg gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggcaacgat acgacgcgca actcgatgag tgggtggcctg	960
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ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaagcagg atgtcgaact gggcggccag accatcaaga agggatgatcg agttgtcatg	1140
tgggtacgct cgggtaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt	1200
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ggaagccgct atattcatga acagctggaa gttggaagtc cgctgcgtat gcgtggccca	1740
cgcaaccatt tcgccctgga tccgggtgcg gaacattacg tgtttggtgc cgggggtatc	1800
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ctgcattatt gtggctgtaa tcgtagcggc atggcttacc tggaacgcgt cgcgggacat	1920
ggtgaccgcg ctgccttgca cgtatctgaa gaaggcaccg gcattgatct ggcggcatta	1980
cttgctgaac cggcggacgg cgtgcaaatc tacgcctgcg gtccgggccg tttattagcg	2040
ggtcttgaag acgcgtctcg taattggccg gatggcgcgc ttcattgtga gcatttcact	2100
tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga gctgcgtgac	2160
tctggcctta ccgttcgcgt cgagccaact cagaccgttt tagacgcttt gcgtgcgaac	2220
aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt	2280
ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgcgcgaat	2340
cgtcagatga tgacttgctg cagtcgtgca tgcggtgatc gtctggctct gcgcctctaa	2400

<210> 40

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 40

Met	Pro	Thr	Leu	Pro	Arg	Thr	Phe	Asp	Asp	Ile	Gln	Ser	Arg	Leu	Ile
1				5					10					15	

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

Lys	Phe	Leu	Met	Ser	Ala	Lys	Arg	Lys	Thr	Phe	Gly	Pro	Arg	Arg	Pro
		35					40					45			

Met	Pro	Glu	Phe	Val	Glu	Thr	Pro	Ile	Pro	Asp	Val	Asn	Thr	Leu	Ala
	50					55					60				

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

Trp	Arg	Ala	Tyr	Phe	Lys	Arg	Leu	Arg	Asp	Glu	Ala	Pro	Val	His	Tyr
				85					90					95	

Gln	Lys	Asn	Ser	Pro	Phe	Gly	Pro	Phe	Trp	Ser	Val	Thr	Arg	Phe	Glu
			100					105					110		

Asp	Ile	Leu	Phe	Val	Asp	Lys	Ser	His	Asp	Leu	Phe	Ser	Ala	Glu	Pro
		115					120					125			

Gln	Ile	Ile	Leu	Gly	Asp	Pro	Pro	Glu	Gly	Leu	Ser	Val	Glu	Met	Phe
	130					135					140				

Ile	Ala	Met	Asp	Pro	Pro	Lys	His	Asp	Val	Gln	Arg	Ser	Ser	Val	Gln
145					150					155					160

Gly	Val	Val	Ala	Pro	Lys	Asn	Leu	Lys	Glu	Met	Glu	Gly	Leu	Ile	Arg
				165					170					175	

Ser	Arg	Thr	Gly	Asp	Val	Leu	Asp	Ser	Leu	Pro	Thr	Asp	Lys	Pro	Phe
			180					185					190		

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Val Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Asp Gly Val Gln Ile Tyr Ala
660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Val Leu Arg Leu
785 790 795

