

SEQUENCE LISTING

<110> PFENEX INC.

<120> METHOD FOR PRODUCTION OF RECOMBINANT E. COLI ASPARAGINASE

<130> 38194-751.601

<140>

<141>

<150> 62/578,302

<151> 2017-10-27

<160> 57

<170> PatentIn version 3.5

<210> 1

<211> 326

<212> PRT

<213> Escherichia coli

<400> 1

Leu Pro Asn Ile Thr Ile Leu Ala Thr Gly Gly Thr Ile Ala Gly Gly
1 5 10 15

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

Glu Asn Leu Val Asn Ala Val Pro Gln Leu Lys Asp Ile Ala Asn Val
35 40 45

Lys Gly Glu Gln Val Val Asn Ile Gly Ser Gln Asp Met Asn Asp Asp
50 55 60

Val Trp Leu Thr Leu Ala Lys Lys Ile Asn Thr Asp Cys Asp Lys Thr
65 70 75 80

Asp Gly Phe Val Ile Thr His Gly Thr Asp Thr Met Glu Glu Thr Ala
85 90 95

Tyr Phe Leu Asp Leu Thr Val Lys Cys Asp Lys Pro Val Val Met Val
100 105 110

Gly Ala Met Arg Pro Ser Thr Ser Met Ser Ala Asp Gly Pro Phe Asn
115 120 125

Leu Tyr Asn Ala Val Val Thr Ala Ala Asp Lys Ala Ser Ala Asn Arg
 130 135 140

Gly Val Leu Val Val Met Asn Asp Thr Val Leu Asp Gly Arg Asp Val
 145 150 155 160

Thr Lys Thr Asn Thr Thr Asp Val Ala Thr Phe Lys Ser Val Asn Tyr
 165 170 175

Gly Pro Leu Gly Tyr Ile His Asn Gly Lys Ile Asp Tyr Gln Arg Thr
 180 185 190

Pro Ala Arg Lys His Thr Ser Asp Thr Pro Phe Asp Val Ser Lys Leu
 195 200 205

Asn Glu Leu Pro Lys Val Gly Ile Val Tyr Asn Tyr Ala Asn Ala Ser
 210 215 220

Asp Leu Pro Ala Lys Ala Leu Val Asp Ala Gly Tyr Asp Gly Ile Val
 225 230 235 240

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

Leu Ala Thr Ala Ala Lys Asn Gly Thr Ala Val Val Arg Ser Ser Arg
 260 265 270

Val Pro Thr Gly Ala Thr Thr Gln Asp Ala Glu Val Asp Asp Ala Lys
 275 280 285

Tyr Gly Phe Val Ala Ser Gly Thr Leu Asn Pro Gln Lys Ala Arg Val
 290 295 300

Leu Leu Gln Leu Ala Leu Thr Gln Thr Lys Asp Pro Gln Gln Ile Gln
 305 310 315 320

Gln Ile Phe Asn Gln Tyr
 325

<210> 2
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 2
 ctcccctaaca ttactattct ggccactggc ggtacgattg caggcggcgg tgactcagcc 60
 accaagtcga attacaccgc cggtaaggtc ggtgtcgaaa acctcgtcaa cgccgtgccg 120
 cagctgaaag atatcgccaa cgtcaagggc gagcaagtgg tgaacatcgg ctcccaagat 180
 atgaacgatg acgtgtggct gacgctggcc aagaaaatca acaccgattg cgacaagacg 240
 gacgggtttg tcatcaccca cggcaccgac actatggaag agactgccta cttcctcgac 300
 ctcacggtga agtgcgataa accggtagtg atggtgggcg ccatgcgccc gagcacctcg 360
 atgagcgcgg acggcccgtt caatctgtac aacgccgtgg taaccgcagc ggacaaggcg 420
 tccgcgaacc gcggtgtatt ggtagtgatg aacgatacgg tgctcgatgg gcgcatgtg 480
 accaagacca ataccactga tgtggccacc ttcaagagcg tgaactatgg cccgctgggc 540
 tacatccata acggcaagat cgattaccag cgtactcccg cccggaagca cacctcgac 600
 acccccttcg acgtgtcgaa actgaacgaa ctgccaagg tcggcatcgt ctacaactac 660
 gccaatgcga gcgatctgcc cgcgaaggcc ctggtggacg ccggctacga cgggatcgta 720
 tcggcgggtg tgggcaatgg taacctgtac aagaccgtgt ttgacaccct ggcgacggcg 780
 gcgaagaacg gcaccgccgt ggtccgcagc agccgcgtgc cactggggc gaccacccaa 840
 gacgccgagg tcgacgacgc gaagtacggc ttcgtagcca gcggcaccct gaaccgcaa 900
 aaggcccggg tcctgctgca gctggcgctc acgcagacga aggacccgca gcaaatacaa 960
 cagatcttca accagtac 978

<210> 3
 <211> 348
 <212> PRT
 <213> Escherichia coli

<400> 3
 Met Glu Phe Phe Lys Lys Thr Ala Leu Ala Ala Leu Val Met Gly Phe
 1 5 10 15

