SEQUENCE LISTING

<110> The Trustees of the University of Pennsylvania
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Leibman, Rachel
Payne, Aimee
Ellebrecht, Christoph T.
Milone, Michael C.

<120> Method of Redirecting T cells to Treat HIV Infection

<130> 046483-7096WO1(01193)

<150> US 62/222,132
<151> 2015-09-22

<150> US 62/253,790
<151> 2015-11-11

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cctggatccg acttcgtgct gacccagagc cctcacagcc tgagcgtgac acctggcgag 120

agcgccagca tcagctgcaa gagcagccac tccctgatcc acggcgaccg gaacaactac 180

ctggcttggt acgtgcagaa gcccggcaga tccccccagc tgctgatcta cctggccagc 240

agcagagcca gcggcgtgcc cgatagattt tctggcagcg gcagcgacaa ggacttcacc 300

ctgaagatca gccgggtgga aaccgaggac gtgggcacct actactgtat gcagggcaga 360

gagagcccct ggacctttgg ccagggcacc aaggtggaca tcaagggcgg cagctccaga 420

agcagctcta gcggaggcgg aggatctggc ggcggaggac aggctcagct ggtgcagtct 480

ggacccgaag tgcggaagcc tggcaccagc gtgaaggtgt cctgtaaagc ccctggcaac 540

accctgaaaa cctacgacct gcactgggtg cgcagcgtgc caggacaggg actgcagtgg 600

atgggctgga tcagccacga gggcgacaag aaagtgatcg tggaacggtt caaggccaaa 660

gtgaccatcg actgggacag aagcaccaac accgcctacc tgcagctgag cggcctgacc 720

tctggcgata ccgccgtgta ctactgcgcc aagggcagca agcaccggct gagagactac 780

gccctgtacg acgatgacgg cgccctgaac tgggccgtgg atgtggacta cctgagcaac 840

ctggaattct ggggccaggg aaccgccgtg accgtgtcat ct 882

<210> 13
<211> 294
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 13

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

His Ala Ala Arg Pro Gly Ser Asp Phe Val Leu Thr Gln Ser Pro His
20 25 30

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

Ser His Ser Leu Ile His Gly Asp Arg Asn Asn Tyr Leu Ala Trp Tyr
50 55 60

Val Gln Lys Pro Gly Arg Ser Pro Gln Leu Leu Ile Tyr Leu Ala Ser
65 70 75 80

Ser Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Asp
85 90 95

Lys Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Thr Glu Asp Val Gly
100 105 110

Thr Tyr Tyr Cys Met Gln Gly Arg Glu Ser Pro Trp Thr Phe Gly Gln
115 120 125

Gly Thr Lys Val Asp Ile Lys Gly Gly Ser Ser Arg Ser Ser Ser Ser

```
    130                 135                 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gln Ala Gln Leu Val Gln Ser
145                 150                 155                 160

Gly Pro Glu Val Arg Lys Pro Gly Thr Ser Val Lys Val Ser Cys Lys
                165                 170                 175

Ala Pro Gly Asn Thr Leu Lys Thr Tyr Asp Leu His Trp Val Arg Ser
            180                 185                 190

Val Pro Gly Gln Gly Leu Gln Trp Met Gly Trp Ile Ser His Glu Gly
        195                 200                 205

Asp Lys Lys Val Ile Val Glu Arg Phe Lys Ala Lys Val Thr Ile Asp
    210                 215                 220

Trp Asp Arg Ser Thr Asn Thr Ala Tyr Leu Gln Leu Ser Gly Leu Thr
225                 230                 235                 240

Ser Gly Asp Thr Ala Val Tyr Tyr Cys Ala Lys Gly Ser Lys His Arg
                245                 250                 255

Leu Arg Asp Tyr Ala Leu Tyr Asp Asp Asp Gly Ala Leu Asn Trp Ala
            260                 265                 270

Val Asp Val Asp Tyr Leu Ser Asn Leu Glu Phe Trp Gly Gln Gly Thr
        275                 280                 285

Ala Val Thr Val Ser Ser
    290
```

<210> 14
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 14
atgggggac ttgaaccctg cagcaggttc ctgctcctgc ctctcctgct ggctgtaagt 60