<210> 41

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido Sintético

<400> 41

atgccaacac tgcccagaac atttgacgac attcagtccc gactgattaa cgccacctcc 60

aggggtggtgc cgatgcagag gcaaattcag ggactgaaat tcttaatgag cgccaagagg 120

aagaccttcg gccacgccg accgatgccc gaattcggtg aaacacccat cccggacgtt 180

aacacgctgg cccttgagga catcgatgtc agcaatccgt ttttataccg gcagggtcag 240

tggcgcgcct atttcaaacg gttgcgtgat gaggcgccgg tccattacca gaagaacagc	300
ccttttcggcc ccttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcggtg accctccgga ggggctgtcg	420
atcgaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgac acgcaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttccaag	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggc acagcatcgg ccaccggcgg ggagtttgcc	720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccc gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggcaacgat acgacgcgca actcgatgag tggtagcctg	960
gtggccatga acgaattccc cagggaattt gaaaaattga aggcaaaacc ggagttgatt	1020
ccgaacatgg tgtaggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaaagcagg atgtcgaact gggcggccag accatcaaga agggtagatc agttgtcatg	1140
tggtagcgt cggtgaaccg ggacgagcgc aaatttgaca accccgatca gttcatcatt	1200
gatcgcaagg acgcacgaaa ccacatgtcg ttcggctatg gggttcaccg ttgcatgggc	1260
aaccgtctgg ctgaactgca actgcgcac cttctgggaag aaataactca gcgttttgac	1320
aacatcgaag tcgtcgaaga gcccagcgg gtgcagtcca acttcgtgcg gggctattcc	1380
aggttgatgg tcaaactgac accgaacagt gtactccatc gtcacaaacc tgtcaccatc	1440
ggcagagccgg ccgctcgtgc tgtgagccgc acggtgaccg ttgagcgtct tgatcgcat	1500
gccgacgatg tccttcgcct ggtccttcgc gatgctggag gtaaaaccct cccgacgtgg	1560
acgcctggcg ctcacatcga cctggatctg ggtgctctga gccgtcagta ttcgctctgc	1620
ggcgtcccg atgctccgtc gtacgaaatc gccgtgcact tagatccgga aagccgtggt	1680
ggaagccgct atattcatga acagctggaa gttggaagtc cgctgcgtat gcgtggccca	1740
cgcaaccatt tcgccctgga tccgggtgcg gaacattacg tgtttgttg cgggggtatc	1800
ggcatcacgc cgggtgctggc aatggcggat catgcccgtg cgcgtggttg gtcgtacgaa	1860
ctgcattatt gtggctgtaa tcgtagcgg atggcttacc tggaacgcgt cgcgggacat	1920
ggtgaccgcg ctgccttgca cgtatctgaa gaaggcacc gcattgatct ggcggcatta	1980

cttgctgaac cggcgccggg cgtgcaaadc tacgcctgcg gtccggggccg tttattagcg 2040
 ggtcttgaag acgcgtctcg taattggccg gatggcgcgcg ttcattgtgga gcatttcact 2100
 tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga gctgcgtgac 2160
 tctggcctta ccgttcgctg cgagccaact cagaccgttt tagacgcttt gcgtgcgaac 2220
 aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt 2280
 ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcgaat 2340
 cgtcagatga tgacttgctg cagtcgtgca tgcgggtgac gtctggtcct gcgcctctaa 2400

<210> 42

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido Sintético

<400> 42

Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
1 5 10 15

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

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
50 55 60

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Ile Glu Met Phe
 130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
 145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
 165 170 175

Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
 180 185 190

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
 195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
 210 215 220

Ser Asp Arg Met Ala Gly Thr Ala Ser Ala Thr Gly Gly Glu Phe Ala
 225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
 245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
 260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
 705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
 740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
 755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
 770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Val Leu Arg Leu
 785 790 795

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido Sintético

<400> 43

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aggggtggtgc cgatgcagct gcaaattcag ggactgaaat tcttaatgag cgccaagagg	120
aagaccttcg gccacgccg accgatgccc gaattcggtg aaacacccat cccggacgtt	180
aacacgctgg cccttgagga catcgatgtc agcaatccgt tttataccg gcagggtcag	240
tgggacgcct atttcaaacg gttgcgtgat gaggcgccg tccattacca gaagaacagc	300
cctttcggcc ctttctggtc ggtaactcgg tttgaagaca tcctgttcgt ggataagagt	360
cacgacctgt tttccgccga gccgcaaadc attctcggtg accctccgga ggggctgtcg	420
atggaaatgt tcatagcgat ggatccgccg aaacacgatg tgcagcgag ctcggtgcag	480
ggagtagtgg caccgaaaaa cctgaaggag atggaggggc tgatccgac aaacaccggc	540
gatgtgcttg acagcctgcc tacagacaaa ccctttaact gggtagctgc tgtttcaaag	600
gaactcacag gccgcatgct ggcgacgctt ctggattttc cttacgagga acgccacaag	660
ctggttgagt ggtcggacag aatggcaggt gcagcatcgg ccaccggcgg ggagtttgcc	720
gatgaaaatg ccatgtttga cgacgcggca gacatggccc ggtctttctc caggctttgg	780
cgggacaagg aggcgcgccg cgcagcaggc gaggagcccg gtttcgattt gatcagcctg	840
ttgcagagca acaaagaaac gaaagacctg atcaatcggc cgatggagtt tatcggtaat	900
ttgacgctgc tcatagtcgc cggcgcggat acgacgcgca actcgatgag tgggtggcctg	960
gtggccatga acgaattccc cagggaattt gaaaaattga aggcaaaacc ggagttgatt	1020
ccgaacatgg tgtcggaaat catccgctgg caaacgccgc tggcctatat gcgccgaatc	1080
gccaagcagg atgtcgaact gggcggccag accatcaaga agggatgatc agttgtcatg	1140
tggtagcgt cggttaaccg ggacgagcgc aaatttgaca acccgcgac gttcatcatt	1200
gatcgcaagg acgcacgaaa ccacatgtcg ttcggctatg gggttcaccg ttgcatgggc	1260
aaccgtctgg ctgaactgca actgcgcac ctcctgggaag aaataactca gcgttttgac	1320
aacatcgaag tcgtcgaaga gcccgagcgg gtgcagtcca acttcgtgcg gggctattcc	1380
aggttgatgg tcaaactgac accgaacagt gtactccatc gtcacatcaacc tgtcaccatc	1440