Ser Gly Ala Ala Leu Ala Leu Pro Asn Ile Thr Ile Leu Ala Thr Gly
 20 25 30

Gly Thr Ile Ala Gly Gly Gly Asp Ser Ala Thr Lys Ser Asn Tyr Thr
 35 40 45

Val Gly Lys Val Gly Val Glu Asn Leu Val Asn Ala Val Pro Gln Leu
 50 55 60

Lys Asp Ile Ala Asn Val Lys Gly Glu Gln Val Val Asn Ile Gly Ser
 65 70 75 80

Gln Asp Met Asn Asp Asn Val Trp Leu Thr Leu Ala Lys Lys Ile Asn
 85 90 95

Thr Asp Cys Asp Lys Thr Asp Gly Phe Val Ile Thr His Gly Thr Asp
 100 105 110

Thr Met Glu Glu Thr Ala Tyr Phe Leu Asp Leu Thr Val Lys Cys Asp
 115 120 125

Lys Pro Val Val Met Val Gly Ala Met Arg Pro Ser Thr Ser Met Ser
 130 135 140

Ala Asp Gly Pro Phe Asn Leu Tyr Asn Ala Val Val Thr Ala Ala Asp
 145 150 155 160

Lys Ala Ser Ala Asn Arg Gly Val Leu Val Val Met Asn Asp Thr Val
 165 170 175

Leu Asp Gly Arg Asp Val Thr Lys Thr Asn Thr Thr Asp Val Ala Thr
 180 185 190

Phe Lys Ser Val Asn Tyr Gly Pro Leu Gly Tyr Ile His Asn Gly Lys
 195 200 205

Ile Asp Tyr Gln Arg Thr Pro Ala Arg Lys His Thr Ser Asp Thr Pro
 210 215 220

Phe Asp Val Ser Lys Leu Asn Glu Leu Pro Lys Val Gly Ile Val Tyr

225		230		235		240
Asn Tyr Ala Asn	Ala Ser Asp Leu Pro	Ala Lys Ala Leu Val	Asp Ala			
	245	250	255			
Gly Tyr Asp Gly	Ile Val Ser Ala	Gly Val Gly Asn	Gly Asn Leu Tyr			
	260	265	270			
Lys Ser Val Phe	Asp Thr Leu Ala	Thr Ala Ala Lys	Thr Gly Thr Ala			
	275	280	285			
Val Val Arg Ser	Ser Arg Val Pro	Thr Gly Ala Thr	Thr Gln Asp Ala			
	290	295	300			
Glu Val Asp Asp	Ala Lys Tyr Gly	Phe Val Ala Ser	Gly Thr Leu Asn			
305	310	315	320			
Pro Gln Lys Ala	Arg Val Leu Leu	Gln Leu Ala Leu	Thr Gln Thr Lys			
	325	330	335			
Asp Pro Gln Gln	Ile Gln Gln Ile	Phe Asn Gln Tyr				
	340	345				

<210> 4

<211> 1047

<212> DNA

<213> Escherichia coli

<400> 4

atggagtttt tcaaaaagac ggcacttgcc gcactggtta tgggttttag tggtgcagca	60
ttggcattac ccaatatcac catttttagca accggcgggga ccattgccgg tggtggtgac	120
tccgcaacca aatctaacta cacagtgggt aaagttggcg tagaaaatct ggttaatgcg	180
gtgccgcaac taaaagacat tgcgaacgtt aaaggcgagc aggtagtga ttcggtctcc	240
caggacatga acgataatgt ctggctgaca ctggcgaaaa aaattaacac cgactgcgat	300
aagaccgacg gcttcgtcat tacccacggt accgacacga tggaagaaac tgcttacttc	360
ctcgacctga cggtgaaatg cgacaaaccg gtggtgatgg tcggcgcaat gcgtccgtcc	420
acgtctatga gcgcagacgg tccattcaac ctgtataacg cggtagtgc cgcagctgat	480
aaagcctccg ccaaccgtgg cgtgctggta gtgatgaatg acaccgtgct tgatggccgt	540

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gacgtcacca aaaccaacac caccgacgta gcgaccttca agtctgttaa ctacggctct      600
ctgggttaca ttcacaacgg taagattgac taccagcgta ccccggcacg taagcatacc      660
agcgacacgc cattcgatgt ctctaagctg aatgaactgc cgaaagtcgg cattgtttat      720
aactacgcta acgcatccga tcttccggct aaagcactgg tagatgcggg ctatgatggc      780
atcgttagcg ctggtgtggg taacggcaac ctgtataaat ctgtgttcga cacgctggcg      840
accgccgcga aaaccggtag tgcagtcgtg cgttcttccc gcgtaccgac gggcgctacc      900
actcaggatg ccgaagtgga tgatgcgaaa tacggcttcg tcgcctctgg cacgctgaac      960
ccgcaaaaag cgcgcttct gctgcaactg gctctgacgc aaaccaaaga tccgcagcag     1020
atccagcaga tcttcaatca gtactaa                                           1047

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<210> 5

<211> 326

<212> PRT

<213> Escherichia coli

<400> 5

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Leu Pro Asn Ile Thr Ile Leu Ala Thr Gly Gly Thr Ile Ala Gly Gly
1           5           10           15

```

```

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

```

```

Glu Asn Leu Val Asn Ala Val Pro Gln Leu Lys Asp Ile Ala Asn Val
          35           40           45

```

```

Lys Gly Glu Gln Val Val Asn Ile Gly Ser Gln Asp Met Asn Asp Asn
          50           55           60

```

```

Val Trp Leu Thr Leu Ala Lys Lys Ile Asn Thr Asp Cys Asp Lys Thr
65           70           75           80

```

```

Asp Gly Phe Val Ile Thr His Gly Thr Asp Thr Met Glu Glu Thr Ala
          85           90           95

```