ggtctccgtc ctgtccaggt ccaggcccag agcgattgca gttgctctac ggtgagcccg 120

ggcgtgctgg cagggatcgt gatgggagac ctggtgctga cagtgctcat tgccctggcc 180

gtgtacttcc tgggccggct ggtccctcgg gggcgagggg ctgcggaggc agcgacccgg 240

aaacagcgta tcactgagac cgagtcgcct tatcaggagc tccagggtca gaggtcggat 300

gtctacagcg acctcaacac acagaggccg tattacaaag tcgagggcgg cggagagggc 360

agaggaagtc ttctaacatg cggtgacgtg gaggagaatc ccggccctag gatggctctg 420

cctgtgacag ctctgctgct gcctctggcc ctgctgctgc atgctgccag acctggatcc 480

cagtctgccc tgactcagcc tccctccgcg tccgggtctc ctggacagtc aatcaccatc 540

tcctgcactg gaaccagcaa taactttgtc tcctggtacc agcaacacgc aggcaaggcc 600

cccaagctcg tcatttatga cgtcaataag cgcccctcag gtgtccctga tcgtttctct 660

ggctccaagt ctggcaacac ggcctccctg accgtctctg gactccagac tgacgatgag 720

gctgtctatt actgcggctc acttgtaggc aactgggatg tgattttcgg cggagggacc 780

aagttgaccg tcctaggcgg aagcagcaga agcagctcta gcggcggagg cggatctggc 840

ggaggggac agatgcagtt acaggagtcg ggccccggac tggtgaagcc ttcggaaacc 900

ctgtccctca cgtgcagtgt gtctggtgcc tccataagtg acagttactg gagctggatc 960

cggcggtccc cagggaaggg acttgagtgg attgggtatg tccacaaaag cggcgacaca 1020

aattacagcc cctccctcaa gagtcgagtc aacttgtcgt tagacacgtc caaaaatcag 1080

gtgtccctga gccttgtggc cgcgaccgct gcggactcgg gcaaatatta ttgcgcgaga 1140

acactgcacg ggaggagaat ttatggaatc gttgccttca atgagtggtt cacctacttc 1200

tacatggacg tctggggcaa tgggactcag gtcaccgtct cctcagctag cggcggaggg 1260

ggatctggag gtgggggttc ctcacccact gaaccaagct ccaaaaccgg taaccccaga 1320

cacctgcatg ttctgattgg gacctcagtg gtcaaaatcc ctttcaccat cctcctcttc 1380

tttctccttc atcgctggtg ctccaacaaa aaaaatgctg ctgtaatgga ccaagagcct 1440

gcagggaaca gaacagtgaa cagcgaggat tctgatgaac aagaccatca ggaggtgtca 1500

tacgcataa 1509

<210> 15
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 15

Met Gly Gly Leu Glu Pro Cys Ser Arg Phe Leu Leu Leu Pro Leu Leu
1 5 10 15

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Val Gln Ala Gln Ser Asp
20 25 30

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
35 40 45

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
50 55 60

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg
65 70 75 80

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

Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr
100 105 110

Lys Val Glu Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly

```
        115                 120                 125

Asp Val Glu Glu Asn Pro Gly Pro Arg Met Ala Leu Pro Val Thr Ala
    130                 135                 140

Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Gly Ser
145                 150                 155                 160

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Asn Asn Phe Val Ser Trp
            180                 185                 190

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

Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser
    210                 215                 220

Gly Asn Thr Ala Ser Leu Thr Val Ser Gly Leu Gln Thr Asp Asp Glu
225                 230                 235                 240

Ala Val Tyr Tyr Cys Gly Ser Leu Val Gly Asn Trp Asp Val Ile Phe
                245                 250                 255

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

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gln Met Gln Leu Gln
        275                 280                 285

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
    290                 295                 300

Cys Ser Val Ser Gly Ala Ser Ile Ser Asp Ser Tyr Trp Ser Trp Ile
```

```
305                 310                 315                 320

Arg Arg Ser Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Val His Lys
                325                 330                 335

Ser Gly Asp Thr Asn Tyr Ser Pro Ser Leu Lys Ser Arg Val Asn Leu
            340                 345                 350

Ser Leu Asp Thr Ser Lys Asn Gln Val Ser Leu Ser Leu Val Ala Ala
        355                 360                 365

Thr Ala Ala Asp Ser Gly Lys Tyr Tyr Cys Ala Arg Thr Leu His Gly
    370                 375                 380

Arg Arg Ile Tyr Gly Ile Val Ala Phe Asn Glu Trp Phe Thr Tyr Phe
385                 390                 395                 400

Tyr Met Asp Val Trp Gly Asn Gly Thr Gln Val Thr Val Ser Ser Ala
                405                 410                 415

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Thr Glu Pro
            420                 425                 430

Ser Ser Lys Thr Gly Asn Pro Arg His Leu His Val Leu Ile Gly Thr
        435                 440                 445

Ser Val Val Lys Ile Pro Phe Thr Ile Leu Leu Phe Phe Leu Leu His
    450                 455                 460

Arg Trp Cys Ser Asn Lys Lys Asn Ala Ala Val Met Asp Gln Glu Pro
465                 470                 475                 480

Ala Gly Asn Arg Thr Val Asn Ser Glu Asp Ser Asp Glu Gln Asp His
                485                 490                 495

Gln Glu Val Ser Tyr Ala Glx
```

500

<210> 16
<211> 834
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 16
atggctctgc ctgtgacagc tctgctgctg cctctggccc tgctgctgca tgctgccaga 60

cctggatccc agtctgccct gactcagcct ccctccgcgt ccgggtctcc tggacagtca 120

atcaccatct cctgcactgg aaccagcaat aactttgtct cctggtacca gcaacacgca 180

ggcaaggccc ccaagctcgt catttatgac gtcaataagc gcccctcagg tgtccctgat 240

cgtttctctg gctccaagtc tggcaacacg gcctccctga ccgtctctgg actccagact 300

gacgatgagg ctgtctatta ctgcggctca cttgtaggca actgggatgt gattttcggc 360

ggagggacca agttgaccgt cctaggcgga agcagcagaa gcagctctag cggcggaggc 420

ggatctggcg gaggggggaca gatgcagtta caggagtcgg gccccggact ggtgaagcct 480

tcggaaaccc tgtccctcac gtgcagtgtg tctggtgcct ccataagtga cagttactgg 540

agctggatcc ggcggtcccc agggaaggga cttgagtgga ttgggtatgt ccacaaaagc 600

ggcgacacaa attacagccc ctccctcaag agtcgagtca acttgtcgtt agacacgtcc 660

aaaaatcagg tgtccctgag ccttgtggcc gcgaccgctg cggactcggg caaatattat 720

tgcgcgagaa cactgcacgg gaggagaatt tatggaatcg ttgccttcaa tgagtggttc 780

acctacttct acatggacgt ctggggcaat gggactcagg tcaccgtctc ctca 834

<210> 17
<211> 278
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 17

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

His Ala Ala Arg Pro Gly Ser Gln Ser Ala Leu Thr Gln Pro Pro Ser
            20                  25                  30

Ala Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr
        35                  40                  45

Ser Asn Asn Phe Val Ser Trp Tyr Gln Gln His Ala Gly Lys Ala Pro
    50                  55                  60

Lys Leu Val Ile Tyr Asp Val Asn Lys Arg Pro Ser Gly Val Pro Asp
65                  70                  75                  80

Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Val Ser
                85                  90                  95

Gly Leu Gln Thr Asp Asp Glu Ala Val Tyr Tyr Cys Gly Ser Leu Val
            100                 105                 110

Gly Asn Trp Asp Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
        115                 120                 125

Gly Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly Ser Gly Gly
    130                 135                 140

Gly Gly Gln Met Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
145                 150                 155                 160

Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Ala Ser Ile Ser
                165                 170                 175

Asp Ser Tyr Trp Ser Trp Ile Arg Arg Ser Pro Gly Lys Gly Leu Glu
```

180 185 190

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

Leu Lys Ser Arg Val Asn Leu Ser Leu Asp Thr Ser Lys Asn Gln Val
210 215 220

Ser Leu Ser Leu Val Ala Ala Thr Ala Ala Asp Ser Gly Lys Tyr Tyr
225 230 235 240

Cys Ala Arg Thr Leu His Gly Arg Arg Ile Tyr Gly Ile Val Ala Phe
245 250 255

Asn Glu Trp Phe Thr Tyr Phe Tyr Met Asp Val Trp Gly Asn Gly Thr
260 265 270

Gln Val Thr Val Ser Ser
275

<210> 18
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 18
atgggggac ttgaaccctg cagcaggttc ctgctcctgc ctctcctgct ggctgtaagt 60

ggtctccgtc ctgtccaggt ccaggcccag agcgattgca gttgctctac ggtgagcccg 120

ggcgtgctgg cagggatcgt gatgggagac ctggtgctga cagtgctcat tgccctggcc 180

gtgtacttcc tgggccggct ggtccctcgg gggcgagggg ctgcggaggc agcgacccgg 240

aaacagcgta tcactgagac cgagtcgcct tatcaggagc tccagggtca gaggtcggat 300

gtctacagcg acctcaacac acagaggccg tattacaaag tcgagggcgg cggagagggc 360

agaggaagtc ttctaacatg cggtgacgtg gaggagaatc ccggccctag gatggctctg 420

cctgtgacag ctctgctgct gcctctggcc ctgctgctgc atgctgccag acctggatcc 480

gagatcgtgc tgacacagag ccctggcacc ctgagcctgt ctccaggcga gacagccatc 540

atcagctgcc ggacaagcca gtacggcagc ctggcctggt atcagcagag gcctggacag 600

gcccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc 660

agcggctcta gatggggccc tgactacaac ctgaccatca gcaacctgga aagcggcgac 720

ttcggcgtgt actactgcca gcagtacgag ttcttcggcc agggcaccaa ggtgcaggtg 780

gacatcaaga gaggcggcag ctccagaagc tccagctctg gcggcggagg atctggcgga 840

ggcggacagg tgcagctggt gcagtctggc ggccagatga agaaacccgg cgagagcatg 900

cggatcagct gcagagcctc cggctacgag ttcatcgact gcaccctgaa ctggattcgg 960

ctggcccctg gcaaaagacc cgagtggatg ggctggctga agcccagagg cggagccgtg 1020

aattacgcca gacctctgca gggcagagtg accatgaccc gggacgtgta cagcgatacc 1080

gccttcctgg aactgcggag cctgaccgtg gatgataccg ccgtgtactt ctgcacccgg 1140

ggcaagaact gcgactacaa ctgggacttc gagcactggg gcagaggcac ccctgtgatc 1200

gtgtctagcg ctagcggcgg agggggatct ggaggtgggg gttcctcacc cactgaacca 1260

agctccaaaa ccggtaaccc cagacacctg catgttctga ttgggacctc agtggtcaaa 1320

atccctttca ccatcctcct cttctttctc cttcatcgct ggtgctccaa caaaaaaaat 1380

gctgctgtaa tggaccaaga gcctgcaggg aacagaacag tgaacagcga ggattctgat 1440

gaacaagacc atcaggaggt gtcatacgca taa 1473

<210> 19
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 19

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Met Gly Gly Leu Glu Pro Cys Ser Arg Phe Leu Leu Leu Pro Leu Leu
1               5                   10                  15

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Val Gln Ala Gln Ser Asp
            20                  25                  30

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
        35                  40                  45

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
    50                  55                  60

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg
65                  70                  75                  80

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

Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr
            100                 105                 110

Lys Val Glu Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
        115                 120                 125

Asp Val Glu Glu Asn Pro Gly Pro Arg Met Ala Leu Pro Val Thr Ala
    130                 135                 140

Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Gly Ser
145                 150                 155                 160

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
                165                 170                 175

Glu Thr Ala Ile Ile Ser Cys Arg Thr Ser Gln Tyr Gly Ser Leu Ala
            180                 185                 190
```

```
Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Val Ile Tyr Ser
        195                 200                 205

Gly Ser Thr Arg Ala Ala Gly Ile Pro Asp Arg Phe Ser Gly Ser Arg
    210                 215                 220

Trp Gly Pro Asp Tyr Asn Leu Thr Ile Ser Asn Leu Glu Ser Gly Asp
225                 230                 235                 240

Phe Gly Val Tyr Tyr Cys Gln Gln Tyr Glu Phe Phe Gly Gln Gly Thr
                245                 250                 255

Lys Val Gln Val Asp Ile Lys Arg Gly Gly Ser Ser Arg Ser Ser Ser
            260                 265                 270

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln
        275                 280                 285

Ser Gly Gly Gln Met Lys Lys Pro Gly Glu Ser Met Arg Ile Ser Cys
    290                 295                 300

Arg Ala Ser Gly Tyr Glu Phe Ile Asp Cys Thr Leu Asn Trp Ile Arg
305                 310                 315                 320

Leu Ala Pro Gly Lys Arg Pro Glu Trp Met Gly Trp Leu Lys Pro Arg
                325                 330                 335

Gly Gly Ala Val Asn Tyr Ala Arg Pro Leu Gln Gly Arg Val Thr Met
            340                 345                 350

Thr Arg Asp Val Tyr Ser Asp Thr Ala Phe Leu Glu Leu Arg Ser Leu
        355                 360                 365

Thr Val Asp Asp Thr Ala Val Tyr Phe Cys Thr Arg Gly Lys Asn Cys
    370                 375                 380
```

```
Asp Tyr Asn Trp Asp Phe Glu His Trp Gly Arg Gly Thr Pro Val Ile
385                 390                 395                 400


Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
                405                 410                 415


Pro Thr Glu Pro Ser Ser Lys Thr Gly Asn Pro Arg His Leu His Val
            420                 425                 430


Leu Ile Gly Thr Ser Val Val Lys Ile Pro Phe Thr Ile Leu Leu Phe
        435                 440                 445


Phe Leu Leu His Arg Trp Cys Ser Asn Lys Lys Asn Ala Ala Val Met
    450                 455                 460


Asp Gln Glu Pro Ala Gly Asn Arg Thr Val Asn Ser Glu Asp Ser Asp
465                 470                 475                 480


Glu Gln Asp His Gln Glu Val Ser Tyr Ala Glx
                485                 490
```

