

LISTADO DE SECUENCIAS

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 Wollacott, Andrew M

<120> GENES DE TOLERANCIA A HERBICIDAS Y MÉTODOS PARA USAR LOS MISMOS

<130> MONS:378US

<150> US 62/064343
 <151> 2014-10-15

<160> 61

<170> PatentIn versión 3.5

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 35 40 45
 Phe His Thr Tyr Gln Val Ile Tyr Phe Pro Gly Gln Ala Ile Thr Asn
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 Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
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 Pro Leu Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
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 Arg Glu Ala Asn Glu Ser Gly Arg Val Ile Gly Asp Asp Trp His Thr
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 Asp Ser Ser Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
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 Ile Asp Val Pro Glu His Gly Gly Asp Thr Gly Phe Leu Ser Met Tyr
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 Thr Ala Tyr Asp Ala Leu Ser Asp Gly Leu Lys Lys Leu Ile Ser Gly
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 Ala Gln Asn Arg Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
 180 185 190
 Ala Asp Gly Asp Arg Glu Thr Val His Pro Leu Val Val Thr His Pro
 195 200 205

Gly Ser Gly Arg Lys Gly Leu Tyr Val Asn Gln Val Tyr Cys Gln Arg
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Ile Glu Gly Met Ser Glu Lys Glu Ser Glu Pro Leu Leu Ser Phe Leu
 225 230 235 240

Phe Ala His Ala Thr Lys Pro Glu Phe Thr Cys Arg Val Arg Trp Lys
 245 250 255

Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Tyr Ala
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Leu Arg Glu Pro Leu Asp Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
35         40         45