```

Tyr Phe Leu Asp Leu Thr Val Lys Cys Asp Lys Pro Val Val Met Val
          100          105          110

```

Gly Ala Met Arg Pro Ser Thr Ser Met Ser Ala Asp Gly Pro Phe Asn
 115 120 125

Leu Tyr Asn Ala Val Val Thr Ala Ala Asp Lys Ala Ser Ala Asn Arg
 130 135 140

Gly Val Leu Val Val Met Asn Asp Thr Val Leu Asp Gly Arg Asp Val
 145 150 155 160

Thr Lys Thr Asn Thr Thr Asp Val Ala Thr Phe Lys Ser Val Asn Tyr
 165 170 175

Gly Pro Leu Gly Tyr Ile His Asn Gly Lys Ile Asp Tyr Gln Arg Thr
 180 185 190

Pro Ala Arg Lys His Thr Ser Asp Thr Pro Phe Asp Val Ser Lys Leu
 195 200 205

Asn Glu Leu Pro Lys Val Gly Ile Val Tyr Asn Tyr Ala Asn Ala Ser
 210 215 220

Asp Leu Pro Ala Lys Ala Leu Val Asp Ala Gly Tyr Asp Gly Ile Val
 225 230 235 240

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

Leu Ala Thr Ala Ala Lys Thr Gly Thr Ala Val Val Arg Ser Ser Arg
 260 265 270

Val Pro Thr Gly Ala Thr Thr Gln Asp Ala Glu Val Asp Asp Ala Lys
 275 280 285

Tyr Gly Phe Val Ala Ser Gly Thr Leu Asn Pro Gln Lys Ala Arg Val
 290 295 300

Leu Leu Gln Leu Ala Leu Thr Gln Thr Lys Asp Pro Gln Gln Ile Gln
 305 310 315 320

Gln Ile Phe Asn Gln Tyr
 325

<210> 6

<211> 351

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 6

Met Lys Ser Ala Leu Lys Asn Val Ile Pro Gly Ala Leu Ala Leu Leu
 1 5 10 15

Leu Leu Phe Pro Val Ala Ala Gln Ala Leu Pro Asn Ile Thr Ile Leu
 20 25 30

Ala Thr Gly Gly Thr Ile Ala Gly Gly Gly Asp Ser Ala Thr Lys Ser
 35 40 45

Asn Tyr Thr Ala Gly Lys Val Gly Val Glu Asn Leu Val Asn Ala Val
 50 55 60

Pro Gln Leu Lys Asp Ile Ala Asn Val Lys Gly Glu Gln Val Val Asn
 65 70 75 80

Ile Gly Ser Gln Asp Met Asn Asp Asp Val Trp Leu Thr Leu Ala Lys
 85 90 95

Lys Ile Asn Thr Asp Cys Asp Lys Thr Asp Gly Phe Val Ile Thr His
 100 105 110

Gly Thr Asp Thr Met Glu Glu Thr Ala Tyr Phe Leu Asp Leu Thr Val
 115 120 125

Lys Cys Asp Lys Pro Val Val Met Val Gly Ala Met Arg Pro Ser Thr
 130 135 140

Ser Met Ser Ala Asp Gly Pro Phe Asn Leu Tyr Asn Ala Val Val Thr
 145 150 155 160

Ala Ala Asp Lys Ala Ser Ala Asn Arg Gly Val Leu Val Val Met Asn
 165 170 175

Asp Thr Val Leu Asp Gly Arg Asp Val Thr Lys Thr Asn Thr Thr Asp
 180 185 190

Val Ala Thr Phe Lys Ser Val Asn Tyr Gly Pro Leu Gly Tyr Ile His
 195 200 205

Asn Gly Lys Ile Asp Tyr Gln Arg Thr Pro Ala Arg Lys His Thr Ser
 210 215 220

Asp Thr Pro Phe Asp Val Ser Lys Leu Asn Glu Leu Pro Lys Val Gly
 225 230 235 240

Ile Val Tyr Asn Tyr Ala Asn Ala Ser Asp Leu Pro Ala Lys Ala Leu
 245 250 255

Val Asp Ala Gly Tyr Asp Gly Ile Val Ser Ala Gly Val Gly Asn Gly
 260 265 270

Asn Leu Tyr Lys Thr Val Phe Asp Thr Leu Ala Thr Ala Ala Lys Asn
 275 280 285

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

Gln Asp Ala Glu Val Asp Asp Ala Lys Tyr Gly Phe Val Ala Ser Gly
 305 310 315 320

Thr Leu Asn Pro Gln Lys Ala Arg Val Leu Leu Gln Leu Ala Leu Thr
 325 330 335

Gln Thr Lys Asp Pro Gln Gln Ile Gln Gln Ile Phe Asn Gln Tyr
 340 345 350

<210> 7

<211> 344

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 7

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

His Ala Leu Pro Asn Ile Thr Ile Leu Ala Thr Gly Gly Thr Ile Ala
 20 25 30

Gly Gly Gly Asp Ser Ala Thr Lys Ser Asn Tyr Thr Ala Gly Lys Val
 35 40 45

Gly Val Glu Asn Leu Val Asn Ala Val Pro Gln Leu Lys Asp Ile Ala
 50 55 60

Asn Val Lys Gly Glu Gln Val Val Asn Ile Gly Ser Gln Asp Met Asn
 65 70 75 80

Asp Asp Val Trp Leu Thr Leu Ala Lys Lys Ile Asn Thr Asp Cys Asp
 85 90 95

Lys Thr Asp Gly Phe Val Ile Thr His Gly Thr Asp Thr Met Glu Glu
 100 105 110

Thr Ala Tyr Phe Leu Asp Leu Thr Val Lys Cys Asp Lys Pro Val Val
 115 120 125

Met Val Gly Ala Met Arg Pro Ser Thr Ser Met Ser Ala Asp Gly Pro
 130 135 140

Phe Asn Leu Tyr Asn Ala Val Val Thr Ala Ala Asp Lys Ala Ser Ala
 145 150 155 160

Asn Arg Gly Val Leu Val Val Met Asn Asp Thr Val Leu Asp Gly Arg
 165 170 175

Asp Val Thr Lys Thr Asn Thr Thr Asp Val Ala Thr Phe Lys Ser Val
 180 185 190

Asn Tyr Gly Pro Leu Gly Tyr Ile His Asn Gly Lys Ile Asp Tyr Gln
 195 200 205

Arg Thr Pro Ala Arg Lys His Thr Ser Asp Thr Pro Phe Asp Val Ser
 210 215 220

Lys Leu Asn Glu Leu Pro Lys Val Gly Ile Val Tyr Asn Tyr Ala Asn
 225 230 235 240

Ala Ser Asp Leu Pro Ala Lys Ala Leu Val Asp Ala Gly Tyr Asp Gly
 245 250 255

Ile Val Ser Ala Gly Val Gly Asn Gly Asn Leu Tyr Lys Thr Val Phe
 260 265 270

Asp Thr Leu Ala Thr Ala Ala Lys Asn Gly Thr Ala Val Val Arg Ser
 275 280 285

Ser Arg Val Pro Thr Gly Ala Thr Thr Gln Asp Ala Glu Val Asp Asp