<210> 20
<211> 798
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 20

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atggccctgc ctgtgacagc cctgctgctg cctctggctc tgctgctgca cgccgctaga       60

cctggatccg agatcgtgct gacacagagc cctggcaccc tgagcctgtc tccaggcgag      120

acagccatca tcagctgccg gacaagccag tacggcagcc tggcctggta tcagcagagg      180

cctggacagg cccccagact cgtgatctac agcggcagca caagagccgc cggaatcccc      240

gatagattca gcggctctag atggggccct gactacaacc tgaccatcag caacctggaa      300
```

agcggcgact tcggcgtgta ctactgccag cagtacgagt tcttcggcca gggcaccaag 360

gtgcaggtgg acatcaagag aggcggcagc tccagaagct ccagctctgg cggcggagga 420

tctggcggag gcggacaggt gcagctggtg cagtctggcg gccagatgaa gaaacccggc 480

gagagcatgc ggatcagctg cagagcctcc ggctacgagt tcatcgactg caccctgaac 540

tggattcggc tggcccctgg caaaagaccc gagtggatgg gctggctgaa gcccagaggc 600

ggagccgtga attacgccag acctctgcag ggcagagtga ccatgacccg ggacgtgtac 660

agcgataccg ccttcctgga actgcggagc ctgaccgtgg atgataccgc cgtgtacttc 720

tgcacccggg gcaagaactg cgactacaac tgggacttcg agcactgggg cagaggcacc 780

cctgtgatcg tgtctagc 798

<210> 21
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 21

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

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

Thr Leu Ser Leu Ser Pro Gly Glu Thr Ala Ile Ile Ser Cys Arg Thr
35 40 45

Ser Gln Tyr Gly Ser Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala
50 55 60

Pro Arg Leu Val Ile Tyr Ser Gly Ser Thr Arg Ala Ala Gly Ile Pro
65 70 75 80

```
Asp Arg Phe Ser Gly Ser Arg Trp Gly Pro Asp Tyr Asn Leu Thr Ile
                85                  90                  95

Ser Asn Leu Glu Ser Gly Asp Phe Gly Val Tyr Tyr Cys Gln Gln Tyr
            100                 105                 110

Glu Phe Phe Gly Gln Gly Thr Lys Val Gln Val Asp Ile Lys Arg Gly
        115                 120                 125

Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Gln Val Gln Leu Val Gln Ser Gly Gly Gln Met Lys Lys Pro Gly
145                 150                 155                 160

Glu Ser Met Arg Ile Ser Cys Arg Ala Ser Gly Tyr Glu Phe Ile Asp
                165                 170                 175

Cys Thr Leu Asn Trp Ile Arg Leu Ala Pro Gly Lys Arg Pro Glu Trp
            180                 185                 190

Met Gly Trp Leu Lys Pro Arg Gly Gly Ala Val Asn Tyr Ala Arg Pro
        195                 200                 205

Leu Gln Gly Arg Val Thr Met Thr Arg Asp Val Tyr Ser Asp Thr Ala
    210                 215                 220

Phe Leu Glu Leu Arg Ser Leu Thr Val Asp Asp Thr Ala Val Tyr Phe
225                 230                 235                 240

Cys Thr Arg Gly Lys Asn Cys Asp Tyr Asn Trp Asp Phe Glu His Trp
                245                 250                 255