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

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Glu Gln Gln Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
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Pro Leu Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
85         90         95

```

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Arg Glu Ala Asn Glu Ser Gly Arg Val Ile Gly Asp Asp Trp His Thr
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Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
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Ile Asp Val Pro Glu His Gly Gly Asp Thr Gly Phe Leu Ser Met Tyr
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Thr Ala Tyr Asp Ala Leu Ser Asp Gly Leu Lys Lys Leu Ile Ser Gly
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Leu Asn Val Val His Ser Ala Thr Arg Val Phe Gly Ser Leu Tyr Gln
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 Ala Gln Asn Arg Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
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 Asp Ala Gly Asp Arg Glu Thr Val His Pro Leu Val Val Thr His Pro
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 Gly Ser Gly Arg Lys Gly Leu Tyr Val Asn Gln Val Tyr Cys Gln Arg
 210 215 220
 Ile Glu Gly Met Ser Glu Lys Glu Ser Glu Pro Leu Leu Ser Phe Leu
 225 230 235 240
 Phe Ala His Ala Thr Lys Pro Glu Phe Thr Cys Arg Val Arg Trp Lys
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 Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Tyr Ala
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Leu Arg Glu Pro Leu Ser Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
          35         40         45

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

Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
65         70         75         80

Pro Leu Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
          85         90         95

Arg Glu Ala Asn Glu Ser Gly Arg Val Ile Gly Asp Asp Trp His Ser
          100        105        110

Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
          115        120        125
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Ile Asp Val Pro Glu His Gly Gly Asp Thr Gly Phe Leu Ser Met Tyr
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 Thr Ala Tyr Asp Ala Leu Ser Asp Gly Leu Lys Lys Leu Ile Ser Gly
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 Ala Gln Asn Arg Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
 180 185 190
 Asp Ala Gly Asp Arg Glu Thr Val His Pro Leu Val Val Thr His Pro
 195 200 205
 Gly Ser Gly Arg Lys Gly Leu Tyr Val Asn Gln Val Tyr Cys Gln Arg
 210 215 220
 Ile Glu Gly Met Ser Glu Lys Glu Ser Glu Pro Leu Leu Ser Phe Leu
 225 230 235 240
 Phe Ala His Ala Thr Lys Pro Glu Phe Thr Cys Arg Val Arg Trp Lys
 245 250 255
 Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Tyr Ala
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 Ile Asn Asp Tyr His Gly Gln Thr Arg Ile Leu His Arg Thr Thr Val
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Leu Arg Glu Pro Leu Asp Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
35 40 45

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

Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
65 70 75 80

Pro Leu Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
85 90 95

Arg Glu Ala Asn Glu Ser Gly Arg Val Leu Gly Asp Asp Trp His Thr
100 105 110

Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
115 120 125

Ile Asp Val Pro Glu His Gly Gly Asp Thr Gly Phe Leu Ser Met Tyr
130 135 140

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

Leu Asn Val Val His Ser Ala Thr Arg Val Phe Gly Ser Leu Tyr Gln
165 170 175

Ala Gln Asn Arg Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
180 185 190

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

Gly Ser Gly Arg Lys Gly Leu Tyr Val Asn Gln Val Tyr Cys Gln Arg
210 215 220

Ile Glu Gly Met Ser Glu Lys Glu Ser Glu Pro Leu Leu Ser Phe Leu
225 230 235 240

Phe Ala His Ala Thr Lys Pro Glu Phe Thr Cys Arg Val Arg Trp Lys
245 250 255

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

Arg Glu Ala Asn Glu Ser Gly Arg Val Ile Gly Glu Asn Trp His Thr
100 105 110

Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Tyr Ala
115 120 125

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

Thr Ala Trp Glu Thr Leu Ser Pro Thr Met Gln Ala Thr Ile Glu Gly
145 150 155 160

Leu Asn Val Val His Ser Ala Thr Arg Val Phe Gly Ser Leu Tyr Gln
165 170 175

Ala Gln Asn Arg Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
180 185 190

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

Glu Thr Gly Arg Lys Gly Leu Tyr Val Asn Gln Val Tyr Cys Gln Arg
210 215 220

Ile Glu Gly Met Ser Glu Lys Glu Ser Glu Pro Leu Leu Ser Phe Leu
225 230 235 240

Phe Ala His Ala Thr Lys Pro Glu Phe Thr Cys Arg Val Arg Trp Gln
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Glu Gly Asp Val Leu Val Trp Asp Asn Leu Cys Thr Gln His Tyr Ala
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			20					25					30		
Leu	Arg	Glu	Pro	Leu	Asp	Asp	Ser	Thr	Trp	Asn	Glu	Ile	Leu	Asp	Ala
		35					40					45			
Phe	His	Thr	Tyr	Gln	Val	Ile	Tyr	Phe	Pro	Gly	Gln	Ala	Ile	Thr	Asn
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Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
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 Pro Ile Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
 85 90 95
 Arg Glu Ala Asn Glu Ser Ser Arg Phe Ile Gly Asp Asp Trp His Thr
 100 105 110
 Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
 115 120 125
 Ile Glu Val Pro Glu Tyr Gly Gly Asp Thr Gly Phe Leu Ser Met Tyr
 130 135 140
 Ser Ala Trp Glu Thr Leu Ser Pro Thr Met Gln Ala Thr Ile Glu Gly
 145 150 155 160
 Leu Asn Val Val His Ser Ala Thr Lys Val Phe Gly Ser Leu Tyr Gln
 165 170 175
 Ala Thr Asn Trp Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
 180 185 190
 Asp Ala Gly Asp Arg Glu Thr Val His Pro Leu Val Val Thr His Pro
 195 200 205
 Val Thr Gly Arg Arg Ala Leu Tyr Cys Asn Gln Val Tyr Cys Gln Lys
 210 215 220
 Ile Gln Gly Met Thr Asp Ala Glu Ser Lys Ser Leu Leu Gln Phe Leu
 225 230 235 240
 Tyr Glu His Ala Thr Lys Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
 245 250 255
 Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ala
 260 265 270
 Val Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
 275 280 285
 Ala Gly Asp Lys Pro Ser Arg
 290 295

<210> 15
 <211> 906
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 15	
atgcacgcgg ctctgacccc gcttaccaac aaataccggt tcatcgacgt tcagccgctg	60
accggtgttt taggtgctga aatcaccggt gttgacctgc gtgaaccgct ggacgactct	120
acctggaacg aaatcctgga cgcgttcac acctaccagg ttatctactt cccgggtcag	180
gcatcacca acgaacagca catcgcgttc tctcgtcgtc tcgggtccggt tgacccggtt	240
ccgattctca aatctatcga aggttaccg gaagttcaga tgatccgtcg cgaagcgaac	300
gaatctagcc gttttattgg tgacgattgg cacaccgact ccaccttcct ggacgcgccg	360

ccagctgcag ttgtgatgcg tgctattgaa gttccggaat acggtggcga caccggtttc	420
ctgtccatgt actctgcttg ggaacacctg tccccgacca tgcaggctac cattgaaggt	480
ctgaacgttg tgcactccgc aaccaaagtg ttcggcagcc tgtaccaggc aaccaactgg	540
cgcttcagca acactagtgt gaaagtgatg gatgtggatg caggcgatcg tgagactgtg	600
cacccgctgg tggtaaacta cccggttacc ggccgtcgtg cgctgtactg caaccaggta	660
tattgccaga aaattcaggg catgactgat gcagagtcaa aatctctgct ccaatttctg	720
tatgagcacg ccactaaatt tgattttact tgccgtgtcc gttggaaaaa ggatcaagta	780
ctgggtatggg ataattctgtg tacgatgcac cgcgccgtac ctgattatgc cggcaaattt	840
cgctatttga cgcgcacgac agtcgcgggg gacaaacctt ctcgccatca ccatcatcat	900
cattag	906

<210> 16
 <211> 888
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 16	
atgcacgcgg cgctgactcc tctaccaac aagtatcgct ttatcgacgt gcagccgctg	60
acaggcgctc tcggtgcaga gattacaggc gtggatctgc gggagcctct cgatgacagc	120
acttggaaatg agatcctgga cgcctttcac acctaccaag tgatctactt tccgggtcaa	180
gctatcacta acgagcagca catcgcgctt tcccgcgggt tcggccctgt ggacccggtg	240
ccgatcttaa agagtatcga gggctatcca gaggtgcaga tgatacggcg cgaggcgaac	300
gagagcagcc ggttcacgga agatgactgg cacaccgatt ccaccttcct ggacgctccg	360
cctgccgccg tggatgatgag agctatcgaa gtgccggagt atggaggatga cacaggcttc	420
ctctccatgt acagtgcctg ggagacactc tcgcctacga tgcaagctac catcgaaggc	480
ttaaactgtg tccactcggc gacgaaggtc ttcgggtcat tgtaccaggc gactaattgg	540
cgcttctcga acaccagcgt gaaagtgatg gacgtggacg ccggagatag agagactgtg	600
caccactcgc tcgtgacgca tcctgttacg ggaaggcgcg cactctactg caaccagggtg	660
tactgccaga agatccaggg aatgacggac gcggagtcca agtccctgtt gcaattcctt	720
tacgagcacg ccaccaagtt cgacttcacc tgccgggtcc ggtggaagaa ggaccaagtc	780
ctgggtgtggg acaacctgtg taccatgcac cgcgccgtcc cggactacgc tgggaaattc	840
agatacctga cccgcaccac cgtggcgggg gacaagccgt cgcgttga	888

<210> 17
 <211> 888
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 17	
atgcacgcgg ctttgacacc tttgaccaac aagtatcggt tcatcgacgt tcaaccactc	60
acaggcgctg tcggcgacga gattaccgga gtggacctga gggagccctt agacgactcc	120
acttggaaacg agatcctcga cgcctttcac acctaccaag ttatctactt tcctggacag	180
gcgatcacca acgagcagca cattgccttc tcaaggagggt tcggaccggt agatccagtt	240
ccaattctca aatccattga gggttatccc gaggtgcaga tgattagacg agaagccaac	300

gagtcctcac ggttcatagg cgacgattgg cacacagaca gcaccttcct tgacgtcct	360
ccggctgccg tggttatgcg cgcaatagag gtgccggagt acggcggcga taccggtttc	420
ctatcaatgt actctgcatg ggagacgctc tcaccaacga tgcaagccac cattgaaggt	480
ctaaacgtgg ttactcagc tactaaggtc ttcggaagtc tttaccaggc gacgaattgg	540
aggttcagta acaccagtgt gaaggatgat gatgtggacg ctggagacag ggagacggtg	600
catccactcg tagttacaca ccctgtaact ggacgcagag ccctttactg caaccaggtt	660
tactgccaga agatccaggg aatgactgat gcggagtcta agtccctgct tcaattcctc	720
tacgaacacg ccaccaaatt cgacttcact tgtcgtgttc ggtggaagaa ggaccaagtg	780
ctcgtgtggg ataacctttg caccatgcac cgagcagtac cagactacgc cgggaaattc	840
cgctatctca cccgcactac agtggccgga gacaagccta gccgctga	888

<210> 18
 <211> 295
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 18

Met His Ala Ala Leu Thr Pro Leu Thr Asn Lys Tyr Arg Phe Ile Asp
 1 5 10 15

Val Gln Pro Leu Thr Gly Val Leu Gly Ala Glu Ile Thr Gly Val Asp
 20 25 30

Leu Arg Glu Pro Leu Asp Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
 35 40 45

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

Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
 65 70 75 80

Pro Leu Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
 85 90 95

Arg Glu Ala Asn Glu Ser Ser Arg Val Ile Gly Asp Asp Trp His Ser
 100 105 110

Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
 115 120 125

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

Ser Ala Trp Glu Thr Leu Ser Pro Thr Met Gln Ala Thr Ile Glu Gly
 145 150 155 160

Leu Asn Val Val His Ser Ala Thr Lys Val Phe Gly Ser Leu Tyr Gln
 165 170 175

Ala Thr Asn Trp Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
 180 185 190

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

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

Ile Gln Gly Met Thr Asp Ala Glu Ser Lys Ser Leu Leu Gln Phe Leu
 225 230 235 240

Tyr Glu His Ala Thr Lys Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
 245 250 255

Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ala
 260 265 270

Ala Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
 275 280 285

Ala Gly Asp Lys Pro Ser Arg
 290 295

<210> 19
 <211> 906
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 19
 atgcacgcgg ctctgacccc gcttaccaac aaataccggt tcatcgacgt tcagccgctg 60
 accggtgttt taggtgctga aatcaccggt gttgacctgc gtgaaccgct ggacgactct 120
 acctggaacg aaatcctgga cgcgttcac acctaccagg ttatctactt cccgggtcag 180
 gcgatcacca acgaacagca catcgcggtc tctcgtcgtc tcggtccggt tgacccggtt 240
 ccgctgctca aatctatcga aggttaccg gaagttcaga tgatccgctc cgaagcgaac 300
 gaatctagcc gtgttattgg tgacgattgg cacagcgact ccaccttcct ggacgcgccg 360
 ccagctgcag ttgtgatgcg tgctattgaa gttccggaat acggtggcga caccggtttc 420
 ctgtccatgt actctgcttg ggaaacctg tccccgacca tgcaggctac cattgaaggt 480
 ctgaacgttg tgcactccgc aaccaaagtg ttcggcagcc tgtaccaggc aaccaactgg 540
 cgcttcagca acactagtgt gaaagtgatg gatgtggatg caggcgatcg tgagactgtg 600
 caccgcgtgg tggttaacta cccggttacc ggccgtcgtg cgctgtactg caaccaggta 660
 tattgccaga aaattcaggg catgactgat gcagagtcaa aatctctgct ccaatttctg 720
 tatgagcacg ccactaaatt tgattttact tgccgtgtcc gttggaaaaa ggatcaagta 780
 ctggtatggg ataattctgtg tacgatgcac cgcgccgcgc ctgattatgc cggcaaattt 840
 cgctatttga cgcgcacgac agtcgcgggg gacaaacctt ctcgccatca ccatcatcat 900
 cattag 906

<210> 20
 <211> 888
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 20
 atgcacgcgg cgctgactcc tctcaccaac aagtatcgct ttatcgacgt gcagccgctg 60
 acaggcgtcc tcggtgcaga gattacaggc gtggatctgc gggagcctct cgatgacagc 120

acttggaa	agatcctgga	cgcccttcac	acctaccaag	tgatctactt	tccgggtcaa	180
gctatcacta	acgagcagca	catcgcggtc	tcccgccggt	tcggccctgt	ggacccggtg	240
ccgctgttaa	agagtatcga	gggctatcca	gaggtgcaga	tgatacggcg	cgaggcgaac	300
gagagcagcc	gggtgatcgg	agatgactgg	cactccgatt	ccaccttcct	ggacgctccg	360
cctgccgccc	tggtgatgag	agctatcgaa	gtgccggagt	atggagggtga	cacaggcttc	420
ctctccatgt	acagtgcctg	ggagacactc	tcgcctacga	tgcaagctac	catcgaaggc	480
ttaaactgtg	tccactcggc	gacgaaggtc	ttcgggtcat	tgtaccaggc	gactaattgg	540
cgcttctcga	acaccagcgt	gaaagtgatg	gacgtggacg	ccggagatag	agagactgtg	600
caccactcgc	tcgtgacgca	tcctgttacg	ggaaggcgcg	cactctactg	caaccagggtg	660
tactgccaga	agatccaggg	aatgacggac	gcggagtcga	agtcctctgtt	gcaattcctt	720
tacgagcacg	ccaccaagtt	cgacttcacc	tgccgggtcc	ggtggaagaa	ggaccaagtc	780
ctggtgtggg	acaacctgtg	taccatgcac	cgcgccgccc	cggactacgc	tgggaaattc	840
agatacctga	cccgaccac	cgtaggcgga	gacaagccgt	cgcggtga		888

<210> 21
 <211> 888
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 21	
atgcacgcag	cccttactcc actgacgaac aagtatcgct tcatcgacgt gcagccactc 60
acgggtgtac	tcggagccga gatcacggga gtggatctgc gcgagccgct cgatgactct 120
acatggaacg	agatcctaga cgctttccac acttatcaag ttatctactt tccaggacaa 180
gccatcacta	acgagcaaca catcgcggtc tcacgtcggt tcgggcctgt tgatcctgtg 240
ccgctcctca	agtcaatcga gggttatcca gaagttcaga tgatccggcg cgaggctaata 300
gagtcatccc	gtgttatcgg tgatgactgg cactcggaca gtacattcct cgacgcacca 360
ccggccgcag	ttgtgatgag ggctatcgaa gtgccggaat acggtggtga cactgggttc 420
ctgtcaatgt	actctgcatg ggagaccctt agtcccacta tgcaagcaac catcgaaggg 480
ctcaacgttg	tgatttcagc tactaaagta ttcggttccc tttatcaggc gacaaactgg 540
cggttcagca	ataccagtgt taaagttatg gatgtggatg ctggagacag ggaaacgggtc 600
caccctcttg	tcgtcacgca cccagttaca gggcgctcag cgctttactg caatcagggtg 660
tactgtcaga	agattcaagg aatgaccgat gcggagtcca aatcactgtt acaattcttg 720
tacgagcacg	ccactaagtt cgatttcacg tgccgagtgc gctggaagaa ggatcaagtg 780
ctcgtttggg	acaacttggt caccatgcac cgggcagctc ccgactacgc gggcaagttc 840
cgttatctca	ctcgcacaaac tgtcgctgga gacaagccct cccgatga 888

<210> 22
 <211> 295
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 22

Met	His	Ala	Ala	Leu	Ser	Pro	Leu	Ser	Gln	Arg	Phe	Glu	Arg	Ile	Ala
1				5					10					15	

Val Gln Pro Leu Thr Gly Val Leu Gly Ala Glu Ile Thr Gly Val Asp
 20 25 30
 Leu Arg Glu Pro Leu Asp Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
 35 40 45
 Phe His Thr Tyr Gln Val Ile Tyr Phe Pro Gly Gln Ala Ile Thr Asn
 50 55 60
 Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
 65 70 75 80
 Pro Leu Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
 85 90 95
 Arg Glu Ala Asn Glu Ser Gly Arg Val Ile Gly Asp Asp Trp His Thr
 100 105 110
 Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Tyr Ala
 115 120 125
 Lys Glu Val Pro Pro Tyr Gly Gly Asp Thr Leu Phe Ala Ser Met Tyr
 130 135 140
 Thr Ala Trp Glu Thr Leu Ser Pro Thr Met Gln Ala Thr Ile Glu Gly
 145 150 155 160
 Leu Asn Val Val His Ser Ala Thr Arg Val Phe Gly Ser Leu Tyr Gln
 165 170 175
 Ala Gln Asn Arg Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
 180 185 190
 Asp Ala Gly Asp Arg Glu Thr Val His Pro Leu Val Val Thr His Pro
 195 200 205
 Glu Thr Gly Arg Lys Gly Leu Tyr Val Asn Gln Val Tyr Cys Gln Arg
 210 215 220
 Ile Glu Gly Met Ser Glu Lys Glu Ser Glu Pro Leu Leu Ser Phe Leu
 225 230 235 240
 Phe Ala His Ala Thr Lys Pro Glu Phe Thr Cys Arg Val Arg Trp Gln
 245 250 255
 Glu Gly Gln Val Leu Val Trp Asp Asn Leu Cys Thr Gln His Phe Ala
 260 265 270
 Val Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
 275 280 285
 Gly Gly Val Arg Pro Ala Arg
 290 295

<210> 23
 <211> 906
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 23
 atgcacgcgg ctctgagccc gcttagccag cgtttcgaac gtatcgcggt tcagccgctg

accggtgttt tagtgctga aatcaccggt gttgacctgc gtgaaccgct ggacgactct	120
acctggaacg aaatcctgga cgcgttcac acctaccagg ttatctactt cccgggtcag	180
gcgatcacca acgaacagca catcgcttc tctcgtcgtc tcggtccggt tgaccgggtt	240
ccgctgctca aatctatcga aggttaccg gaagttcaga tgatccgtcg cgaagcgaac	300
gaatctggtc gtgttattgg tgacgactgg cacaccgact ctaccttcct ggacgcgccg	360
ccagctgcag ttgtgatgta cgctaaagaa gtgccgccat acggtggcga caccctgttc	420
gcgtccatgt acaccgcttg ggaaccctg tccccgacca tgcaggctac cattgaaggt	480
ctgaacgttg tgcactccgc aactcgtgtt ttcggctccc tgtaccaggc acagaaccgt	540
cgcttcagca aactagcgt taaagtgatg gatgtggatg caggcgatcg tgaaactgtg	600
caccgcgtgg tggttaactca cccgaaact ggccgtaaag gcctgtacgt gaaccaggta	660
tattgccagc gtattgaagg catgagttag aaagagtcgg agccgtgct ctcatttctg	720
tttgcacacg ccactaaacc agagtttact tgccgtgtcc gttggcaaga gggccaggta	780
ctggtatggg ataactgtg tacgcaacac ttcgccgtac ctgattatgc cggcaagttt	840
cgctatttga cgcgcacgac agtcggcggg gtccgcctg cccgccatca ccatcaccat	900
cattag	906

<210> 24
 <211> 888
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 24	
atgcacgcgg ccctgtctcc tctgtcccag cggttcgagc gcatcgcggt ccagccgcta	60
acgggtgtcc tgggcgcgga aatcaccgga gttgatctga gagagccttt agacgacagc	120
acctggaacg agatcctcga tgcctttcac acataccaag ttatctactt tccgggcaa	180
gccatcacga acgagcagca catcgcttt agccggagggt ttggcccggt tgatccggtt	240
cctctgctta agtcaattga gggttacca gaggtgcaga tgatccgccg cgaggccaac	300
gaatctgggc gtgtcatagg cgacgattgg catacggaca gcaccttct cgacgctcct	360
ccggccgcag tcgtgatgta cgcgaaggag gtgccgcctt acggcggcga taccctgttc	420
gcgtcgtatg acacggcctg ggagacgctc agcccgacca tgcaagccac aatagagggt	480
ctaaatgtgg tccactccgc gacgcgggtg ttcgggagcc tctaccaggc gcagaacaga	540
cggttctcga acacatcagt caaggtgatg gacgtggatg ccggagatcg tgaaactgtt	600
caccacttg tggtcacca tccagagacg ggaaggaaag gactttacgt gaaccagggtg	660
tactgccagc ggatcgaggg catgtccgag aaggagagt agccattgct gagctttcta	720
ttcgcgacg caactaagcc cgagttcacg tgccgcgtcc gatggcaaga gggccaagtt	780
ctcgtctggg ataacttgtg cacacagcac ttcgcggttc ccgattacgc cggaaagttc	840
cgctatctca cacgcaccac tgtgggaggc gttcgtccc cgcggtga	888

<210> 25
 <211> 295
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 25

Met His Ala Ala Leu Thr Pro Leu Thr Asn Lys Tyr Arg Phe Ile Asp
 1 5 10 15
 Val Gln Pro Leu Thr Gly Val Leu Gly Ala Glu Ile Thr Gly Val Asp
 20 25 30
 Leu Arg Glu Pro Leu Asp Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
 35 40 45
 Phe His Thr Tyr Gln Val Ile Tyr Phe Pro Gly Gln Ala Ile Thr Asn
 50 55 60
 Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
 65 70 75 80
 Pro Leu Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
 85 90 95
 Arg Glu Ala Asn Glu Ser Gly Arg Val Ile Gly Asp Asp Trp His Thr
 100 105 110
 Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Tyr Ala
 115 120 125
 Arg Glu Val Pro Pro Tyr Gly Gly Asp Thr Gly Phe Leu Ser Met Tyr
 130 135 140
 Thr Ala Trp Glu Thr Leu Ser Pro Thr Met Gln Ala Thr Ile Glu Gly
 145 150 155 160
 Leu Asn Val Val His Ser Ala Thr Arg Val Phe Gly Ser Leu Tyr Gln
 165 170 175
 Ala Gln Asn Arg Arg Tyr Ser Asn Thr Ser Val Lys Val Met Asp Val
 180 185 190
 Asp Ala Gly Asp Arg Glu Thr Val His Pro Leu Val Val Ser His Pro
 195 200 205
 Val Thr Gly Arg Arg Ala Leu Tyr Cys Asn Gln Val Tyr Cys Gln Arg
 210 215 220
 Ile Glu Gly Met Thr Asp Ala Glu Ser Lys Ser Leu Leu Gln Phe Leu
 225 230 235 240
 Tyr Glu His Ala Thr Lys Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
 245 250 255
 Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ala
 260 265 270
 Val Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
 275 280 285
 Ala Gly Asp Lys Pro Ser Arg
 290 295

<210> 26
 <211> 906
 <212> ADN

<213> Secuencia Artificial

<220>

<223> Recombinante

<400> 26

atgcacgcgg ctctgacccc gcttaccaac aaataccggt tcatcgacgt tcagccgctg	60
accggtgttt taggtgctga aatcaccggt gttgacctgc gtgaaccgct ggacgactct	120
acctggaacg aaatcctgga cgcgttccac acctaccagg ttatctactt cccgggtcag	180
gcgatcacca acgaacagca catcgcgttc tctcgtcgct tcgggtccggt tgacccggtt	240
ccgctgctca aatctatcga aggttaccg gaagttcaga tgatccgtcg cgaagcgaac	300
gaatctggtc gtgttattgg tgacgattgg cacaccgact ccaccttcct ggacgcgccg	360
ccagctgcag ttgtgatgta cgctcgtgaa gttccgccgt acggtggcga caccggtttc	420
ctgtccatgt acaccgcttg ggaaccctg tccccgacca tgcaggctac cattgaaggt	480
ctgaacgttg tgactccgc aaccctgtg ttcggcagcc tgtaccaggc acagaaccgt	540
cgctacagca aactagtgt gaaagtgatg gatgtggatg caggcgatcg tgagactgtg	600
caccgcgtgg tggatatcga cccggttacc ggccgtcggt cgctgtactg caaccaggta	660
tattgccagc gtattgaggg catgactgat gcagagtcaa aatctctgct ccaatttctg	720
tatgagcacg cactaaatt tgattttact tgccgtgtcc gttggaaaaa ggatcaagta	780
ctggtatggg ataactctgtg tacgatgcac cgcgcgttac ctgattatgc cggcaaattt	840
cgctatttga cgcgcacgac agtcgcgggg gacaaacctt ctcgccatca ccatcatcat	900
cattag	906

<210> 27

<211> 888

<212> ADN

<213> Secuencia Artificial

<220>

<223> Recombinante

<400> 27

atgcacgcgtg ctctgactcc actcacaac aagtacgggt tcatcgacgt gcaaccgctg	60
accggcgctct tgggtgcgga aatcaccggc gtggacttgc gggagccgct ggatgacagc	120
acatggaacg agatcctcga tgcgttccac acctaccaag tgatctattt cccaggccag	180
gccattacga acgagcagca catcgcgttc agtcgaaggt tcgggcctgt ggacccggtt	240
ccgctgctta agagtatcga gggctaccg gaagtacaga tgattcgccg cgaagcgaat	300
gagtcggggc gagtgatcgg cgatgactgg cacaccgaca gcacgttcct cgacgcgccg	360
cctgccgctg tcgtgatgta cgcacgggag gtgccacct acggcggaga tacgggattc	420
ctttcaatgt acacggcatg ggagacactc tctccgacca tgcaagcaac gatagagggc	480
ttgaacgtgg tgactccgc caccgaggtc ttcggcagcc tctaccaagc ccagaaccgc	540
cggtagctca aactagcgt gaaagtgatg gacgtggatg cgggcgaccg ggagaccgtg	600
catcctctag ttgtgagcca cccggtgact ggccgacggg cgctgtactg caaccaggtc	660
tattgccagc gcatcgaggg catgaccgac gcggagtcca aatctctgct ccaattcctg	720
tacgagcacg ccacgaagtt cgacttcacc tgccgggttc gctggaagaa ggatcaagtg	780