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ggcgagccgg ccgctcgtgc tgtgagccgc acggtgaccg ttgagcgtct tgatcgcatt      1500
gccgacgatg tccttcgcct ggtccttcgc gatgctggag gtaaaaccct cccgacgtgg      1560
acgcctggcg ctacacatcga cctggatctg ggtgctctga gccgtcagta ttcgctctgc      1620
ggcgctccgg atgctccgtc gtacgaaatc gccgtgact tagatccgga aagccgtggt      1680
ggaagccgct atattcatga acagctggaa gttggaagtc cgctgcgtat gcgtggccca      1740
cgcaaccatt tcgccctgga tccgggtgcg gaacattacg tgtttggtgc cgggggtatc      1800
ggcatcacgc cggtgctggc aatggcggat catgcccggt cgcggtggtg gtcgtacgaa      1860
ctgcattatt gtggtcgtaa tcgtagcggg atggcctacc tggaacgcgt cgcgggacat      1920
ggtgaccgcg ctgccttgca cgtatctgaa gaaggcaccg gcattgatct ggcggcatta      1980
cttgctgaac cggcgccggg cgtgcaaatc tacgcctgcg gtccggggccg tttattagcg      2040
ggtcttgaag acgcgtctcg taattggccg gatggcgcgc ttcattgtga gcatttact      2100
tcgagtttag ccgctttgga tccggatgtc gaacatgcct ttgatttgga gctgcgtgac      2160
tctggcctta ccgttcgctg cgagccaact cagaccgttt tagacgcttt gcgtgcgaac      2220
aatatcgacg tcccgtcgga ttgcgaagag gggctgtgtg gttcttgca agtagccgtt      2280
ctggatggcg aggttgatca ccgtgatacc gttctgacta aggccgagcg cgccgcgaat      2340
cgtcagatga tgacttgctg cagtcgtgca tgcggtgatc gtctggtcct gcgcctctaa      2400

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<210> 44

<211> 799

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polipéptido
Sintético

<400> 44

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Met Pro Thr Leu Pro Arg Thr Phe Asp Asp Ile Gln Ser Arg Leu Ile
1           5           10           15

```

```

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

```

```

Lys Phe Leu Met Ser Ala Lys Arg Lys Thr Phe Gly Pro Arg Arg Pro
          35           40           45

```