Gly Arg Gly Thr Pro Val Ile Val Ser Ser
            260                 265
```

<210> 22
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 22
atgggggac ttgaaccctg cagcaggttc ctgctcctgc ctctcctgct ggctgtaagt 60

ggtctccgtc ctgtccaggt ccaggcccag agcgattgca gttgctctac ggtgagcccg 120

ggcgtgctgg cagggatcgt gatgggagac ctggtgctga cagtgctcat tgccctggcc 180

gtgtacttcc tgggccggct ggtccctcgg gggcgagggg ctgcggaggc agcgacccgg 240

aaacagcgta tcactgagac cgagtcgcct tatcaggagc tccagggtca gaggtcggat 300

gtctacagcg acctcaacac acagaggccg tattacaaag tcgagggcgg cggagagggc 360

agaggaagtc ttctaacatg cggtgacgtg gaggagaatc ccggccctag gatggctctg 420

cctgtgacag ctctgctgct gcctctggcc ctgctgctgc atgctgccag acctggatcc 480

gacatccaga tgacccagag ccccagcagc ctgtctgcca gagtgggcga caccgtgacc 540

atcacctgtc aggccaacgg ctacctgaac tggtatcagc agcggagagg caaggccccc 600

aagctgctga tctacgacgg cagcaagctg gaaagaggcg tgcccgccag attcagcggc 660

agaagatggg gccaggagta caacctgacc atcaacaacc tgcagcccga ggacgtggcc 720

acatactttt gccaggtgta cgagttcatc gtgcccggca cccggctgga tctgaagggc 780

ggaagcagca gaagcagctc tagcggcgga ggcggatctg gcggaggggg acaggtgcac 840

ctgagtcagt ctggcgccgc tgtgacaaag ccaggcgctt ctgtgcgggt gtcctgtgaa 900

gccagcggct acaagatcag cgaccacttc atccactggt ggcggcaggc tccaggacag 960

ggactgcagt gggtgggatg gatcaacccc aagaccggcc agcccaacaa ccccagacag 1020

ttccagggca gagtgtccct gaccagacag gccagctggg acttcgacac ctacagcttc 1080

tacatggacc tgaaggccgt gcggagcgac gacaccgcca tctacttttg cgccagacag 1140

agaagcgact tctgggattt cgacgtgtgg ggcagcggca cccaagtgac cgtgtcatct 1200

gctagcggcg gaggggggatc tggaggtggg ggttcctcac ccactgaacc aagctccaaa 1260

accggtaacc ccagacacct gcatgttctg attgggacct cagtggtcaa aatccctttc 1320

accatcctcc tcttctttct ccttcatcgc tggtgctcca acaaaaaaaa tgctgctgta 1380

atggaccaag agcctgcagg gaacagaaca gtgaacagcg aggattctga tgaacaagac 1440

catcaggagg tgtcatacgc ataa 1464

<210> 23
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 23

Met Gly Gly Leu Glu Pro Cys Ser Arg Phe Leu Leu Leu Pro Leu Leu
1 5 10 15

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Val Gln Ala Gln Ser Asp
20 25 30

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
35 40 45

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
50 55 60

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg
65 70 75 80

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

Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr

```
            100                 105                 110

Lys Val Glu Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
        115                 120                 125

Asp Val Glu Glu Asn Pro Gly Pro Arg Met Ala Leu Pro Val Thr Ala
    130                 135                 140

Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Gly Ser
145                 150                 155                 160

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

Asp Thr Val Thr Ile Thr Cys Gln Ala Asn Gly Tyr Leu Asn Trp Tyr
            180                 185                 190

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

Lys Leu Glu Arg Gly Val Pro Ala Arg Phe Ser Gly Arg Arg Trp Gly
    210                 215                 220

Gln Glu Tyr Asn Leu Thr Ile Asn Asn Leu Gln Pro Glu Asp Val Ala
225                 230                 235                 240

Thr Tyr Phe Cys Gln Val Tyr Glu Phe Ile Val Pro Gly Thr Arg Leu
                245                 250                 255

Asp Leu Lys Gly Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly
            260                 265                 270

Ser Gly Gly Gly Gly Gln Val His Leu Ser Gln Ser Gly Ala Ala Val
        275                 280                 285

Thr Lys Pro Gly Ala Ser Val Arg Val Ser Cys Glu Ala Ser Gly Tyr
```

```
    290                 295                 300

Lys Ile Ser Asp His Phe Ile His Trp Trp Arg Gln Ala Pro Gly Gln
305                 310                 315                 320

Gly Leu Gln Trp Val Gly Trp Ile Asn Pro Lys Thr Gly Gln Pro Asn
                325                 330                 335

Asn Pro Arg Gln Phe Gln Gly Arg Val Ser Leu Thr Arg Gln Ala Ser
            340                 345                 350

Trp Asp Phe Asp Thr Tyr Ser Phe Tyr Met Asp Leu Lys Ala Val Arg
        355                 360                 365

Ser Asp Asp Thr Ala Ile Tyr Phe Cys Ala Arg Gln Arg Ser Asp Phe
    370                 375                 380

Trp Asp Phe Asp Val Trp Gly Ser Gly Thr Gln Val Thr Val Ser Ser
385                 390                 395                 400

Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Thr Glu
                405                 410                 415

Pro Ser Ser Lys Thr Gly Asn Pro Arg His Leu His Val Leu Ile Gly
            420                 425                 430

Thr Ser Val Val Lys Ile Pro Phe Thr Ile Leu Leu Phe Phe Leu Leu
        435                 440                 445

His Arg Trp Cys Ser Asn Lys Lys Asn Ala Ala Val Met Asp Gln Glu
    450                 455                 460

Pro Ala Gly Asn Arg Thr Val Asn Ser Glu Asp Ser Asp Glu Gln Asp
465                 470                 475                 480

His Gln Glu Val Ser Tyr Ala Glx
```

<210> 24
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 24
gacatccaga tgacccagag ccccagcagc ctgtctgcca gagtgggcga caccgtgacc 60

atcacctgtc aggccaacgg ctacctgaac tggtatcagc agcggagagg caaggccccc 120

aagctgctga tctacgacgg cagcaagctg gaaagaggcg tgcccgccag attcagcggc 180

agaagatggg gccaggagta caacctgacc atcaacaacc tgcagcccga ggacgtggcc 240

acatactttt gccaggtgta cgagttcatc gtgcccggca cccggctgga tctgaagggc 300

ggaagcagca gaagcagctc tagcggcgga ggcggatctg gcggaggggg acaggtgcac 360

ctgagtcagt ctggcgccgc tgtgacaaag ccaggcgctt ctgtgcgggt gtcctgtgaa 420

gccagcggct acaagatcag cgaccacttc atccactggt ggcggcaggc tccaggacag 480

ggactgcagt gggtgggatg gatcaacccc aagaccggcc agcccaacaa ccccagacag 540

ttccagggca gagtgtccct gaccagacag gccagctggg acttcgacac ctacagcttc 600

tacatggacc tgaaggccgt gcggagcgac gacaccgcca tctacttttg cgccagacag 660

agaagcgact tctgggattt cgacgtgtgg ggcagcggca cccaagtgac cgtgtcatct 720

<210> 25
<211> 263
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 25

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