 290 295 300

Ala Lys Tyr Gly Phe Val Ala Ser Gly Thr Leu Asn Pro Gln Lys Ala
 305 310 315 320

Arg Val Leu Leu Gln Leu Ala Leu Thr Gln Thr Lys Asp Pro Gln Gln
 325 330 335

Ile Gln Gln Ile Phe Asn Gln Tyr
 340

<210> 8

<211> 357

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 8

Met Ile Arg Asp Asn Arg Leu Lys Thr Ser Leu Leu Arg Gly Leu Thr
 1 5 10 15

Leu Thr Leu Leu Ser Leu Thr Leu Leu Ser Pro Ala Ala His Ala Leu
 20 25 30

Pro Asn Ile Thr Ile Leu Ala Thr Gly Gly Thr Ile Ala Gly Gly Gly
 35 40 45

Asp Ser Ala Thr Lys Ser Asn Tyr Thr Ala Gly Lys Val Gly Val Glu
 50 55 60

Asn Leu Val Asn Ala Val Pro Gln Leu Lys Asp Ile Ala Asn Val Lys
 65 70 75 80

Gly Glu Gln Val Val Asn Ile Gly Ser Gln Asp Met Asn Asp Asp Val
 85 90 95

Trp Leu Thr Leu Ala Lys Lys Ile Asn Thr Asp Cys Asp Lys Thr Asp
 100 105 110

Gly Phe Val Ile Thr His Gly Thr Asp Thr Met Glu Glu Thr Ala Tyr
 115 120 125

Phe Leu Asp Leu Thr Val Lys Cys Asp Lys Pro Val Val Met Val Gly
 130 135 140

Ala Met Arg Pro Ser Thr Ser Met Ser Ala Asp Gly Pro Phe Asn Leu
 145 150 155 160

Tyr Asn Ala Val Val Thr Ala Ala Asp Lys Ala Ser Ala Asn Arg Gly
 165 170 175

Val Leu Val Val Met Asn Asp Thr Val Leu Asp Gly Arg Asp Val Thr
 180 185 190

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

Pro Leu Gly Tyr Ile His Asn Gly Lys Ile Asp Tyr Gln Arg Thr Pro
 210 215 220

Ala Arg Lys His Thr Ser Asp Thr Pro Phe Asp Val Ser Lys Leu Asn
 225 230 235 240

Glu Leu Pro Lys Val Gly Ile Val Tyr Asn Tyr Ala Asn Ala Ser Asp
 245 250 255

Leu Pro Ala Lys Ala Leu Val Asp Ala Gly Tyr Asp Gly Ile Val Ser
 260 265 270

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

Ala Thr Ala Ala Lys Asn Gly Thr Ala Val Val Arg Ser Ser Arg Val
 290 295 300

Pro Thr Gly Ala Thr Thr Gln Asp Ala Glu Val Asp Asp Ala Lys Tyr
 305 310 315 320

Gly Phe Val Ala Ser Gly Thr Leu Asn Pro Gln Lys Ala Arg Val Leu
 325 330 335

Leu Gln Leu Ala Leu Thr Gln Thr Lys Asp Pro Gln Gln Ile Gln Gln
 340 345 350

Ile Phe Asn Gln Tyr
 355

<210> 9

<211> 350

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 9

Met Lys Leu Lys Arg Leu Met Ala Ala Met Thr Phe Val Ala Ala Gly
 1 5 10 15

Val Ala Thr Ala Asn Ala Val Ala Leu Pro Asn Ile Thr Ile Leu Ala
 20 25 30

Thr Gly Gly Thr Ile Ala Gly Gly Gly Asp Ser Ala Thr Lys Ser Asn
 35 40 45

Tyr Thr Ala Gly Lys Val Gly Val Glu Asn Leu Val Asn Ala Val Pro
 50 55 60

Gln Leu Lys Asp Ile Ala Asn Val Lys Gly Glu Gln Val Val Asn Ile
65 70 75 80

Gly Ser Gln Asp Met Asn Asp Asp Val Trp Leu Thr Leu Ala Lys Lys
85 90 95

Ile Asn Thr Asp Cys Asp Lys Thr Asp Gly Phe Val Ile Thr His Gly
100 105 110

Thr Asp Thr Met Glu Glu Thr Ala Tyr Phe Leu Asp Leu Thr Val Lys
115 120 125

Cys Asp Lys Pro Val Val Met Val Gly Ala Met Arg Pro Ser Thr Ser
130 135 140

Met Ser Ala Asp Gly Pro Phe Asn Leu Tyr Asn Ala Val Val Thr Ala
145 150 155 160

Ala Asp Lys Ala Ser Ala Asn Arg Gly Val Leu Val Val Met Asn Asp
165 170 175

Thr Val Leu Asp Gly Arg Asp Val Thr Lys Thr Asn Thr Thr Asp Val
180 185 190

Ala Thr Phe Lys Ser Val Asn Tyr Gly Pro Leu Gly Tyr Ile His Asn
195 200 205

Gly Lys Ile Asp Tyr Gln Arg Thr Pro Ala Arg Lys His Thr Ser Asp
210 215 220

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

Val Tyr Asn Tyr Ala Asn Ala Ser Asp Leu Pro Ala Lys Ala Leu Val
245 250 255

Asp Ala Gly Tyr Asp Gly Ile Val Ser Ala Gly Val Gly Asn Gly Asn
260 265 270

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

Thr Ala Val Val Arg Ser Ser Arg Val Pro Thr Gly Ala Thr Thr Gln
 290 295 300

Asp Ala Glu Val Asp Asp Ala Lys Tyr Gly Phe Val Ala Ser Gly Thr
 305 310 315 320

Leu Asn Pro Gln Lys Ala Arg Val Leu Leu Gln Leu Ala Leu Thr Gln
 325 330 335

Thr Lys Asp Pro Gln Gln Ile Gln Gln Ile Phe Asn Gln Tyr
 340 345 350

<210> 10

<211> 349

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 10

Met Gln Asn Tyr Lys Lys Phe Leu Leu Ala Ala Ala Val Ser Met Ala
 1 5 10 15

Phe Ser Ala Thr Ala Met Ala Leu Pro Asn Ile Thr Ile Leu Ala Thr
 20 25 30

Gly Gly Thr Ile Ala Gly Gly Gly Asp Ser Ala Thr Lys Ser Asn Tyr
 35 40 45

Thr Ala Gly Lys Val Gly Val Glu Asn Leu Val Asn Ala Val Pro Gln
 50 55 60

Leu Lys Asp Ile Ala Asn Val Lys Gly Glu Gln Val Val Asn Ile Gly
 65 70 75 80

Ser Gln Asp Met Asn Asp Asp Val Trp Leu Thr Leu Ala Lys Lys Ile
 85 90 95

Asn Thr Asp Cys Asp Lys Thr Asp Gly Phe Val Ile Thr His Gly Thr
 100 105 110

Asp Thr Met Glu Glu Thr Ala Tyr Phe Leu Asp Leu Thr Val Lys Cys