```

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
50           55           60

```

110

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

Trp Asp Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
115 120 125

Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Met Glu Met Phe
130 135 140

Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
145 150 155 160

Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
165 170 175

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

Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
195 200 205

Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
210 215 220

Ser Asp Arg Met Ala Gly Ala Ala Ser Ala Thr Gly Gly Glu Phe Ala
225 230 235 240

Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
245 250 255

Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
260 265 270

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

Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
 290 295 300

Ile Val Ala Gly Ala Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
 305 310 315 320

Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
 340 345 350

Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
 355 360 365

Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
 370 375 380

Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
 385 390 395 400

Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
 405 410 415

Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
 420 425 430

Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
 435 440 445

Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
 450 455 460

Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
 465 470 475 480

Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
 485 490 495

Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
 500 505 510

Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
 515 520 525

Asp Leu Gly Ala Leu Ser Arg Gln Tyr Ser Leu Cys Gly Ala Pro Asp
 530 535 540

Ala Pro Ser Tyr Glu Ile Ala Val His Leu Asp Pro Glu Ser Arg Gly
 545 550 555 560

Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
 565 570 575

Met Arg Gly Pro Arg Asn His Phe Ala Leu Asp Pro Gly Ala Glu His
 580 585 590

Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
 595 600 605

Ala Asp His Ala Arg Ala Arg Gly Trp Ser Tyr Glu Leu His Tyr Cys
 610 615 620

Gly Arg Asn Arg Ser Gly Met Ala Tyr Leu Glu Arg Val Ala Gly His
 625 630 635 640

Gly Asp Arg Ala Ala Leu His Val Ser Glu Glu Gly Thr Arg Ile Asp
 645 650 655

Leu Ala Ala Leu Leu Ala Glu Pro Ala Pro Gly Val Gln Ile Tyr Ala
 660 665 670

Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
 675 680 685

Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
 690 695 700

Ala Leu Asp Pro Asp Val Glu His Ala Phe Asp Leu Glu Leu Arg Asp
 705 710 715 720

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

Leu Arg Ala Asn Asn Ile Asp Val Pro Ser Asp Cys Glu Glu Gly Leu
 740 745 750

Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
 755 760 765

Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
 770 775 780

Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Val Leu Arg Leu
 785 790 795

<210> 45

<211> 2400

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de Secuencia Artificial: Polinucleótido
 Sintético

<400> 45

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 35 40 45

Met Pro Glu Phe Val Glu Thr Pro Ile Pro Asp Val Asn Thr Leu Ala
 50 55 60

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

Trp Arg Ala Tyr Phe Lys Arg Leu Arg Asp Glu Ala Pro Val His Tyr
 85 90 95

Gln Lys Asn Ser Pro Phe Gly Pro Phe Trp Ser Val Thr Arg Phe Glu
 100 105 110

Asp Ile Leu Phe Val Asp Lys Ser His Asp Leu Phe Ser Ala Glu Pro
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Gln Ile Ile Leu Gly Asp Pro Pro Glu Gly Leu Ser Thr Glu Met Phe
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Ile Ala Met Asp Pro Pro Lys His Asp Val Gln Arg Ser Ser Val Gln
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Gly Val Val Ala Pro Lys Asn Leu Lys Glu Met Glu Gly Leu Ile Arg
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Ser Arg Thr Gly Asp Val Leu Asp Ser Leu Pro Thr Asp Lys Pro Phe
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Asn Trp Val Pro Ala Val Ser Lys Glu Leu Thr Gly Arg Met Leu Ala
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Thr Leu Leu Asp Phe Pro Tyr Glu Glu Arg His Lys Leu Val Glu Trp
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Ser Asp Arg Met Ala Gly Thr Ala Ser Ala Thr Gly Gly Glu Phe Ala
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Asp Glu Asn Ala Met Phe Asp Asp Ala Ala Asp Met Ala Arg Ser Phe
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Ser Arg Leu Trp Arg Asp Lys Glu Ala Arg Arg Ala Ala Gly Glu Glu
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Pro Gly Phe Asp Leu Ile Ser Leu Leu Gln Ser Asn Lys Glu Thr Lys
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Asp Leu Ile Asn Arg Pro Met Glu Phe Ile Gly Asn Leu Thr Leu Leu
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Ile Val Ala Gly Asn Asp Thr Thr Arg Asn Ser Met Ser Gly Gly Leu
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Val Ala Met Asn Glu Phe Pro Arg Glu Phe Glu Lys Leu Lys Ala Lys
 325 330 335

Pro Glu Leu Ile Pro Asn Met Val Ser Glu Ile Ile Arg Trp Gln Thr
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Pro Leu Ala Tyr Met Arg Arg Ile Ala Lys Gln Asp Val Glu Leu Gly
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Gly Gln Thr Ile Lys Lys Gly Asp Arg Val Val Met Trp Tyr Ala Ser
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Gly Asn Arg Asp Glu Arg Lys Phe Asp Asn Pro Asp Gln Phe Ile Ile
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Asp Arg Lys Asp Ala Arg Asn His Met Ser Phe Gly Tyr Gly Val His
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Arg Cys Met Gly Asn Arg Leu Ala Glu Leu Gln Leu Arg Ile Leu Trp
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Glu Glu Ile Leu Lys Arg Phe Asp Asn Ile Glu Val Val Glu Glu Pro
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Glu Arg Val Gln Ser Asn Phe Val Arg Gly Tyr Ser Arg Leu Met Val
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Lys Leu Thr Pro Asn Ser Val Leu His Arg His Gln Pro Val Thr Ile
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Gly Glu Pro Ala Ala Arg Ala Val Ser Arg Thr Val Thr Val Glu Arg
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Leu Asp Arg Ile Ala Asp Asp Val Leu Arg Leu Val Leu Arg Asp Ala
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Gly Gly Lys Thr Leu Pro Thr Trp Thr Pro Gly Ala His Ile Asp Leu
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Gly Ser Arg Tyr Ile His Glu Gln Leu Glu Val Gly Ser Pro Leu Arg
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Tyr Val Phe Val Ala Gly Gly Ile Gly Ile Thr Pro Val Leu Ala Met
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Cys Gly Pro Gly Arg Leu Leu Ala Gly Leu Glu Asp Ala Ser Arg Asn
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Trp Pro Asp Gly Ala Leu His Val Glu His Phe Thr Ser Ser Leu Ala
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Ser Gly Leu Thr Val Arg Val Glu Pro Thr Gln Thr Val Leu Asp Ala
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Cys Gly Ser Cys Glu Val Ala Val Leu Asp Gly Glu Val Asp His Arg
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Asp Thr Val Leu Thr Lys Ala Glu Arg Ala Ala Asn Arg Gln Met Met
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Thr Cys Cys Ser Arg Ala Cys Gly Asp Arg Leu Val Leu Arg Leu
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