```
1               5                   10                  15

His Ala Ala Arg Pro Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
            20                  25                  30

Ser Leu Ser Ala Arg Val Gly Asp Thr Val Thr Ile Thr Cys Gln Ala
        35                  40                  45

Asn Gly Tyr Leu Asn Trp Tyr Gln Gln Arg Arg Gly Lys Ala Pro Lys
    50                  55                  60

Leu Leu Ile Tyr Asp Gly Ser Lys Leu Glu Arg Gly Val Pro Ala Arg
65                  70                  75                  80

Phe Ser Gly Arg Arg Trp Gly Gln Glu Tyr Asn Leu Thr Ile Asn Asn
                85                  90                  95

Leu Gln Pro Glu Asp Val Ala Thr Tyr Phe Cys Gln Val Tyr Glu Phe
            100                 105                 110

Ile Val Pro Gly Thr Arg Leu Asp Leu Lys Gly Gly Ser Ser Arg Ser
        115                 120                 125

Ser Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gln Val His Leu
    130                 135                 140

Ser Gln Ser Gly Ala Ala Val Thr Lys Pro Gly Ala Ser Val Arg Val
145                 150                 155                 160

Ser Cys Glu Ala Ser Gly Tyr Lys Ile Ser Asp His Phe Ile His Trp
                165                 170                 175

Trp Arg Gln Ala Pro Gly Gln Gly Leu Gln Trp Val Gly Trp Ile Asn
            180                 185                 190

Pro Lys Thr Gly Gln Pro Asn Asn Pro Arg Gln Phe Gln Gly Arg Val
```

195 200 205

Ser Leu Thr Arg Gln Ala Ser Trp Asp Phe Asp Thr Tyr Ser Phe Tyr
210 215 220

Met Asp Leu Lys Ala Val Arg Ser Asp Asp Thr Ala Ile Tyr Phe Cys
225 230 235 240

Ala Arg Gln Arg Ser Asp Phe Trp Asp Phe Asp Val Trp Gly Ser Gly
245 250 255

Thr Gln Val Thr Val Ser Ser
260

<210> 26
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 26
atgggggac ttgaaccctg cagcaggttc ctgctcctgc ctctcctgct ggctgtaagt 60

ggtctccgtc ctgtccaggt ccaggcccag agcgattgca gttgctctac ggtgagcccg 120

ggcgtgctgg cagggatcgt gatgggagac ctggtgctga cagtgctcat tgccctggcc 180

gtgtacttcc tgggccggct ggtccctcgg gggcgagggg ctgcggaggc agcgacccgg 240

aaacagcgta tcactgagac cgagtcgcct tatcaggagc tccagggtca gaggtcggat 300

gtctacagcg acctcaacac acagaggccg tattacaaag tcgagggcgg cggagagggc 360

agaggaagtc ttctaacatg cggtgacgtg gaggagaatc ccggccctag gatggctctg 420

cctgtgacag ctctgctgct gcctctggcc ctgctgctgc atgctgccag acctggatcc 480

gagatcgtgc tgacacagag ccctggcacc ctgagcctgt ctccaggcga gacagccatc 540

atcagctgcc ggacaagcca gtacggcagc ctggcctggt atcagcagag gcctggacag 600

gcccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc 660

agcggctcta gatggggccc tgactacaac ctgaccatca gcaacctgga aagcggcgac 720

ttcggcgtgt actactgcca gcagtacgag ttcttcggcc agggcaccaa ggtgcaggtg 780

gacatcaaga gaggtggttc ctctagatct tcctcctctg gtggcggtgg ctcgggcggt 840

ggtgggcagg tgcagctggt gcagtctggc ggccagatga agaaacccgg cgagagcatg 900

cggatcagct gcagagcctc cggctacgag ttcatcgacg ccaccctgaa ctggattcgg 960

ctggcccctg gcaaaagacc cgagtggatg ggctggctga agcccagagg cggagccgtg 1020

aattacgcca gacctctgca gggcagagtg accatgaccc gggacgtgta cagcgatacc 1080

gccttcctgg aactgcggag cctgaccgtg gatgataccg ccgtgtactt ctgcacccgg 1140

ggcaagaaca gcgactacaa ctgggacttc gagcactggg gcagaggcac ccctgtgatc 1200

gtgtctagcg ctagcggcgg agggggatct ggaggtgggg gttcctcacc cactgaacca 1260

agctccaaaa ccggtaaccc cagacacctg catgttctga ttgggacctc agtggtcaaa 1320

atccctttca ccatcctcct cttctttctc cttcatcgct ggtgctccaa caaaaaaaat 1380

gctgctgtaa tggaccaaga gcctgcaggg aacagaacag tgaacagcga ggattctgat 1440

gaacaagacc atcaggaggt gtcatacgca taa 1473

<210> 27
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 27

Met Gly Gly Leu Glu Pro Cys Ser Arg Phe Leu Leu Leu Pro Leu Leu
1 5 10 15

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Val Gln Ala Gln Ser Asp
20 25 30

```
Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
        35                  40                  45

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
    50                  55                  60

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg
65                  70                  75                  80

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

Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr
            100                 105                 110

Lys Val Glu Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
        115                 120                 125

Asp Val Glu Glu Asn Pro Gly Pro Arg Met Ala Leu Pro Val Thr Ala
    130                 135                 140

Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Gly Ser
145                 150                 155                 160

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
                165                 170                 175

Glu Thr Ala Ile Ile Ser Cys Arg Thr Ser Gln Tyr Gly Ser Leu Ala
            180                 185                 190

Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Val Ile Tyr Ser
        195                 200                 205

Gly Ser Thr Arg Ala Ala Gly Ile Pro Asp Arg Phe Ser Gly Ser Arg
    210                 215                 220
```

```
Trp Gly Pro Asp Tyr Asn Leu Thr Ile Ser Asn Leu Glu Ser Gly Asp
225                 230                 235                 240


Phe Gly Val Tyr Tyr Cys Gln Gln Tyr Glu Phe Phe Gly Gln Gly Thr
                245                 250                 255


Lys Val Gln Val Asp Ile Lys Arg Gly Gly Ser Ser Arg Ser Ser Ser
            260                 265                 270


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln
        275                 280                 285


Ser Gly Gly Gln Met Lys Lys Pro Gly Glu Ser Met Arg Ile Ser Cys
    290                 295                 300


Arg Ala Ser Gly Tyr Glu Phe Ile Asp Ala Thr Leu Asn Trp Ile Arg
305                 310                 315                 320


Leu Ala Pro Gly Lys Arg Pro Glu Trp Met Gly Trp Leu Lys Pro Arg
                325                 330                 335


Gly Gly Ala Val Asn Tyr Ala Arg Pro Leu Gln Gly Arg Val Thr Met
            340                 345                 350


Thr Arg Asp Val Tyr Ser Asp Thr Ala Phe Leu Glu Leu Arg Ser Leu
        355                 360                 365


Thr Val Asp Asp Thr Ala Val Tyr Phe Cys Thr Arg Gly Lys Asn Ser
    370                 375                 380


Asp Tyr Asn Trp Asp Phe Glu His Trp Gly Arg Gly Thr Pro Val Ile
385                 390                 395                 400


Val Ser Ser Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
                405                 410                 415
```

```
Pro Thr Glu Pro Ser Ser Lys Thr Gly Asn Pro Arg His Leu His Val
            420                 425                 430


Leu Ile Gly Thr Ser Val Val Lys Ile Pro Phe Thr Ile Leu Leu Phe
        435                 440                 445


Phe Leu Leu His Arg Trp Cys Ser Asn Lys Lys Asn Ala Ala Val Met
    450                 455                 460


Asp Gln Glu Pro Ala Gly Asn Arg Thr Val Asn Ser Glu Asp Ser Asp
465                 470                 475                 480


Glu Gln Asp His Gln Glu Val Ser Tyr Ala Glx
                485                 490


<210>  28
<211>  729
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificially Synthesized

<400>  28
gagatcgtgc tgacacagag ccctggcacc ctgagcctgt ctccaggcga gacagccatc       60