 115 120 125

Asp Lys Pro Val Val Met Val Gly Ala Met Arg Pro Ser Thr Ser Met
 130 135 140

Ser Ala Asp Gly Pro Phe Asn Leu Tyr Asn Ala Val Val Thr Ala Ala
 145 150 155 160

Asp Lys Ala Ser Ala Asn Arg Gly Val Leu Val Val Met Asn Asp Thr
 165 170 175

Val Leu Asp Gly Arg Asp Val Thr Lys Thr Asn Thr Thr Asp Val Ala
 180 185 190

Thr Phe Lys Ser Val Asn Tyr Gly Pro Leu Gly Tyr Ile His Asn Gly
 195 200 205

Lys Ile Asp Tyr Gln Arg Thr Pro Ala Arg Lys His Thr Ser Asp Thr
 210 215 220

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

Tyr Asn Tyr Ala Asn Ala Ser Asp Leu Pro Ala Lys Ala Leu Val Asp
 245 250 255

Ala Gly Tyr Asp Gly Ile Val Ser Ala Gly Val Gly Asn Gly Asn Leu
 260 265 270

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

Ala Val Val Arg Ser Ser Arg Val Pro Thr Gly Ala Thr Thr Gln Asp
 290 295 300

Ala Glu Val Asp Asp Ala Lys Tyr Gly Phe Val Ala Ser Gly Thr Leu
 305 310 315 320

Asn Pro Gln Lys Ala Arg Val Leu Leu Gln Leu Ala Leu Thr Gln Thr
 325 330 335

Lys Asp Pro Gln Gln Ile Gln Gln Ile Phe Asn Gln Tyr
 340 345

<210> 11

<211> 346

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 11

Met Phe Ala Lys Leu Val Ala Val Ser Leu Leu Thr Leu Ala Ser Gly
 1 5 10 15

Gln Leu Leu Ala Leu Pro Asn Ile Thr Ile Leu Ala Thr Gly Gly Thr
 20 25 30

Ile Ala Gly Gly Gly Asp Ser Ala Thr Lys Ser Asn Tyr Thr Ala Gly
 35 40 45

Lys Val Gly Val Glu Asn Leu Val Asn Ala Val Pro Gln Leu Lys Asp
 50 55 60

Ile Ala Asn Val Lys Gly Glu Gln Val Val Asn Ile Gly Ser Gln Asp
 65 70 75 80

Met Asn Asp Asp Val Trp Leu Thr Leu Ala Lys Lys Ile Asn Thr Asp
 85 90 95

Cys Asp Lys Thr Asp Gly Phe Val Ile Thr His Gly Thr Asp Thr Met
 100 105 110

Glu Glu Thr Ala Tyr Phe Leu Asp Leu Thr Val Lys Cys Asp Lys Pro
 115 120 125

Val Val Met Val Gly Ala Met Arg Pro Ser Thr Ser Met Ser Ala Asp
 130 135 140

Gly Pro Phe Asn Leu Tyr Asn Ala Val Val Thr Ala Ala Asp Lys Ala
 145 150 155 160

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

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

Ser Val Asn Tyr Gly Pro Leu Gly Tyr Ile His Asn Gly Lys Ile Asp
 195 200 205

Tyr Gln Arg Thr Pro Ala Arg Lys His Thr Ser Asp Thr Pro Phe Asp
 210 215 220

Val Ser Lys Leu Asn Glu Leu Pro Lys Val Gly Ile Val Tyr Asn Tyr
 225 230 235 240

Ala Asn Ala Ser Asp Leu Pro Ala Lys Ala Leu Val Asp Ala Gly Tyr
 245 250 255

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

Val Phe Asp Thr Leu Ala Thr Ala Ala Lys Asn Gly Thr Ala Val Val
 275 280 285

Arg Ser Ser Arg Val Pro Thr Gly Ala Thr Thr Gln Asp Ala Glu Val
 290 295 300

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

Lys Ala Arg Val Leu Leu Gln Leu Ala Leu Thr Gln Thr Lys Asp Pro
 325 330 335

Gln Gln Ile Gln Gln Ile Phe Asn Gln Tyr
 340 345

<210> 12

<211> 350

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 12

Met	Lys	Leu	Lys	Arg	Leu	Met	Ala	Ala	Met	Thr	Phe	Val	Ala	Ala	Gly
1				5					10					15	

Val	Ala	Thr	Val	Asn	Ala	Val	Ala	Leu	Pro	Asn	Ile	Thr	Ile	Leu	Ala
			20					25					30		

Thr	Gly	Gly	Thr	Ile	Ala	Gly	Gly	Gly	Asp	Ser	Ala	Thr	Lys	Ser	Asn
		35					40						45		

Tyr	Thr	Ala	Gly	Lys	Val	Gly	Val	Glu	Asn	Leu	Val	Asn	Ala	Val	Pro
	50					55					60				

Gln	Leu	Lys	Asp	Ile	Ala	Asn	Val	Lys	Gly	Glu	Gln	Val	Val	Asn	Ile
65					70					75				80	

Gly	Ser	Gln	Asp	Met	Asn	Asp	Asp	Val	Trp	Leu	Thr	Leu	Ala	Lys	Lys
				85					90					95	

Ile	Asn	Thr	Asp	Cys	Asp	Lys	Thr	Asp	Gly	Phe	Val	Ile	Thr	His	Gly
			100					105					110		

Thr	Asp	Thr	Met	Glu	Glu	Thr	Ala	Tyr	Phe	Leu	Asp	Leu	Thr	Val	Lys
		115					120					125			

Cys	Asp	Lys	Pro	Val	Val	Met	Val	Gly	Ala	Met	Arg	Pro	Ser	Thr	Ser
	130					135					140				

Met	Ser	Ala	Asp	Gly	Pro	Phe	Asn	Leu	Tyr	Asn	Ala	Val	Val	Thr	Ala
145					150					155					160

Ala	Asp	Lys	Ala	Ser	Ala	Asn	Arg	Gly	Val	Leu	Val	Val	Met	Asn	Asp
				165					170					175	

Thr Val Leu Asp Gly Arg Asp Val Thr Lys Thr Asn Thr Thr Asp Val
 180 185 190

Ala Thr Phe Lys Ser Val Asn Tyr Gly Pro Leu Gly Tyr Ile His Asn
 195 200 205

Gly Lys Ile Asp Tyr Gln Arg Thr Pro Ala Arg Lys His Thr Ser Asp
 210 215 220

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

Val Tyr Asn Tyr Ala Asn Ala Ser Asp Leu Pro Ala Lys Ala Leu Val
 245 250 255

Asp Ala Gly Tyr Asp Gly Ile Val Ser Ala Gly Val Gly Asn Gly Asn
 260 265 270

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

Thr Ala Val Val Arg Ser Ser Arg Val Pro Thr Gly Ala Thr Thr Gln
 290 295 300

Asp Ala Glu Val Asp Asp Ala Lys Tyr Gly Phe Val Ala Ser Gly Thr