ctagtgtggg acaacctctg cactatgcac agggctgtgc cgactatgc tggcaaattc	840
cgttacctta cccggaccac tgtggcgggc gacaagccaa gcagatga	888

<210> 28

<211> 295
<212> PRT
<213> Secuencia Artificial

<220>
<223> Recombinante

<400> 28

Met His Ala Ala Leu Thr Pro Leu Thr Asn Lys Tyr Arg Phe Ile Asp
1 5 10 15
Val Gln Pro Leu Thr Gly Val Leu Gly Ala Glu Ile Thr Gly Val Asp
20 25 30
Leu Arg Glu Pro Leu Asp Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
35 40 45
Phe His Thr Tyr Gln Val Ile Tyr Phe Pro Gly Gln Ala Ile Thr Asn
50 55 60
Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
65 70 75 80
Pro Leu Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
85 90 95
Arg Glu Ala Asn Glu Ser Gly Arg Val Ile Gly Asp Asp Trp His Thr
100 105 110
Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
115 120 125
Ile Glu Val Pro Glu Tyr Gly Gly Asp Thr Gly Phe Leu Ser Met Tyr
130 135 140
Ser Ala Trp Glu Thr Leu Ser Pro Thr Met Gln Ala Thr Ile Glu Gly
145 150 155 160
Leu Asn Val Val His Ser Ala Thr Lys Val Phe Gly Ser Leu Tyr Gln
165 170 175
Ala Thr Asn Trp Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
180 185 190
Asp Ala Gly Asp Arg Glu Thr Val His Pro Leu Val Val Thr His Pro
195 200 205
Val Thr Gly Arg Arg Ala Leu Tyr Cys Asn Gln Val Tyr Cys Gln Lys
210 215 220
Ile Gln Gly Met Thr Asp Ala Glu Ser Lys Ser Leu Leu Gln Phe Leu
225 230 235 240
Tyr Glu His Ala Thr Lys Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
245 250 255
Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ala
260 265 270
Val Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
275 280 285

Ala Gly Asp Lys Pro Ser Arg
290 295

<210> 29
<211> 906
<212> ADN
<213> Secuencia Artificial

<220>

<223> Recombinante

<400> 29
atgcacgcgg ctctgacccc gcttaccaac aaataccggt tcatcgacgt tcagccgctg 60
accggtgttt taggtgctga aatcaccggt gttgacctgc gtgaaccgct ggacgactct 120
acctggaacg aaatcctgga cgcgttcac acctaccagg ttatctactt cccgggtcag 180
gcgatcacca acgaacagca catcgcggtc tctcgtcgtc tcgggtccggt tgaccgggtt 240
ccgctgctca aatctatcga aggttacccg gaagttcaga tgatccgtcg cgaagcgaac 300
gaatctggtc gtgttattgg tgacgattgg cacaccgact ccaccttcct ggacgcgccg 360
ccagctgcag ttgtgatgcg tgctattgaa gttccggaat acgggtggcg caccgggttc 420
ctgtccatgt actctgcttg gaaaccctg tccccgacca tgcaggctac cattgaaggt 480
ctgaacgttg tgcaactccg aaccaaagtg ttcggcagcc tgtaccaggc aaccaactgg 540
cgcttcagca acactagtgt gaaagtgatg gatgtggatg caggcgatcg tgagactgtg 600
caccgcgtgg tggttaactca cccggttacc ggccgtcgtg cgctgtactg caaccaggta 660
tattgccaga aaattcaggg catgactgat gcagagtaa aatctctgct ccaatttctg 720
tatgagcacg ccactaaatt tgattttact tgccgtgtcc gttggaaaaa ggatcaagta 780
ctggtatggg ataactctgtg tacgatgcac cgcgccgtac ctgattatgc cggcaaattt 840
cgctatttga cgcgcacgac agtcgcgggg gacaaacctt ctcccatca ccatcatcat 900
cattag 906

<210> 30
<211> 888
<212> ADN
<213> Secuencia Artificial

<220>

<223> Recombinante

<400> 30
atgcacgcgg cgctgactcc tctcaccaac aagtatcgct ttatcgacgt gcagccgctg 60
acaggcgctc tcggtgcaga gattacaggc gtggatctgc gggagcctct cgatgacagc 120
acttggaatg agatcctgga cgcctttcac acctaccaag tgatctactt tccgggtcaa 180
gctatcacta acgagcagca catcgcggtc tcccgcgggt tcggccctgt ggaccgggtg 240
ccgctgttaa agagtatcga gggctatcca gaggtgcaga tgatacggcg cgaggcgaac 300
gagagcggcc ggggtgatcg agatgactgg cacaccgatt ccaccttcct ggacgctccg 360
cctgccgccg tggatgatgag agctatcgaa gtgccggagt atggagggtga cacaggcttc 420
ctctccatgt acagtgcctg ggagacactc tcgcctacga tgcaagctac catcgaaggc 480
ttaaacgtgg tccactcggc gacgaaggtc ttcgggtcat tgtaccaggc gactaattgg 540
cgcttctcga acaccagcgt gaaagtgatg gacgtggacg ccggagatag agagactgtg 600
caccactcgc tcgtgacgca tcctgttacg ggaaggcgcg cactctactg caaccagggtg 660
tactgccaga agatccaggg aatgacggac gcggagtcga agtcctctgtt gcaattcctt 720
tacgagcacg ccaccaagtt cgacttcacc tgccgggtcc ggtggaagaa ggaccaagtc 780

ctggtgtggg acaacctgtg taccatgcac cgcgccgtcc cggactacgc tgggaaattc 840
agatacctga cccgcaccac cgtggcgga gacaagccgt cgcgttga 888

<210> 31
<211> 295
<212> PRT
<213> Secuencia Artificial

<220>
<223> Recombinante

<400> 31

Met His Ala Ala Leu Ser Pro Leu Ser Gln Lys Tyr Arg Phe Ile Asp
1 5 10 15

Val Gln Pro Leu Thr Gly Val Leu Gly Ala Glu Ile Thr Gly Val Thr
20 25 30

Leu Arg Glu Pro Leu Asp Asp Asn Thr Trp Asn Glu Ile Leu Asp Ala
35 40 45

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

Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
65 70 75 80

Pro Leu Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
85 90 95

Arg Glu Ala Asn Glu Ser Gly Arg Val Ile Gly Asp Asp Trp His Thr
100 105 110

Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Tyr Ala
115 120 125

Arg Glu Val Pro Pro Tyr Gly Gly Asp Thr Gly Phe Leu Ser Met Tyr
130 135 140

Ser Ala Trp Asp Thr Leu Ser Asp Thr Met Lys Ala Thr Ile Glu Gly
145 150 155 160

Leu Asn Val Val His Ser Ala Thr Arg Val Phe Gly Ser Leu Tyr Gln
165 170 175

Ala Gln Asn Arg Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
180 185 190

Asp Ala Gly Asp Arg Glu Thr Val His Pro Leu Val Val Ser His Pro
195 200 205

Val Thr Gly Arg Arg Ala Leu Tyr Cys Asn Gln Val Tyr Cys Gln Arg
210 215 220

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

Tyr Glu His Ala Thr Arg Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
245 250 255

Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ala
260 265 270

Val Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
275 280 285

Ala Gly Asp Lys Pro Ser Arg
290 295

<210> 32
<211> 906
<212> ADN
<213> Secuencia Artificial

<220>
<223> Recombinante

<400> 32
atgcacgcgg ctctgagccc gcttagccag aaataccggt tcatcgacgt tcagccgctg 60
accggtgttt taggtgctga aatcaccggt gttaccctgc gtgaaccgct ggacgacaac 120
acctggaacg aaatcctgga cgcgttcac acctaccagg ttatctactt cccgggtcag 180
gcgatcacca acgaacagca catcgcggtc tctcgtcgct tcgggccggt tgacccggtt 240
ccgctgctca aatctatcga aggttacccg gaagttcaga tgatccgtcg cgaagcgaac 300
gaatctggtc gtgttattgg tgacgattgg cacaccgact ccaccttcct ggacgcgccg 360
ccagctgcag ttgtgatgta cgctcgtgaa gttccgccgt acggtggcga caccgggttc 420
ctgtccatgt actctgcttg ggacaccctg tccgacacca tgaaagctac cattgaaggt 480
ctgaacgttg tgactccgc aaccctgttg ttcggcagcc tgtaccaggc acagaaccgt 540
cgcttcagca aactagtgtg gaaagtgatg gatgtggatg caggcgatcg tgagactgtg 600
caccgcgtgg tggatatcga cccgggtacc ggccgtcggt cgctgtactg caaccaggta 660
tattgccagc gtattgaggg catgactgat gcagagtcaa aaccactgct ccaatttctg 720
tatgagcacg cactcgtttt tgattttact tgccgtgtcc gttggaaaaa ggatcaagta 780
ctggtatggg ataactgttg tacgatgcac cgcgcgttac ctgattatgc cggcaaattt 840
cgctatttga cgcgcacgac agtcgcgggg gacaaacctt ctcgccatca ccatcatcat 900
cattag 906

<210> 33
<211> 888
<212> ADN
<213> Secuencia Artificial

<220>
<223> Recombinante

<400> 33
atgcacgccg ccctctctcc tcttagccag aagtaccgat tcatcgacgt ccagccgctc 60
actggcgtag tgggcgctga gataacgggt gtgacctga gggagccgct ggacgacaac 120
acttgaacg agatccttga cgccttccat acttatcaag ttatctactt tcctggacaa 180
gcgattacga atgagcagca catcgcggtc tcccggaggt tcgggccagt cgatccggtg 240
ccgtactca agtccatcga aggataccca gaagtcaga tgatccgtcg tgaggcaaac 300
gagtcggcc gggatcatcg cgacgattgg cacaccgact ctaccttcct tgacgcgcct 360
ccggccgcag tggatcatgta cggccgcgag gtgcctccct acggcggcga tacgggcttc 420
ctcagtatgt actctgcatg ggacacccta agcgacacca tgaaggccac catcgaaggt 480
ctgaacgtcg tgactcggc aacacgagtc ttcggatcac tctaccaagc acagaatcgc 540
cgcttctcga acacctcggg taaggtgatg gacgtggatg cgggtgacag ggaaaccgtt 600

catcctctgg tggctctcgca tccggttacg ggacgccgcg ctctctactg caaccaggtg	660
tactgtcaaa ggatcgaagg aatgacagat gctgagagca agccgttgct ccaattcctc	720
tatgaacacg caacaaggtt cgacttcacc tgccgggttc gatggaagaa ggatcaagtg	780
ctagtctggg acaacctctg caccatgcac cgggccgtgc cggactatgc tgggaaattc	840
cgttacctga cccgcacgac cgtcgcggga gacaagccgt cgagatga	888

<210> 34
 <211> 295
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 34

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

Tyr Glu His Ala Thr Lys Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
245 250 255

Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ser
260 265 270

Val Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
275 280 285

Ala Gly Asp Lys Pro Ser Arg
290 295

<210> 35
<211> 906
<212> ADN
<213> Secuencia Artificial

<220>
<223> Recombinante

<400> 35	
atgcacgcgg ctctgacccc gcttaccaac aaataccggt tcatcgacgt tcagccgctg	60
accggtgttt taggtgctga aatcaccggt gttgacctgc gtgaaccgct ggacgactct	120
acctggaacg aaatcctgga cgcgttcac acctaccagg ttatctactt cccgggtcag	180
gcgatcacca acgaacagca catcgcggtc tctcgtcgtc tcgggtccgtg tgacccggtt	240
ccgctgctca aatctatcga aggttacccg gaagttcaga tgatccgtcg cgaagcgaac	300
gaatctggtc gtgttattgg tgacgattgg cagcgggact ccaccttcct ggacgcgccg	360
ccagctgcag ttgtgatgcy tgctattgaa gttccggaat acggtggcga caccggtttc	420
ctgtccatgt actctgcttg ggaaaccttg tccccgacca tgcaggctac cattgaaggt	480
ctgaacgttg tgcactccgc aaccaaagtg ttcggcagcc tgtaccaggc aaccaactgg	540
cgcttcagca acactagtgt gaaagtgatg gatgtggatg caggcgatcg tgagactgtg	600
caccgcgtgg tggtaaacta cccggttacc ggccgtcgtg cgctgtactg caaccaggtg	660
tattgccaga aaattcaggg catgactgat gcagagtcaa aatctctgct ccaatttctg	720
tatgagcacg cactaaatt tgattttact tgccgtgtcc gttggaaaaa ggatcaagta	780
ctggtatggg ataactctgtg tacgatgcac cgcagcgtag ctgattatgc cggcaaattt	840
cgctatttga cgcgcacgac agtcgcgggg gacaaacctt ctcgccatca ccatcatcat	900
cattag	906

<210> 36
<211> 888
<212> ADN
<213> Secuencia Artificial

<220>
<223> Recombinante

<400> 36	
atgcacgcgg cgctgactcc tctcaccaac aagtatcgct ttatcgacgt gcagccgctg	60
acaggcgtcc tcggtgcaga gattacaggc gtggatctgc gggagcctct cgatgacagc	120
acttggaaag agatcctgga cgcctttcac acctaccaag tgatctactt tccgggtcaa	180
gctatcacta acgagcagca catcgcggtc tcccgcgggt tcggccctgt ggacccggtg	240
ccgctgttaa agagtatcga gggctatcca gaggtgcaga tgatacggcg cgaggcgaac	300
gagagcggcc ggggtgatcg agatgactgg cagcgggatt ccaccttcct ggacgtccg	360
cctgccgccg tgggtgatgag agctatcgaa gtgccggagt atggaggatga cacaggcttc	420

ctctccatgt acagtgcctg ggagacactc tcgcctacga tgcaagctac catcgaaggc	480
ttaaactgtg tccactcggc gacgaaggtc ttcgggtcat tgtaccaggc gactaattgg	540
cgcttctcga acaccagcgt gaaagtgatg gacgtggacg ccggagatag agagactgtg	600
caccactcg tcgtgacgca tcctgttacg ggaaggcgcg cactctactg caaccagggtg	660
tactgccaga agatccaggg aatgacggac gcggagtcga agtccctgtt gcaattcctt	720
tacgagcacg ccaccaagtt cgacttcacc tgccgggtcc ggtggaagaa ggaccaagtc	780
ctggtgtggg acaacctgtg taccatgcac cgctccgtcc cggactacgc tgggaaattc	840
agatacctga cccgcaccac cgtggcgga gacaagccgt cgcggtga	888

<210> 37
 <211> 295
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 37

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

Ile Gln Gly Met Thr Asp Ala Glu Ser Lys Ser Leu Leu Gln Phe Leu
 225 230 235 240

Tyr Glu His Ala Thr Lys Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
 245 250 255

Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ser
 260 265 270

Val Pro Asp Tyr Gly Asn Ala Phe Arg Tyr Leu Thr Arg Thr Thr Val
 275 280 285

Ala Gly Asp Lys Pro Ser Arg
 290 295

<210> 38
 <211> 906
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 38	
atgcacgcgg ctctgacccc gcttaccaac aaataccggt tcatcgacgt tcagccgctg	60
accggtgttt taggtgctga aatcaccggt gttgacctgc gtgaaccgct ggacgactct	120