 305 310 315 320

Leu Asn Pro Gln Lys Ala Arg Val Leu Leu Gln Leu Ala Leu Thr Gln
 325 330 335

Thr Lys Asp Pro Gln Gln Ile Gln Gln Ile Phe Asn Gln Tyr
 340 345 350

<210> 13

<211> 349

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 13

Met Pro Pro Arg Ser Ile Ala Ala Cys Leu Gly Leu Leu Gly Leu Leu
 1 5 10 15

Met Ala Thr Gln Ala Ala Ala Leu Pro Asn Ile Thr Ile Leu Ala Thr
 20 25 30

Gly Gly Thr Ile Ala Gly Gly Gly Asp Ser Ala Thr Lys Ser Asn Tyr
 35 40 45

Thr Ala Gly Lys Val Gly Val Glu Asn Leu Val Asn Ala Val Pro Gln
 50 55 60

Leu Lys Asp Ile Ala Asn Val Lys Gly Glu Gln Val Val Asn Ile Gly
 65 70 75 80

Ser Gln Asp Met Asn Asp Asp Val Trp Leu Thr Leu Ala Lys Lys Ile
 85 90 95

Asn Thr Asp Cys Asp Lys Thr Asp Gly Phe Val Ile Thr His Gly Thr
 100 105 110

Asp Thr Met Glu Glu Thr Ala Tyr Phe Leu Asp Leu Thr Val Lys Cys
 115 120 125

Asp Lys Pro Val Val Met Val Gly Ala Met Arg Pro Ser Thr Ser Met
 130 135 140

Ser Ala Asp Gly Pro Phe Asn Leu Tyr Asn Ala Val Val Thr Ala Ala
 145 150 155 160

Asp Lys Ala Ser Ala Asn Arg Gly Val Leu Val Val Met Asn Asp Thr
 165 170 175

Val Leu Asp Gly Arg Asp Val Thr Lys Thr Asn Thr Thr Asp Val Ala
 180 185 190

Thr Phe Lys Ser Val Asn Tyr Gly Pro Leu Gly Tyr Ile His Asn Gly
 195 200 205

Lys Ile Asp Tyr Gln Arg Thr Pro Ala Arg Lys His Thr Ser Asp Thr
 210 215 220

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

Tyr Asn Tyr Ala Asn Ala Ser Asp Leu Pro Ala Lys Ala Leu Val Asp
 245 250 255

Ala Gly Tyr Asp Gly Ile Val Ser Ala Gly Val Gly Asn Gly Asn Leu
 260 265 270

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

Ala Val Val Arg Ser Ser Arg Val Pro Thr Gly Ala Thr Thr Gln Asp
 290 295 300

Ala Glu Val Asp Asp Ala Lys Tyr Gly Phe Val Ala Ser Gly Thr Leu
 305 310 315 320

Asn Pro Gln Lys Ala Arg Val Leu Leu Gln Leu Ala Leu Thr Gln Thr
 325 330 335

Lys Asp Pro Gln Gln Ile Gln Gln Ile Phe Asn Gln Tyr
 340 345

<210> 14

<211> 25

<212> PRT

<213> Pseudomonas fluorescens

<400> 14

Met Lys Ser Ala Leu Lys Asn Val Ile Pro Gly Ala Leu Ala Leu Leu
 1 5 10 15

Leu Leu Phe Pro Val Ala Ala Gln Ala
 20 25

<210> 15

<211> 75

<212> DNA

<213> Pseudomonas fluorescens

<400> 15

atgaaatctg cattgaagaa cgttattccg ggcgccctgg cccttctgct gctattcccc 60
 gtcgccgccc aggca 75

<210> 16
 <211> 18
 <212> PRT
 <213> Pseudomonas fluorescens

<400> 16
 Met Arg Gln Leu Phe Phe Cys Leu Met Leu Met Val Ser Leu Thr Ala
 1 5 10 15

His Ala

<210> 17
 <211> 54
 <212> DNA
 <213> Pseudomonas fluorescens

<400> 17
 atgcgacaac tatttttctg ttgatgctg atggtgtcgc tcacggcgca cgcc 54

<210> 18
 <211> 31
 <212> PRT
 <213> Pseudomonas fluorescens

<400> 18
 Met Ile Arg Asp Asn Arg Leu Lys Thr Ser Leu Leu Arg Gly Leu Thr
 1 5 10 15

Leu Thr Leu Leu Ser Leu Thr Leu Leu Ser Pro Ala Ala His Ala
 20 25 30

<210> 19
 <211> 93
 <212> DNA
 <213> Pseudomonas fluorescens

<400> 19
 atgatccgtg acaaccgact caagacatcc cttctgcgcg gcctgaccct caccctactc 60
 agcctgaccc tgctctcgcc cgcggcccat gcc 93

<210> 20

<211> 24
 <212> PRT
 <213> *Pseudomonas fluorescens*

<400> 20
 Met Lys Leu Lys Arg Leu Met Ala Ala Met Thr Phe Val Ala Ala Gly
 1 5 10 15

Val Ala Thr Ala Asn Ala Val Ala
 20

<210> 21
 <211> 72
 <212> DNA
 <213> *Pseudomonas fluorescens*

<400> 21
 atgaaactga aacgtttgat ggcggcaatg acttttgtcg ctgctggcgt tgcgaccgcc 60
 aacgcggtgg cc 72

<210> 22
 <211> 23
 <212> PRT
 <213> *Pseudomonas fluorescens*

<400> 22
 Met Gln Asn Tyr Lys Lys Phe Leu Leu Ala Ala Ala Val Ser Met Ala
 1 5 10 15

Phe Ser Ala Thr Ala Met Ala
 20

<210> 23
 <211> 69
 <212> DNA
 <213> *Pseudomonas fluorescens*

<400> 23
 atgcagaact ataaaaaatt ccttctggcc gcggccgtct cgatggcggt cagcgccacg 60
 gccatggca 69

<210> 24
 <211> 20
 <212> PRT
 <213> *Pseudomonas fluorescens*

<400> 24

Met Phe Ala Lys Leu Val Ala Val Ser Leu Leu Thr Leu Ala Ser Gly
 1 5 10 15

Gln Leu Leu Ala
 20

<210> 25

<211> 60

<212> DNA

<213> *Pseudomonas fluorescens*

<400> 25

atgtttgcca aactcgttgc tgtttcctg ctgactctgg cgagcggcca gttgcttgct 60

<210> 26

<211> 24

<212> PRT

<213> *Pseudomonas fluorescens*

<400> 26

Met Lys Leu Lys Arg Leu Met Ala Ala Met Thr Phe Val Ala Ala Gly
 1 5 10 15

Val Ala Thr Val Asn Ala Val Ala
 20

<210> 27

<211> 72

<212> DNA

<213> *Pseudomonas fluorescens*

<400> 27

atgaaactga aacgtttgat ggcggcaatg acttttgtcg ctgctggcgt tgcgaccgtc 60

aacgcggtgg cc 72

<210> 28

<211> 23

<212> PRT

<213> *Pseudomonas fluorescens*

<400> 28

Met Pro Pro Arg Ser Ile Ala Ala Cys Leu Gly Leu Leu Gly Leu Leu
 1 5 10 15

Met Ala Thr Gln Ala Ala Ala

20

<210> 29
 <211> 69
 <212> DNA
 <213> *Pseudomonas fluorescens*

<400> 29
 atgccgcctc gttctatcgc cgcatgtctg gggctgctgg gcttgctcat ggctaccag 60
 gccgccgcc 69

<210> 30
 <211> 22
 <212> PRT
 <213> *Escherichia coli*

<400> 30
 Met Glu Phe Phe Lys Lys Thr Ala Leu Ala Ala Leu Val Met Gly Phe
 1 5 10 15

Ser Gly Ala Ala Leu Ala
 20

<210> 31
 <211> 33
 <212> PRT
 <213> *Pseudomonas fluorescens*

<400> 31
 Met Gln Asn Arg Thr Val Glu Ile Gly Val Gly Leu Phe Leu Leu Ala
 1 5 10 15

Gly Ile Leu Ala Leu Leu Leu Leu Ala Leu Arg Val Ser Gly Leu Ser
 20 25 30

Ala

<210> 32
 <211> 99
 <212> DNA
 <213> *Pseudomonas fluorescens*

<400> 32
 atgcaaaacc gcactgtgga aatcggtgtc ggccttttct tgctggctgg catcctggct 60

ttactgttgt tggccctgcg agtcagcggc ctttcggcc

99

<210> 33

<211> 21

<212> PRT

<213> Pseudomonas fluorescens

<400> 33

Met Asn Arg Ser Ser Ala Leu Leu Leu Ala Phe Val Phe Leu Ser Gly

1

5

10

15

Cys Gln Ala Met Ala

20

<210> 34

<211> 63

<212> DNA

<213> Pseudomonas fluorescens

<400> 34

atgaatagat cttccgcgtt gtcctcgct tttgtcttcc tcagcggctg ccaggccatg

60

gcc

63

<210> 35

<211> 21

<212> PRT

<213> Pseudomonas fluorescens

<400> 35

Met Arg Leu Thr Gln Ile Ile Ala Ala Ala Ala Ile Ala Leu Val Ser

1

5

10

15

Thr Phe Ala Leu Ala

20

<210> 36

<211> 63

<212> DNA

<213> Pseudomonas fluorescens

<400> 36

atgcgcttga cccagattat tgccgccgca gccattgcgt tggtttccac ctttgcgctc

60

gcc

63

<210> 37

<211> 29
 <212> PRT
 <213> *Pseudomonas fluorescens*

<400> 37
 Met Gln Ser Leu Pro Phe Ser Ala Leu Arg Leu Leu Gly Val Leu Ala
 1 5 10 15

Val Met Val Cys Val Leu Leu Thr Thr Pro Ala Arg Ala
 20 25

<210> 38
 <211> 87
 <212> DNA
 <213> *Pseudomonas fluorescens*

<400> 38
 atgcaaagcc tgccgttctc tgcgttacgc ctgctcgggtg tgctggcagt catggtctgc 60
 gtgctgttga cgacgccagc ccgtgcc 87

<210> 39
 <211> 22
 <212> PRT
 <213> *Pseudomonas fluorescens*

<400> 39
 Met Arg Asn Leu Ile Leu Ser Ala Ala Leu Val Thr Ala Ser Leu Phe
 1 5 10 15

Gly Met Thr Ala Gln Ala
 20

<210> 40
 <211> 66
 <212> DNA
 <213> *Pseudomonas fluorescens*

<400> 40
 atgcgtaatc tgatcctcag cgccgctctc gtcactgccg gcctcttcgg catgaccgca 60
 caagct 66

<210> 41
 <211> 21
 <212> PRT
 <213> *Pseudomonas fluorescens*

<400> 41

Met Arg Asn Leu Leu Arg Gly Met Leu Val Val Ile Cys Cys Met Ala
 1 5 10 15

Gly Ile Ala Ala Ala
 20

<210> 42

<211> 63

<212> DNA

<213> Pseudomonas fluorescens

<400> 42

atgagaaacc ttcttcgagg aatgcttgct gttatttgct gtatggcagg gatagcggcg 60
 gcg 63

<210> 43

<211> 24

<212> PRT

<213> Pseudomonas fluorescens

<400> 43

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

Gly Leu Pro Ser Thr Ala His Ala
 20

<210> 44

<211> 72

<212> DNA

<213> Pseudomonas fluorescens

<400> 44

atgctttttc gcacattact ggcgagcctt accttttgctg tcatcgccgg cttaccgtcc 60
 acggcccacg cg 72

<210> 45

<211> 6

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 consensus RBS sequence

<400> 45
aggagg 6

<210> 46
<211> 6
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
RBS2 sequence

<400> 46
ggagcg 6

<210> 47
<211> 6
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
RBS34 sequence

<400> 47
ggagcg 6

<210> 48
<211> 6
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
RBS41 sequence

<400> 48
aggagt 6

<210> 49
<211> 6
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
RBS43 sequence

<400> 49
ggagtg 6

<210> 50
 <211> 6
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown:
 RBS48 sequence

<400> 50
 gagtaa 6

<210> 51
 <211> 6
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown:
 RBS1 sequence

<400> 51
 agagag 6

<210> 52
 <211> 6
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown:
 RBS35 sequence

<400> 52
 aaggca 6

<210> 53
 <211> 6
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown:
 RBS49 sequence

<400> 53
 ccgaac 6

<210> 54
 <211> 325
 <212> PRT
 <213> *Pseudomonas fluorescens*

<400> 54

Met Gln Ser Ala Asn Asn Val Met Val Leu Tyr Thr Gly Gly Thr Ile
 1 5 10 15

Gly Met Gln Ala Ser Ala Asn Gly Leu Ala Pro Ala Ser Gly Phe Glu
 20 25 30

Val Arg Met Arg Glu Gln Phe Ala Gly Ala Asp Leu Pro Ala Trp Arg
 35 40 45

Phe Gln Glu Met Ser Pro Leu Ile Asp Ser Ala Asn Met Asn Pro Ala
 50 55 60

Tyr Trp Gln Arg Leu Arg Ser Ala Val Val Glu Ala Val Asp Ala Gly
 65 70 75 80

Cys Asp Ala Val Leu Ile Leu His Gly Thr Asp Thr Leu Ala Tyr Ser
 85 90 95