acctggaacg aaatcctgga cgcgttcac acctaccagg ttatctactt cccgggtcag	180
gcgatcacca acgaacagca catcgcggtc tctcgtcgtc tcgggtccgtg tgacccggtt	240
ccgatttctca aatctatcga aggttaccg gaagttcaga tgatccgtcg cgaagcgaac	300
gaatctggtc gtgttattgg tgacgattgg cacaccgact ccaccttcct ggacgcgccg	360
ccagctgcag ttgtgatgcg tgctattgaa gttccggaat acggtggcga caccggtttc	420
ctgtccatgt actctgcttg ggaaacctg tccccgacca tgcaggctac cattgaaggt	480
ctgaacgttg tgactccgc aaccaaagtg ttcggcagcc tgtaccaggc aaccaactgg	540
cgcttcagca acactagtgt gaaagtgatg gatgtggatg caggcgatcg tgagactgtg	600
caccgcgtgg tggtaaacta cccggttacc ggccgtcgtg cgctgtactg caaccaggtg	660
tattgccaga aaattcaggg catgactgat gcagagtcaa aatctctgct ccaatttctg	720
tatgagcacg cactaaatt tgattttact tgccgtgtcc gttggaaaaa ggatcaagta	780
ctggtatggg ataactctgtg tacgatgcac cgcagcgtac ctgattatgg caatgcgttt	840
cgctatttga cgcgcacgac agtcgcgggg gacaaacctt ctcgccatca ccatcatcat	900
cattag	906

<210> 39
 <211> 888
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 39	
atgcacgcgg cgctgactcc tctaccaac aagtatcgct ttatcgacgt gcagccgctg	60
acaggcgtcc tcggtgcaga gattacaggc gtggatctgc gggagcctct cgatgacagc	120
acttggaaatg agatcctgga cgcctttcac acctaccaag tgatctactt tccgggtcaa	180
gctatcacta acgagcagca catcgcggtc tcccgcgggt tcggccctgt ggacccggtg	240

ccgatcttaa agagtatcga gggctatcca gaggtgcaga tgatacggcg cgaggcgaac 300

gagagcggcc gggatgatcgg agatgactgg cacaccgatt ccaccttcct ggacgctccg 360

cctgccgccg tggatgatgag agctatcgaa gtgccggagt atggaggtga cacaggcttc 420

ctctccatgt acagtgcctg ggagacactc tcgcctacga tgcaagctac catcgaaggc 480

ttaaactgtg tccactcggc gacgaaggtc ttcgggtcat tgtaccaggc gactaattgg 540

cgcttctcga acaccagcgt gaaagtgatg gacgtggacg ccggagatag agagactgtg 600

caccactcg tcgtgacgca tcctgttacg ggaaggcgcg cactctactg caaccagggtg 660

tactgccaga agatccaggg aatgacggac gcggaagtcga agtcctgtt gcaattcctt 720

tacgagcacg ccaccaagtt cgacttcacc tgccgggtcc ggtggaagaa ggaccaagtc 780

ctggtgtggg acaactgtg taccatgcac cgctccgtcc cggactacgg caacgccttc 840

agatacctga cccgcaccac cgtggcgga gacaagccgt cgcgttga 888

<210> 40
 <211> 295
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 40

Met His Ala Ala Leu Thr Pro Leu Thr Asn Lys Tyr Arg Phe Ile Asp
 1 5 10 15

Val Gln Pro Leu Thr Gly Val Leu Gly Ala Glu Ile Thr Gly Val Asp
 20 25 30

Leu Arg Glu Pro Leu Asp Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
 35 40 45

Phe His Thr Tyr Gln Val Ile Tyr Phe Pro Ala Gln Gln Ile Thr Asn
 50 55 60

Glu Gln His Ile Ser Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
 65 70 75 80

Pro Leu Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
 85 90 95

Arg Glu Ala Asn Glu Ser Gly Arg Ile Leu Gly Asp Asp Trp His Thr
 100 105 110

Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
 115 120 125

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

Ser Ala Trp Asp Thr Leu Ser Asp Thr Met Lys Ala Thr Ile Glu Gly
 145 150 155 160

Leu Asn Val Val His Ser Ala Thr Arg Val Phe Gly Ser Leu Tyr Gln
 165 170 175

Ala Gln Asn Trp Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
 180 185 190

Asp Ala Gly Asp Arg Glu Thr Val His Pro Leu Val Val Ser His Pro
 195 200 205
 Val Thr Gly Arg Arg Ala Leu Tyr Cys Asn Gln Val Tyr Cys Gln Arg
 210 215 220
 Ile Glu Gly Met Thr Asp Ala Glu Ser Lys Cys Leu Leu Gln Phe Leu
 225 230 235 240
 Tyr Glu His Ala Thr Lys Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
 245 250 255
 Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ala
 260 265 270
 Val Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
 275 280 285
 Ala Gly Asp Arg Pro Ala Arg
 290 295

<210> 41
 <211> 906
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 41
 atgcacgcgg ctctgacccc gcttaccaac aaataccggt tcatcgacgt tcagccgctg 60
 accggtgttt taggtgctga aatcaccggt gttgacctgc gtgaaccgct ggacgactct 120
 acctggaacg aaatcctgga cgcgttcac acctaccagg ttatctactt cccggcgag 180
 cagatcacca acgaacagca catctctttc tctcgtcgt tccggtccggt tgacccggtt 240
 ccgctgctca aatctatcga aggttacccg gaagttcaga tgatccgctc cgaagcgaac 300
 gaattctggtc gtatcctggg tgacgattgg cacaccgact ccaccttcct ggacgcgccg 360
 ccagctgcag ttgtgatgcg tgctattgaa gttccggaat acggtggcga caccggtttc 420
 ctgtccatgt actctgcttg ggacacacctg tccgacacca tgaaagctac cattgaaggt 480
 ctgaacgttg tgactccgc aaccggtggt ttcggcagcc tgtaccaggc acagaactgg 540
 cgcttcagca acactagtgt gaaagtgatg gatgtggatg caggcgatcg tgagactgtg 600
 caccgctggt tggatatcca cccggttacc ggccgtcgtg cgctgtactg caaccaggtg 660
 tattgccagc gtattgaggg catgactgat gcagagtcaa aatgcctgct ccaatttctg 720
 tatgagcacg ccactaaatt tgattttact tgccgtgtcc gttggaaaaa ggatcaagta 780
 ctggtatggg ataattctgtg tacgatgcac cgcgccgtac ctgattatgc cggcaaattt 840
 cgctatttga cgcgcacgac agtcgcgggg gaccgccctg cccgccatca ccatcatcat 900
 cattag 906

<210> 42
 <211> 888
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 42
 atgcacgcgg ccttaacgcc actcacgaac aagtatcgct tcatcgacgt ccagccgctc 60

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

Ala Gln Asn Trp Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
180 185 190

Asp Ala Gly Asp Arg Glu Thr Val His Pro Leu Val Val Ser His Pro
195 200 205

Val Thr Gly Arg Arg Ala Leu Tyr Cys Asn Gln Val Tyr Cys Gln Arg
210 215 220

Ile Glu Gly Met Thr Asp Ala Glu Ser Lys Cys Leu Leu Gln Phe Leu
225 230 235 240

Tyr Glu His Ala Thr Lys Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
245 250 255

Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Leu Ala
260 265 270

Val Pro Asp Tyr Asp Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
275 280 285

Ala Gly Asp Lys Pro Ser Arg
290 295

<210> 44
<211> 906
<212> ADN
<213> Secuencia Artificial

<220>
<223> Recombinante

<400> 44
atgcacgcgg ctctgacccc gcttaccaac aaataccggt tcatcgacgt tcagccgctg 60
tgcggtgttt taggtgctga aatcaccggt gttgacctgc gtgaaccgct ggacgactct 120
acctggaacg aaatcctgga cgcgttcac acctaccagg ttatctactt cccgggtcag 180
gcgatcacca acgaacagca catcgcggtc tctcgtcgct tcgggccggt tgaccgggtt 240
ccgctgctca aatctatcga aggttacccg gaagttcaga tgatccgtcg cgaagcgaac 300
gaatctggtc gtatcctggg tgacgattgg cacaccgact ccaccttcct ggacgcgccg 360
ccagctgcag ttgtgatgcg tgctattgaa gttccggaat acggtggcga caccgggttc 420
ctgtccatgt actctgcttg ggacaccctg tccgacacca tgaaagctac cattgaaggt 480
ctgaacgttg tgactccgc aaccctgtg ttcggcagcc tgtaccaggc acagaactgg 540
cgcttcagca aactagtgt gaaagtgatg gatgtggatg caggcgatcg tgagactgtg 600
caccgcgtgg tggatatcga cccgggtacc ggccgtcgtg cgctgtactg caaccaggta 660
tattgccagc gtattgaggg catgactgat gcagagtcaa aatgcctgct ccaatttctg 720
tatgagcacg cactaaatt tgattttact tgccgtgtcc gttggaaaaa ggatcaagta 780
ctggtatggg ataactgtg tacgatgcac ctggccgtac ctgattatga cggcaaattt 840
cgctatttga cgcgcacgac agtcgcgggg gacaaacctt ctcgccatca ccatcatcat 900
cattag 906

<210> 45
<211> 888
<212> ADN
<213> Secuencia Artificial

<220>

<223> Recombinante

<400> 45

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tgtggcgctcc tgggcgcaga aatcacgggc gtggatctcc gcgagcctct ggacgacagc    120
acctggaacg aaatcctgga tgctttccac acttaccaag tgatctactt tcccggacaa     180
gccatcacta acgagcagca catcgctttc tcacggcgct tcggcccggg agatccgggtg    240
ccgctactca agtcaattga aggctatccg gaggtgcaaa tgattcgccg cgaagctaac     300
gagagcgggc gcatactggg cgacgactgg catactgact ccaccttcct cgatgctcca    360
ccagccgcag tggatgatcg tgccatcgaa gttcccagat atggtggcga cacgggtttc     420
ctgtctatgt actccgcttg ggatacactg tctgacacga tgaaggctac catcgagggc    480
ctgaatgtcg tccacagtgc tacgcgcgtg ttcgggtcac tgtaccaggc gcagaactgg     540
aggttcagca acaccagtgt caaggatgat gacgttgatg ctggagacag ggaaactgtg    600
catcctcttg tggctctcca tccagttacc gggaggagag cactctactg caaccagggt    660
tactgccagc gcatcgaggg catgaccgat gcggagtcga agtgtctgtt acagttcttg    720
tacgagcacg cgacgaagtt cgacttcacg tgccgggtgc ggtggaagaa ggaccaagtt    780
ctcgtctggg acaatctctg cacgatgcac ctgccggtc cggactacga cggcaaattc     840
agatacttga cccgaacaac agtagcggga gataagcctt cccgttga                    888
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<210> 46

<211> 295

<212> PRT

<213> Secuencia Artificial

<220>

<223> Recombinante

<400> 46

Met His Ala Ala Leu Thr Pro Leu Thr Asn Lys Tyr Arg Phe Ile Asp
1 5 10 15

Val Gln Pro Leu Thr Gly Val Leu Gly Ala Glu Ile Thr Gly Val Asp
20 25 30

Leu Arg Glu Pro Leu Asp Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
35 40 45

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

Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
65 70 75 80

Pro Ile Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
85 90 95

Arg Glu Ala Asn Glu Ser Ser Arg Tyr Ile Gly Asp Asp Trp His Ala
100 105 110

Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
115 120 125

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

Ser Ala Trp Glu Thr Leu Ser Pro Thr Met Gln Ala Thr Ile Glu Gly
145 150 155 160

Leu Asn Val Val His Ser Ala Thr Lys Val Phe Gly Ser Leu Tyr Gln
165 170 175

Ala Thr Asn Trp Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
180 185 190

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

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

Ile Gln Gly Met Thr Asp Ala Glu Ser Lys Ser Leu Leu Gln Phe Leu
225 230 235 240

Tyr Glu His Ala Thr Lys Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
245 250 255

Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ala
260 265 270

Val Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
275 280 285

Ala Gly Asp Lys Pro Ser Arg
290 295

<210> 47
<211> 295
<212> PRT
<213> Secuencia Artificial

<220>
<223> Recombinante

<400> 47

Met His Ala Ala Leu Thr Pro Leu Thr Asn Lys Tyr Arg Phe Ile Asp
1 5 10 15

Val Gln Pro Leu Thr Gly Val Leu Gly Ala Glu Ile Thr Gly Val Asp
20 25 30

Leu Arg Glu Pro Leu Asp Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
35 40 45

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

Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
65 70 75 80

Pro Ile Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
85 90 95

Arg Glu Ala Asn Glu Ser Ser Arg Tyr Ile Gly Asp Asp Trp His Ala
100 105 110

Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
115 120 125

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

<210> 48
 <211> 295
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 48

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

Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
115 120 125

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

Ser Ala Trp Glu Thr Leu Ser Pro Thr Met Gln Ala Thr Ile Glu Gly
145 150 155 160

Leu Asn Val Val His Ser Ala Thr Lys Val Phe Gly Ser Leu Tyr Gln
165 170 175

Ala Thr Asn Trp Arg Phe Ser Gly Thr Ser Val Lys Val Met Asp Val
180 185 190

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

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

Ile Gln Gly Met Thr Asp Ala Glu Ser Lys Ser Leu Leu Gln Phe Leu
225 230 235 240

Tyr Glu His Ala Thr Gln Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
245 250 255

Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ala
260 265 270

Val Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
275 280 285

Ala Gly Asp Lys Pro Ser Arg
290 295

<210> 49
<211> 295
<212> PRT