Ala Ala Ala Met Ser Phe Gln Leu Leu Gly Leu Pro Ala Pro Val Val
 100 105 110

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

Glu Asn Val Ser Gly Ala Leu Thr Ala Leu Gly Glu Gly Leu Lys Pro
 130 135 140

Gly Val His Leu Tyr Phe His Gly Ala Leu Met Ala Pro Thr Arg Cys
 145 150 155 160

Ala Lys Ile Arg Ser Phe Gly Arg Asn Pro Phe Ala Ala Leu Gln Arg
 165 170 175

Asn Gly Gly Val Ala Leu Ala Asp Lys Leu Pro Ala Ala Leu Ala Tyr
 180 185 190

Arg Asn Asp Lys Ala Pro Ala Asn Val Gly Val Leu Pro Leu Val Pro
 195 200 205

Gly Ile Ala Ala Ala Gln Leu Asp Ala Leu Ile Asp Ser Gly Ile Gln
 210 215 220

Ala Leu Val Leu Glu Cys Phe Gly Ser Gly Thr Gly Pro Ser Asp Asn
 225 230 235 240

Pro Ala Phe Leu Ala Ser Leu Lys Arg Ala Gln Asp Gln Glu Val Val
 245 250 255

Val Val Ala Ile Thr Gln Cys His Glu Gly Gly Val Glu Leu Asp Val
 260 265 270

Tyr Glu Ala Gly Ser Arg Leu Arg Ser Val Gly Val Leu Ser Gly Gly
 275 280 285

Gly Met Thr Arg Glu Ala Ala Phe Gly Lys Leu Asn Ala Leu Ile Gly
 290 295 300

Ala Gly Leu Asp Ser Ala Glu Ile Arg Arg Leu Val Glu Leu Asp Leu
 305 310 315 320

Cys Gly Glu Leu Ser
 325

<210> 55
 <211> 362
 <212> PRT
 <213> *Pseudomonas fluorescens*

<400> 55
 Met Lys Ser Ala Leu Lys Asn Val Ile Pro Gly Ala Leu Ala Leu Leu
 1 5 10 15

Leu Leu Phe Pro Val Ala Ala Gln Ala Lys Glu Val Glu Ser Lys Thr
 20 25 30

Lys Leu Ser Asn Val Val Ile Leu Ala Thr Gly Gly Thr Ile Ala Gly
 35 40 45

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

Gly Ile Glu Gln Leu Ile Ala Gly Val Pro Glu Leu Ser Gln Ile Ala
 65 70 75 80

Asn Val Arg Gly Glu Gln Val Met Gln Ile Ala Ser Glu Ser Ile Asn
 85 90 95

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

Asn Lys Asp Val Asp Gly Ile Val Ile Thr His Gly Thr Asp Thr Leu
 115 120 125

Glu Glu Thr Ala Tyr Phe Leu Asn Leu Val Glu Lys Thr Asp Lys Pro
 130 135 140

Ile Val Val Val Gly Ser Met Arg Pro Gly Thr Ala Met Ser Ala Asp
 145 150 155 160

Gly Met Leu Asn Leu Tyr Asn Ala Val Ala Val Ala Gly Ser Lys Glu
 165 170 175

Ala Arg Gly Lys Gly Val Leu Val Thr Met Asn Asp Glu Ile Gln Ser
 180 185 190

Gly Arg Asp Val Ser Lys Met Ile Asn Ile Lys Thr Glu Ala Phe Lys
 195 200 205

Ser Pro Trp Gly Pro Met Gly Met Val Val Glu Gly Lys Ser Tyr Trp
 210 215 220

Phe Arg Leu Pro Ala Lys Arg His Thr Met Asp Ser Glu Phe Asp Ile
 225 230 235 240

Lys Thr Ile Lys Ser Leu Pro Asp Val Glu Ile Ala Tyr Gly Tyr Gly
 245 250 255

Asn Val Ser Asp Thr Ala Tyr Lys Ala Leu Ala Gln Ala Gly Ala Lys
 260 265 270

Ala Ile Ile His Ala Gly Thr Gly Asn Gly Ser Val Ser Ser Lys Val
275 280 285

Val	Pro	Ala	Leu	Val	Glu	Leu	Arg	Lys	Gln	Gly	Val	Gln	Ile	Ile	Arg
	290					295					300				

Ser Ser His Val Asn Ala Gly Gly Met Val Leu Arg Asn Ala Glu Gln
305 310 315 320

Pro Asp Asp Lys Tyr Asp Trp Val Ala Ala Leu Asp Leu Asn Pro Gln
325 330 335

Lys Ala Arg Ile Leu Ala Met Val Ala Leu Thr Lys Thr Gln Asp Ser
340 345 350

Lys Glu Leu Gln Arg Ile Phe Trp Glu Tyr
355 360

<210> 56

<211> 167

<212> PRT

<213> *Pseudomonas fluorescens*

<400> 56

Val	Arg	Lys	Leu	Thr	Gln	Leu	Val	Leu	Leu	Ala	Thr	Val	Leu	Val	Thr
1				5				10					15		

Thr Pro Ala Phe Ala Glu Met Lys Ile Ala Val Leu Asn Tyr Gln Met
20 25 30

Ala Leu Leu Glu Ser Asp Ala Ala Lys Arg Tyr Ala Val Asp Ala Glu
35 40 45

Lys Lys Phe Gly Pro Gln Leu Thr Lys Leu Lys Thr Leu Glu Ser Ser
50 55 60

Ala Lys Gly Ile Gln Asp Arg Leu Val Ala Gly Gly Asp Lys Met Gln
65 70 75 80

Gln Gly Glu Arg Glu Arg Leu Glu Leu Glu Phe Lys Gln Lys Ala Arg
85 90 95

Asp Tyr Gln Phe Gln Ser Lys Glu Leu Asn Glu Ala Lys Ala Val Ala
 100 105 110

Asp Arg Glu Met Leu Lys Gln Leu Lys Pro Lys Leu Asp Ser Ala Val
 115 120 125

Glu Glu Val Ile Lys Lys Gly Ala Phe Asp Leu Val Phe Glu Arg Gly
 130 135 140

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

Glu Arg Met Asn Gln Leu Lys
 165

<210> 57

<211> 504

<212> DNA

<213> *Pseudomonas fluorescens*

<400> 57

gtgcgtaagt tgactcaatt ggtcttgctg gccactgtgc tggtcaccac cccggccttc	60
gccgaaatga aaatcgccgt tctgaactat cagatggccc tgctggaatc cgatgcggcc	120
aagcgatacg ccgtggatgc cgagaagaag ttcgggtccgc aactgaccaa gctcaagaca	180
ctggaaagca gcgccaaagg catccaggac cgcctggtag ccggtggcga caagatgcag	240
caaggcgagc gcgagcgtct ggagcttgaa ttcaagcaaa aggcccgtga ctaccagttc	300
caatccaagg agctgaacga agccaaggct gtggccgacc gcgaaatgct caagcagctc	360
aagcctaaat tggacagcgc tgtggaagaa gtcataaga agggcgcctt tgacctggtg	420
ttcgagcgtg gcgccgtgat cgacgtcaag cctcaatacg acatcacccg ccaggtgatc	480
gagcgcata accagctgaa gtga	504