<213> Secuencia Artificial

<220>
<223> Recombinante

<400> 49

Met His Ala Ala Leu Thr Pro Leu Thr Asn Lys Tyr Arg His Ile Asp
1 5 10 15

Val Gln Pro Leu Thr Gly Val Leu Gly Ala Glu Ile Thr Gly Val Asp
20 25 30

Leu Arg Glu Pro Leu Asp Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
35 40 45

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

Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
65 70 75 80

Pro Ile Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
85 90 95

Arg Glu Ala Asn Glu Ser Ser Arg Tyr Ile Gly Asp Asp Trp His Ala
100 105 110

Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
115 120 125

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

Ser Ala Trp Glu Thr Leu Ser Pro Ala Met Gln Ala Thr Ile Glu Gly
145 150 155 160

Leu Asn Val Val His Ser Ala Thr Lys Val Phe Gly Ser Leu Tyr Gln
165 170 175

Ala Thr Asn Trp Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
180 185 190

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

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

Ile Gln Gly Met Thr Asp Ala Glu Ser Lys Ser Leu Leu Gln Phe Leu
225 230 235 240

Tyr Glu His Ala Thr Gln Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
245 250 255

Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ala
260 265 270

Val Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
275 280 285

Ala Gly Asp Lys Pro Ser Arg
290 295

<210> 50
<211> 295
<212> PRT
<213> Secuencia Artificial

<220>
<223> Recombinante

<400> 50

Met His Ala Ala Leu Thr Pro Leu Thr Asn Lys Tyr Arg Phe Ile Asp
1 5 10 15

Val Gln Pro Leu Thr Gly Val Leu Gly Ala Glu Ile Thr Gly Val Asp
20 25 30

Leu Arg Glu Pro Leu Asp Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
35 40 45

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

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

<210> 51
 <211> 295
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 51

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

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

Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
65 70 75 80

Pro Ile Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
85 90 95

Arg Glu Ala Asn Glu Ser Ser Arg Tyr Ile Gly Asp Asp Trp His Ala
100 105 110

Asp Ser Thr Phe Leu Asp Ala Pro Pro Ala Ala Val Val Met Arg Ala
115 120 125

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

Ser Ala Trp Glu Thr Leu Ser Pro Thr Met Gln Ala Thr Ile Glu Gly
145 150 155 160

Leu Asn Val Val His Ser Ala Thr Lys Val Phe Gly Ser Leu Tyr Gln
165 170 175

Ala Thr Asn Trp Arg Phe Ser Asn Thr Ser Val Lys Val Met Asp Val
180 185 190

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

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

Ile Gln Gly Met Thr Asp Ala Glu Ser Lys Ser Leu Leu Gln Phe Leu
225 230 235 240

Tyr Glu His Ala Thr Gln Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
245 250 255

Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ala
260 265 270

Val Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
275 280 285

Ala Gly Asp Lys Pro Ser Arg
290 295

<210> 52
<211> 295
<212> PRT
<213> Secuencia Artificial

<220>
<223> Recombinante

<400> 52

Met His Ala Ala Leu Thr Pro Leu Thr Asn Lys Tyr Arg His Ile Asp
1 5 10 15

Val Gln Pro Leu Thr Gly Val Leu Gly Ala Glu Ile Thr Gly Val Asp
20 25 30

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

<210> 53
 <211> 888
 <212> ADN
 <213> Secuencia Artificial
 <220>
 <223> Recombinante
 <400> 53

atgcacgcgg ctttgacacc tttagaccaac aagtatcggg tcatcgacgt tcaaccactc	60
acaggcgtgc tcggcgacaga gattaccgga gtggacctga gggagccctt agacgactcc	120
acttgaacg agatcctcga cgcccttcac acctaccaag ttatctactt tcctggacag	180
gcgatcacca acgagcagca cattgccttc tcaaggagggt tcggaccgggt agatccagtt	240
ccaatttctca aatccattga gggttatccc gaggtgcaga tgattagacg agaagccaac	300
gagtcctcac ggtacatagg cgacgattgg cacgcagaca gcaccttcct tgacgctcct	360
ccggctgccg tggttatgcg cgcaatagag gtgccggagt acggcggcga taccggtttc	420
ctatcaatgt actctgcatg ggagacgctc tcaccaacga tgcaagccac cattgaagggt	480
ctaaacgtgg ttactcagc tactaagggtc ttcggaagtc tttaccaggc gacgaattgg	540
agggttcagta acaccagtgt gaagggtgatg gatgtggacg ctggagacag ggagacgggtg	600
catccactcg tagttacaca ccctgtaact ggacgcagag ccctttactg caaccagggtt	660
tactgccaga agatccagggt aatgactgat gcggagtcta agtccctgct tcaattcctc	720
tacgaacacg ccaccaaatt cgacttcact tgtcgtgttc ggtggaagaa ggaccaagtg	780
ctcgtgtggg ataacctttg caccatgcac cgagcagtag cagactacgc cgggaaattc	840
cgctatctca cccgcactac agtggccgga gacaagccta gccgctga	888

<210> 54
 <211> 888
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 54	
atgcacgcgg ctttgacacc tttagaccaac aagtatcggg tcatcgacgt tcaaccactc	60
acaggcgtgc tcggcgacaga gattaccgga gtggacctga gggagccctt agacgactcc	120
acttgaacg agatcctcga cgcccttcac acctaccaag ttatctactt tcctggacag	180
gcgatcacca acgagcagca cattgccttc tcaaggagggt tcggaccgggt agatccagtt	240
ccaatttctca aatccattga gggttatccc gaggtgcaga tgattagacg agaagccaac	300
gagtcctcac ggtacatagg cgacgattgg cacgcagaca gcaccttcct tgacgctcct	360
ccggctgccg tggttatgcg cgcaatagag gtgccggagt acggcggcga taccggtttc	420
ctatcaatgt actctgcatg ggagacgctc tcaccaacga tgcaagccac cattgaagggt	480
ctaaacgtgg ttactcagc tactaagggtc ttcggaagtc tttaccaggc gacgaattgg	540
agggttcagt gaaccagtgt gaagggtgatg gatgtggacg ctggagacag ggagacgggtg	600
catccactcg tagttacaca ccctgtaact ggacgcagag ccctttactg caaccagggtt	660
tactgccaga agatccagggt aatgactgat gcggagtcta agtccctgct tcaattcctc	720
tacgaacacg ccacccaatt cgacttcact tgtcgtgttc ggtggaagaa ggaccaagtg	780
ctcgtgtggg ataacctttg caccatgcac cgagcagtag cagactacgc cgggaaattc	840
cgctatctca cccgcactac agtggccgga gacaagccta gccgctga	888

<210> 55
 <211> 888
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 55	
atgcacgcgg ctttgacacc tttagaccaac aagtatcggc atatcgacgt tcaaccactc	60

acaggcgtgc tcggcgca gattaccgga gtggacctga gggagccctt agacgactcc	120
acttggaacg agatcctcga cgcttttcac acctaccaag ttatctactt tcctggacag	180
gcgatcacca acgagcagca cattgccttc tcaaggaggt tcggaccggt agatccagtt	240
ccaatttca aatccattga gggttatccc gaggtgcaga tgattagacg agaagccaac	300
gagtcctcac ggtacatagg cgacgattgg cacgcagaca gcaccttcct tgacgctcct	360
ccggctgccg tggttatgca cgcaatagag gtgccggagt acggcggcga taccggtttc	420
ctatcaatgt actctgcatg ggagacgctc tcaccaacga tgcaagccac cattgaaggt	480
ctaaacgtgg ttactcagc tactaaggtc ttcggaagtc tttaccaggc gacgaattgg	540
aggttcagtg gaaccagtgt gaaggatgat gatgtggacg ctggagacag ggagacggtg	600
catccactcg tagttacaca ccctgtaact ggacgcagag ccctttactg caaccaggtt	660
tactgccaga agatccaggg aatgactgat gcggagtcta agtccctgct tcaattcctc	720
tacgaacacg ccaccaatt cgacttcact tgtcgtgttc ggtggaagaa ggaccaagt	780
ctcgtgtggg ataacctttg caccatgcac cgagcagtag cagactacgc cgggaaattc	840
cgctatctca ccgcactac agtggccgga gacaagccta gccgctga	888

<210> 56
 <211> 888
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Recombinante

<400> 56	
atgcacgcgg ctttgacacc tttgaccaac aagtatcggc atatcgacgt tcaaccactc	60
acaggcgtgc tcggcgca gattaccgga gtggacctga gggagccctt agacgactcc	120
acttggaacg agatcctcga cgcttttcac acctaccaag ttatctactt tcctggacag	180
gcgatcacca acgagcagca cattgccttc tcaaggaggt tcggaccggt agatccagtt	240
ccaatttca aatccattga gggttatccc gaggtgcaga tgattagacg agaagccaac	300
gagtcctcac ggtacatagg cgacgattgg cacgcagaca gcaccttcct tgacgctcct	360
ccggctgccg tggttatgca cgcaatagag gtgccggagt acggcggcga taccggtttc	420
ctatcaatgt actctgcatg ggagacgctc tcaccagcta tgcaagccac cattgaaggt	480
ctaaacgtgg ttactcagc tactaaggtc ttcggaagtc tttaccaggc gacgaattgg	540
aggttcagta acaccagtgt gaaggatgat gatgtggacg ctggagacag ggagacggtg	600
catccactcg tagttacaca ccctgtaact ggacgcagag ccctttactg caaccagatt	660
tactgccaga agatccaggg aatgactgat gcggagtcta agtccctgct tcaattcctc	720
tacgaacacg ccaccaatt cgacttcact tgtcgtgttc ggtggaagaa ggaccaagt	780
ctcgtgtggg ataacctttg caccatgcac cgagcagtag cagactacgc cgggaaattc	840
cgctatctca ccgcactac agtggccgga gacaagccta gccgctga	888

<210> 57
 <211> 888
 <212> ADN
 <213> Secuencia Artificial

<220>
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acttgaacg agatcctcga cgcccttcac acctaccaag ttatctactt tcctggacag	180
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gagtcctcac ggtacatagg cgacgattgg cacgcagaca gcaccttcct tgacgctcct	360
ccggctgccg tggttatgcg cgcaatagag gtgccggagt acggcggcga taccggtttc	420
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tactgccaga agatccaggg aatgactgat gcggagtcta agtccctgct tcaattcctc	720
tacgaacacg ccacccaatt cgacttcact tgtcgtgttc ggtggaagaa ggaccaagtg	780
ctcgtgtggg ataacctttg caccatgcac cgagcagtag cagactacgc cgggaaattc	840
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tactgccaga agatccaggg aatgactgat gcggagtcta agtccttgct tcaattcctc	720
tacgaacacg ccaccaatt cgacttcact tgtcgtgttc ggtggaagaa ggaccaagtg	780
ctcgtgtggg ataacctttg caccatgcac cgagcagtac cagactacgc cgggaaattc	840
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<210> 60
 <211> 295
 <212> PRT
 <213> Sphingobium herbicidovorans

<400> 60

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Val	Gln	Pro	Leu	Thr	Gly	Val	Leu	Gly	Ala	Glu	Ile	Thr	Gly	Val	Asp	20	25	30	
Leu	Arg	Glu	Pro	Leu	Asp	Asp	Ser	Thr	Trp	Asn	Glu	Ile	Leu	Asp	Ala	35	40	45	
Phe	His	Thr	Tyr	Gln	Val	Ile	Tyr	Phe	Pro	Gly	Gln	Ala	Ile	Thr	Asn	50	55	60	
Glu	Gln	His	Ile	Ala	Phe	Ser	Arg	Arg	Phe	Gly	Pro	Val	Asp	Pro	Val	65	70	75	80
Pro	Leu	Leu	Lys	Ser	Ile	Glu	Gly	Tyr	Pro	Glu	Val	Gln	Met	Ile	Arg	85	90	95	
Arg	Glu	Ala	Asn	Glu	Ser	Gly	Arg	Val	Ile	Gly	Asp	Asp	Trp	His	Thr	100	105	110	
Asp	Ser	Thr	Phe	Leu	Asp	Ala	Pro	Pro	Ala	Ala	Val	Val	Met	Arg	Ala	115	120	125	
Ile	Asp	Val	Pro	Glu	His	Gly	Gly	Asp	Thr	Gly	Phe	Leu	Ser	Met	Tyr	130	135	140	
Thr	Ala	Trp	Glu	Thr	Leu	Ser	Pro	Thr	Met	Gln	Ala	Thr	Ile	Glu	Gly	145	150	155	160
Leu	Asn	Val	Val	His	Ser	Ala	Thr	Arg	Val	Phe	Gly	Ser	Leu	Tyr	Gln	165	170	175	
Ala	Gln	Asn	Arg	Arg	Phe	Ser	Asn	Thr	Ser	Val	Lys	Val	Met	Asp	Val	180	185	190	

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

Gly Ser Gly Arg Lys Gly Leu Tyr Val Asn Gln Val Tyr Cys Gln Arg
210 215 220

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

Tyr Glu His Ala Thr Arg Phe Asp Phe Thr Cys Arg Val Arg Trp Lys
245 250 255

Lys Asp Gln Val Leu Val Trp Asp Asn Leu Cys Thr Met His Arg Ala
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Val Pro Asp Tyr Ala Gly Lys Phe Arg Tyr Leu Thr Arg Thr Thr Val
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Gly Gly Val Arg Pro Ala Arg
290 295

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Met His Ala Ala Leu Xaa Pro Leu Xaa Xaa Xaa Xaa Xaa Ile Xaa
1          5          10          15

Val Gln Pro Leu Thr Gly Val Leu Gly Ala Glu Ile Thr Gly Val Asp
20          25          30

Leu Arg Glu Pro Leu Asp Asp Ser Thr Trp Asn Glu Ile Leu Asp Ala
35          40          45

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

Glu Gln His Ile Ala Phe Ser Arg Arg Phe Gly Pro Val Asp Pro Val
65          70          75          80

Pro Xaa Leu Lys Ser Ile Glu Gly Tyr Pro Glu Val Gln Met Ile Arg
85          90          95

Arg Glu Ala Asn Glu Ser Xaa Arg Xaa Ile Gly Asp Asp Trp His Xaa
100         105         110

```


REIVINDICACIONES

1. Una molécula de ADN recombinante caracterizada porque comprende una secuencia de ácido nucleico que codifica un polipéptido que comprende una secuencia de aminoácido seleccionada a partir del grupo que consiste de la SEQ ID NO: 51.

2. La molécula de ADN recombinante de conformidad con la reivindicación 1, caracterizada porque la secuencia de ácido nucleico seleccionada a partir del grupo que consiste de la SEQ ID NO: 58.

3. La molécula de ADN recombinante de conformidad con la reivindicación 1, caracterizada porque la molécula de ADN recombinante está operablemente ligada a un promotor heterólogo funcional en una célula vegetal.

4. La molécula de ADN recombinante de conformidad con la reivindicación 3, caracterizada porque la molécula de ADN recombinante es además operablemente ligada a una molécula de ADN que codifica un péptido de tránsito de cloroplasto.

5. Un constructo de ADN, caracterizado porque comprende un promotor heterólogo funcional en una célula vegetal operablemente ligada a la molécula de ADN recombinante de conformidad con la reivindicación 1.

6. El constructo de ADN de conformidad con la reivindicación 5, caracterizado porque comprende además, una molécula de ADN que codifica un péptido de tránsito de cloroplasto operablemente ligado a la molécula de ADN recombinante.

7. El constructo de ADN de conformidad con la reivindicación 5, caracterizado porque el constructo de ADN está presente en el genoma de una

planta transgénica.

8. Un polipéptido, caracterizado porque comprende una secuencia de aminoácido seleccionada a partir del grupo que consiste de la SEQ ID NO:51.

9. Un método para conferir tolerancia a los herbicidas a una planta, semilla, célula, o parte de la planta, caracterizado porque comprende transformar en tal planta, semilla, célula, o parte de la planta con un ácido nucleico que codifica el polipéptido de conformidad con la reivindicación 8 donde la expresión de dicho polipéptido confiere tolerancia a herbicidas a dicha planta, semilla o parte de planta.

10. El método de conformidad con la reivindicación 9, caracterizado porque tal planta, semilla, célula o parte de la planta comprende un constructo de ADN que comprende un promotor heterólogo funcional en una célula vegetal operablemente ligada a una molécula de ADN recombinante que comprende una secuencia de ácido nucleico que codifica un polipéptido que comprende una secuencia de aminoácido seleccionada a partir del grupo que consiste de la SEQ ID NO:51.

11. El método de conformidad con la reivindicación 11, caracterizado porque la planta, semilla, célula o parte de la planta comprende tolerancia a un herbicida seleccionado a partir del grupo que consiste de herbicidas de AOPP, herbicidas de fenoxiácido, y herbicidas de piridiniloxilácidos.

12. El método de acuerdo con la reivindicación 11, caracterizado porque además comprende regenerar una planta transgénica tolerante al herbicida a partir de la semilla, célula o parte de planta transformada.

13. El método de conformidad con la reivindicación 12, caracterizado porque tal planta transgénica tolerante al herbicida comprende tolerancia a un

herbicida seleccionado a partir del grupo que consiste de herbicidas de AOPP, herbicidas de fenoxiácido, y herbicidas de piridiniloxilácidos.

14. Un método para controlar malezas en un área de crecimiento de la planta, caracterizado porque comprende poner en contacto un área de crecimiento de la planta que comprende una planta o semilla que comprende una molécula de ADN recombinante que comprende una secuencia de ácido nucleico que codifica una proteína que comprende una secuencia de aminoácido seleccionada a partir del grupo que consiste de la SEQ ID NO:14 con un herbicida seleccionado a partir del grupo que consiste de herbicidas de AOPP, herbicidas de fenoxiácido, y herbicidas de piridiniloxilácidos, en donde la planta o semilla es tolerante al herbicidas.

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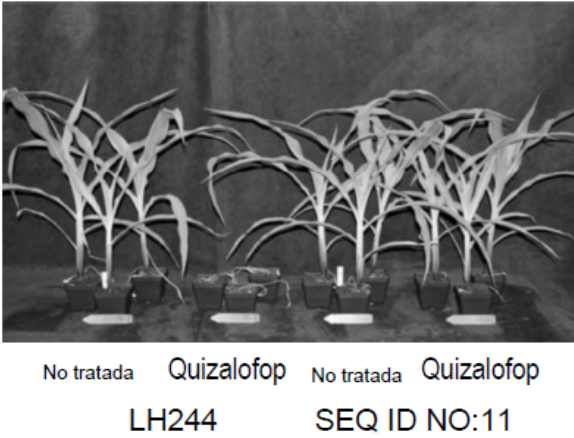


FIG.1A

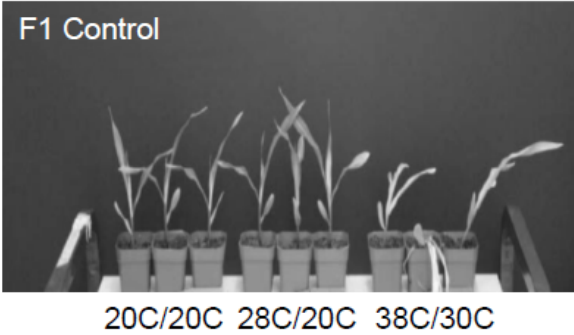


FIG.1B

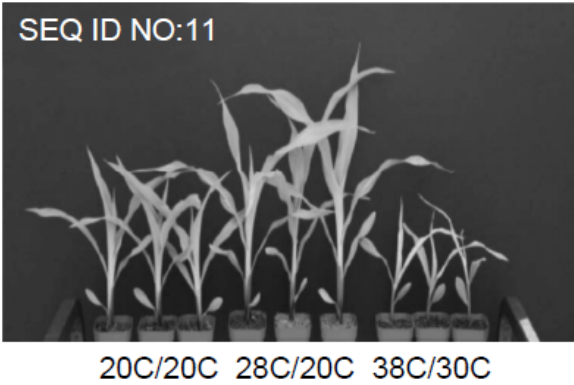


FIG.1C

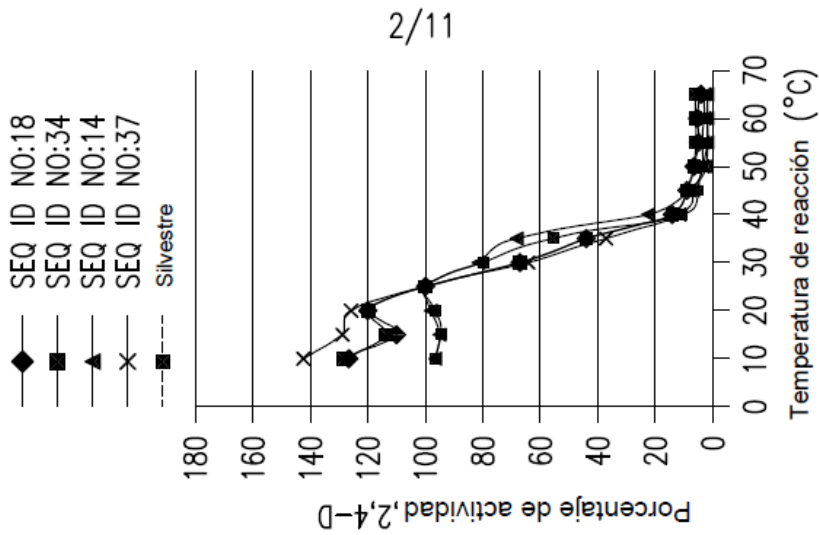
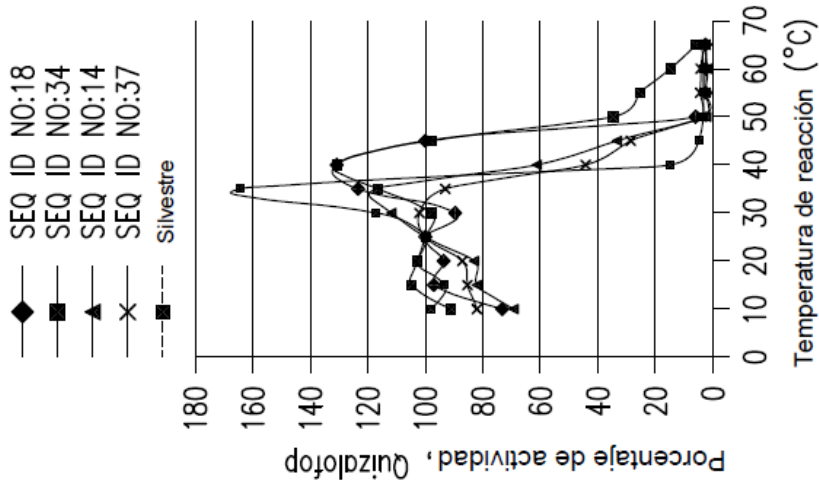
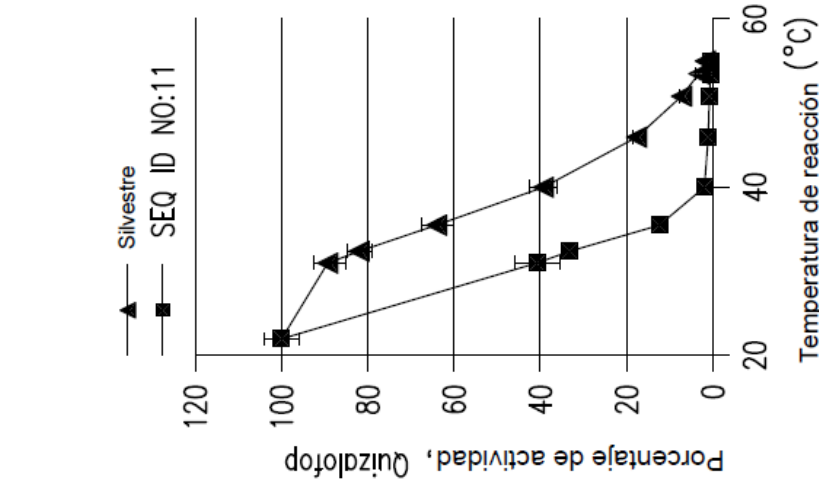


FIG.2A

FIG.2B

FIG.2C

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MHAALSPLSQRFERIAVQPLTGVLGAEITGVDLREPLDDSTWNEIL
DAFHTYQVIYFPGQAITNEQHIAFSRRFGPVDVPVLLKSIEGYPEV
QMIRREANESGRVIGDDWHIDSTFLDAPPAAVVMRAIDVPEHGGDT
GFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFSN
TSVKVMDVDAGDRETVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTD
AESKPLLQFLYEHATRFDFTCRVRWKKDQVLVDNLCTMHRAVPDY
AGKFRYLTRTTVGGVRPAR

FIG.3

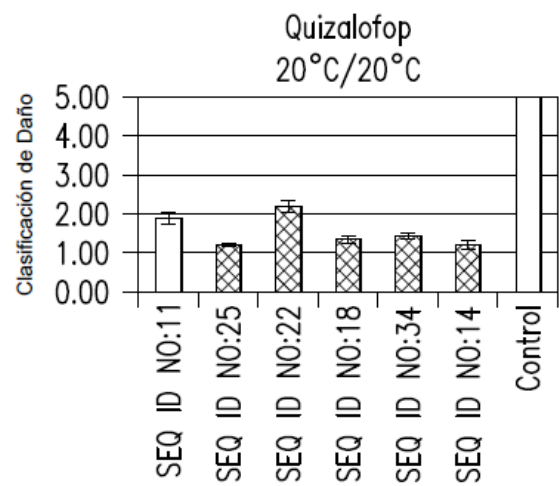


FIG.4A

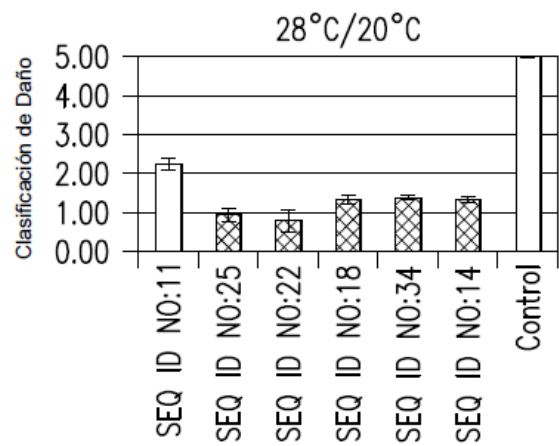


FIG.4B

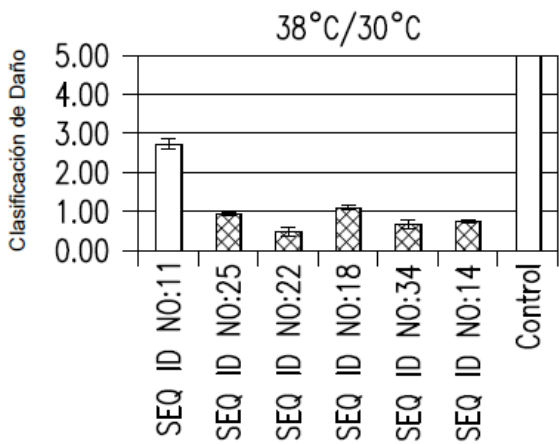


FIG.4C

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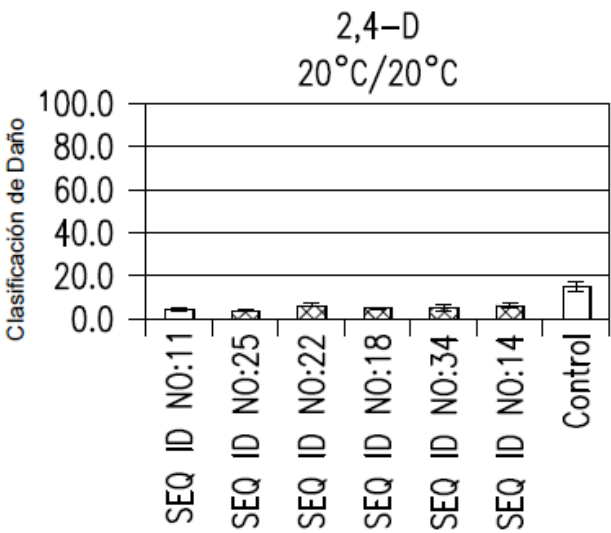


FIG.4D

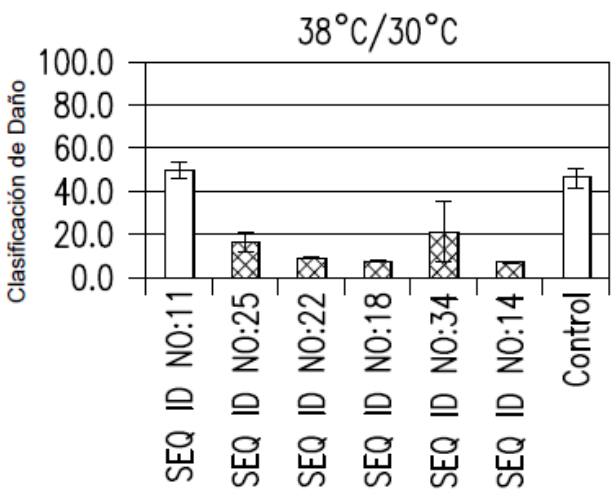


FIG.4E

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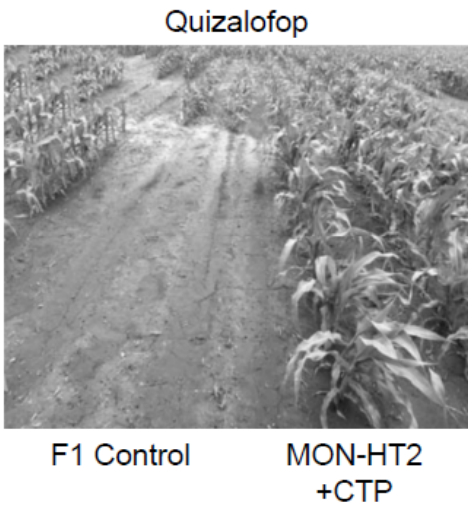


FIG.5A

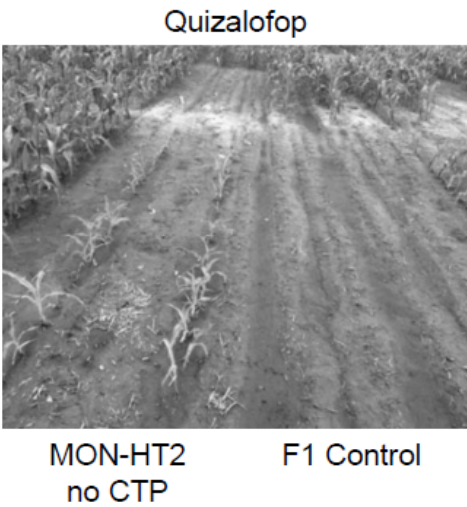


FIG.5B

SEQ ID NO:60	LSMYTAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPGS	210
SEQ ID NO:1	LSMYTAYDALSDGLKKLIISGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPGS	210
SEQ ID NO:4	LSMYTAYDALSDGLKKLIISGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPGS	210
SEQ ID NO:7	LSMYTAYDALSDGLKKLIISGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPGS	210
SEQ ID NO:9	LSMYTAYDALSDGLKKLIISGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPGS	210
SEQ ID NO:11	TSMYTAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPEIT	210
SEQ ID NO:14	LSMYSAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPVIT	210
SEQ ID NO:18	LSMYSAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPVIT	210
SEQ ID NO:22	ASMYTAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPEIT	210
SEQ ID NO:25	LSMYTAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVSHPVIT	210
SEQ ID NO:28	LSMYSAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPVIT	210
SEQ ID NO:31	LSMYSAMDITLSDITMKATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVSHPVIT	210
SEQ ID NO:34	LSMYSAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPVIT	210
SEQ ID NO:37	LSMYSAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPVIT	210
SEQ ID NO:40	LSMYSAMDITLSDITMKATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVSHPVIT	210
SEQ ID NO:43	LSMYSAMDITLSDITMKATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVSHPVIT	210
SEQ ID NO:46	LSMYSAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPVIT	210
SEQ ID NO:47	LSMYSAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPVIT	210
SEQ ID NO:48	LSMYSAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPVIT	210
SEQ ID NO:49	LSMYSAMETLSPAMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPVIT	210
SEQ ID NO:50	LSMYSAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPVIT	210
SEQ ID NO:51	LSMYSAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPVIT	210
SEQ ID NO:52	LSMYSAMETLSPITMQATIEGLNVVHSATRVFGSLYQAQNRREFSNTSVKVMMDVdAGDRETMPLVVTHPVIT	210
Consenso	LSMYAw•tLS•tm•atIJeGLNVVHSAT•VFGSLYQA•N•RfSnTSVKVMMDVdGdGdRETdVHPLVVtHP•t	210

FIG.6C

SEQ ID NO:60	GRKGLYNQMYCQRIEGMTDAESKPLQLFLYEHAITKFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280
SEQ ID NO:1	GRKGLYNQMYCQRIEGMSEKESPLSFLFAHAITKPEFTCRVRMKKQQLVWDNLCTMHYAINDYHGQT	280
SEQ ID NO:4	GRKGLYNQMYCQRIEGMSEKESPLSFLFAHAITKPEFTCRVRMKKQQLVWDNLCTMHYAINDYHGQT	280
SEQ ID NO:7	GRKGLYNQMYCQRIEGMSEKESPLSFLFAHAITKPEFTCRVRMKKQQLVWDNLCTMHYAINDYHGQT	280
SEQ ID NO:9	GRKGLYNQMYCQRIEGMSEKESPLSFLFAHAITKPEFTCRVRMKKQQLVWDNLCTMHYAINDYHGQT	280
SEQ ID NO:11	GRKGLYNQMYCQRIEGMSEKESPLSFLFAHAITKPEFTCRVRMQEGDVLVWDNLCTQHYAVPDYAGKF	280
SEQ ID NO:14	GRRALYCNQMYCCKIQGMTDAESKSLQLFLYEHAITKFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280
SEQ ID NO:18	GRRALYCNQMYCCKIQGMTDAESKSLQLFLYEHAITKFDFTCRVRMKKQQLVWDNLCTMHRAPDYAGKF	280
SEQ ID NO:22	GRKGLYNQMYCQRIEGMSEKESPLSFLFAHAITKPEFTCRVRMQEGQVLVWDNLCTQHF AVPDYAGKF	280
SEQ ID NO:25	GRRALYCNQMYCQRIEGMTDAESKSLQLFLYEHAITKFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280
SEQ ID NO:28	GRRALYCNQMYCCKIQGMTDAESKSLQLFLYEHAITKFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280
SEQ ID NO:31	GRRALYCNQMYCQRIEGMTDAESKPLQLFLYEHAITKFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280
SEQ ID NO:34	GRRALYCNQMYCCKIQGMTDAESKSLQLFLYEHAITKFDFTCRVRMKKQQLVWDNLCTMHSVPDYAGKF	280
SEQ ID NO:37	GRRALYCNQMYCCKIQGMTDAESKSLQLFLYEHAITKFDFTCRVRMKKQQLVWDNLCTMHSVPDYGNAF	280
SEQ ID NO:40	GRRALYCNQMYCQRIEGMTDAESKCLQLFLYEHAITKFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280
SEQ ID NO:43	GRRALYCNQMYCQRIEGMTDAESKCLQLFLYEHAITKFDFTCRVRMKKQQLVWDNLCTMHLAVPDYDGKF	280
SEQ ID NO:46	GRRALYCNQMYCCKIQGMTDAESKSLQLFLYEHAITKFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280
SEQ ID NO:47	GRRALYCNQMYCCKIQGMTDAESKSLQLFLYEHAITQFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280
SEQ ID NO:48	GRRALYCNQMYCCKIQGMTDAESKSLQLFLYEHAITQFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280
SEQ ID NO:49	GRRALYCNQIYCCKIQGMTDAESKSLQLFLYEHAITQFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280
SEQ ID NO:50	GRRALYCNQIYCCKIQGMTDAESKSLQLFLYEHAITQFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280
SEQ ID NO:51	GRRALYCNQMYCCKIQGMTDAESKSLQLFLYEHAITQFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280
SEQ ID NO:52	GRRALYCNQMYCCKIQGMTDAESKSLQLFLYEHAITQFDFTCRVRMKKQQLVWDNLCTMHRVPDYAGKF	280

Consenso GR·LY·NQMYCQ·I·GMtdE\$K·LLdFLyeHAT·fdFTCRVRWkkdqVLVWDNLCTH·avpDYagkf 280

FIG.6D

SEQ ID NO:60	R	Y	L	T	R	T	T	V	G	G	V	R	P	A	R	295
SEQ ID NO:1	R	I	L	H	R	T	T	V	G	G	V	R	P	A	R	295
SEQ ID NO:4	R	I	L	H	R	T	T	V	G	G	V	R	P	A	R	295
SEQ ID NO:7	R	I	L	H	R	T	T	V	G	G	V	R	P	A	R	295
SEQ ID NO:9	R	I	L	H	R	T	T	V	G	G	V	R	P	A	R	295
SEQ ID NO:11	R	Y	L	T	R	T	T	V	G	G	V	R	P	A	R	295
SEQ ID NO:14	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:18	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:22	R	Y	L	T	R	T	T	V	G	G	V	R	P	A	R	295
SEQ ID NO:25	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:28	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:31	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:34	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:37	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:40	R	Y	L	T	R	T	T	V	A	G	D	R	P	A	R	295
SEQ ID NO:43	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:46	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:47	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:48	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:49	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:50	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:51	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
SEQ ID NO:52	R	Y	L	T	R	T	T	V	A	G	D	K	P	S	R	295
Consenso	R	Y	L	T	R	T	T	V	·	G	·	·	P	·	R	295

FIG.6E