atcagctgcc ggacaagcca gtacggcagc ctggcctggt atcagcagag gcctggacag      120

gcccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc      180

agcggctcta gatggggccc tgactacaac ctgaccatca gcaacctgga aagcggcgac      240

ttcggcgtgt actactgcca gcagtacgag ttcttcggcc agggcaccaa ggtgcaggtg      300

gacatcaaga gaggcggcag ctccagaagc tccagctctg gcggcggagg atctggcgga      360

ggcggacagg tgcagctggt gcagtctggc ggccagatga agaaacccgg cgagagcatg      420

cggatcagct gcagagcctc cggctacgag ttcatcgaca gcaccctgaa ctggattcgg      480

ctggcccctg gcaaaagacc cgagtggatg ggctggctga agcccagagg cggagccgtg      540
```

aattacgcca gacctctgca gggcagagtg accatgaccc gggacgtgta cagcgatacc 600

gccttcctgg aactgcggag cctgaccgtg gatgataccg ccgtgtactt ctgcacccgg 660

ggcaagaacg ccgactacaa ctgggacttc gagcactggg gcagaggcac ccctgtgatc 720

gtgtctagc 729

<210> 29
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 29

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

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

Thr Leu Ser Leu Ser Pro Gly Glu Thr Ala Ile Ile Ser Cys Arg Thr
35 40 45

Ser Gln Tyr Gly Ser Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala
50 55 60

Pro Arg Leu Val Ile Tyr Ser Gly Ser Thr Arg Ala Ala Gly Ile Pro
65 70 75 80

Asp Arg Phe Ser Gly Ser Arg Trp Gly Pro Asp Tyr Asn Leu Thr Ile
85 90 95

Ser Asn Leu Glu Ser Gly Asp Phe Gly Val Tyr Tyr Cys Gln Gln Tyr
100 105 110

Glu Phe Phe Gly Gln Gly Thr Lys Val Gln Val Asp Ile Lys Arg Gly

115 120 125

Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Gln Val Gln Leu Val Gln Ser Gly Gly Gln Met Lys Lys Pro Gly
145 150 155 160

Glu Ser Met Arg Ile Ser Cys Arg Ala Ser Gly Tyr Glu Phe Ile Asp
165 170 175

Ser Thr Leu Asn Trp Ile Arg Leu Ala Pro Gly Lys Arg Pro Glu Trp
180 185 190

Met Gly Trp Leu Lys Pro Arg Gly Gly Ala Val Asn Tyr Ala Arg Pro
195 200 205

Leu Gln Gly Arg Val Thr Met Thr Arg Asp Val Tyr Ser Asp Thr Ala
210 215 220

Phe Leu Glu Leu Arg Ser Leu Thr Val Asp Asp Thr Ala Val Tyr Phe
225 230 235 240

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

Gly Arg Gly Thr Pro Val Ile Val Ser Ser
260 265

<210> 30
<211> 1857
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 30

atggggggac ttgaaccctg cagcaggttc ctgctcctgc ctctcctgct ggctgtaagt 60

ggtctccgtc ctgtccaggt ccaggcccag agcgattgca gttgctctac ggtgagcccg 120

ggcgtgctgg cagggatcgt gatgggagac ctggtgctga cagtgctcat tgccctggcc 180

gtgtacttcc tgggccggct ggtccctcgg gggcgagggg ctgcggaggc agcgacccgg 240

aaacagcgta tcactgagac cgagtcgcct tatcaggagc tccagggtca gaggtcggat 300

gtctacagcg acctcaacac acagaggccg tattacaaag tcgagggcgg cggagagggc 360

agaggaagtc ttctaacatg cggtgacgtg gaggagaatc ccggccctag gatggctctg 420

cctgtgacag ctctgctgct gcctctggcc ctgctgctgc atgctgccag acctggatcc 480

aagaaagtgg tgcttggcaa gaagggcgac accgtggaac tgacctgcac cgccagccag 540

aagaagtcca tccagttcca ctggaagaac agcaaccaga tcaagatcct gggcaaccag 600

ggcagcttcc tgaccaaggg ccccagcaag ctgaacgaca gagccgactc tcggcggagc 660

ctgtgggacc agggcaattt cccactgatc atcaagaacc tgaagatcga ggacagcgac 720

acctacatct gcgaggtgga agatcagaaa gaagaggtgc agctgctggt gttcggcctg 780

accgccaact ccgacaccca tctgctgcag ggccagagcc tgaccctgac actggaaagc 840

cctccaggca gcagcccgag cgtgcagtgt agaagcccca gaggcaagaa catccagggc 900

ggcaagaccc tgagcgtgtc ccagcttgaa ctgcaggata gcggcacctg gacctgtacc 960

gtgctgcaga accagaagaa agtggaattc aagatcgaca tcgtcgtgct cgccttccag 1020

aaagccagct ccatcgtgta caagaaggag ggcgaacagg tggaattttc cttccccctg 1080

gccttcactg tggaaaagct gaccggcagc ggcgagctgt ggtggcaggc tgaaagagcc 1140

agctccagca agtcctggat caccttcgac ctgaagaaca aagaggtgtc cgtgaagaga 1200

gtgacccagg accccaagct gcagatgggc aagaagctgc ccctgcatct gacactgcca 1260

caggcccttc cacagtatgc cggctctggc aatctcactc ttgctcttga agccaagacc 1320

ggcaagctgc accaggaagt gaacctggtc gtgatgcggg ccacccagct gcagaagaat 1380

ctgacctgcg aagtgtgggg ccctaccagc cctaagctga tgctgagcct gaagctggaa 1440

aacaaagaag ccaaggtgtc caagcgcgag aaggccgtgt gggtgctgaa tcctgaggcc 1500

ggcatgtggc agtgtctgct gagcgattct ggccaggtgc tgctcgaaag caacatcaag 1560

gtgctgccca cctggtccac tccagtgcag cctgctagcg gcggaggggg atctggaggt 1620

gggggttcct cacccactga accaagctcc aaaaccggta accccagaca cctgcatgtt 1680

ctgattggga cctcagtggt caaaatccct ttcaccatcc tcctcttctt tctccttcat 1740

cgctggtgct ccaacaaaaa aaatgctgct gtaatggacc aagagcctgc agggaacaga 1800

acagtgaaca gcgaggattc tgatgaacaa gaccatcagg aggtgtcata cgcataa 1857

<210> 31
<211> 619
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 31

Met Gly Gly Leu Glu Pro Cys Ser Arg Phe Leu Leu Leu Pro Leu Leu
1 5 10 15

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Val Gln Ala Gln Ser Asp
20 25 30

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
35 40 45

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
50 55 60

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg
65 70 75 80

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

```
Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr
            100                 105                 110

Lys Val Glu Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
        115                 120                 125

Asp Val Glu Glu Asn Pro Gly Pro Arg Met Ala Leu Pro Val Thr Ala
    130                 135                 140

Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Gly Ser
145                 150                 155                 160

Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys
                165                 170                 175

Thr Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn
            180                 185                 190

Gln Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro
        195                 200                 205

Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln
    210                 215                 220

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

Thr Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu
                245                 250                 255

Val Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln
            260                 265                 270

Ser Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val
        275                 280                 285
```

```
Gln Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu
    290                 295                 300

Ser Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr
305                 310                 315                 320

Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val
                325                 330                 335

Leu Ala Phe Gln Lys Ala Ser Ser Ile Val Tyr Lys Lys Glu Gly Glu
            340                 345                 350

Gln Val Glu Phe Ser Phe Pro Leu Ala Phe Thr Val Glu Lys Leu Thr
        355                 360                 365

Gly Ser Gly Glu Leu Trp Trp Gln Ala Glu Arg Ala Ser Ser Ser Lys
    370                 375                 380

Ser Trp Ile Thr Phe Asp Leu Lys Asn Lys Glu Val Ser Val Lys Arg
385                 390                 395                 400

Val Thr Gln Asp Pro Lys Leu Gln Met Gly Lys Lys Leu Pro Leu His
                405                 410                 415

Leu Thr Leu Pro Gln Ala Leu Pro Gln Tyr Ala Gly Ser Gly Asn Leu
            420                 425                 430

Thr Leu Ala Leu Glu Ala Lys Thr Gly Lys Leu His Gln Glu Val Asn
        435                 440                 445

Leu Val Val Met Arg Ala Thr Gln Leu Gln Lys Asn Leu Thr Cys Glu
    450                 455                 460

Val Trp Gly Pro Thr Ser Pro Lys Leu Met Leu Ser Leu Lys Leu Glu
465                 470                 475                 480
```

```
Asn Lys Glu Ala Lys Val Ser Lys Arg Glu Lys Ala Val Trp Val Leu
                485                 490                 495

Asn Pro Glu Ala Gly Met Trp Gln Cys Leu Leu Ser Asp Ser Gly Gln
            500                 505                 510

Val Leu Leu Glu Ser Asn Ile Lys Val Leu Pro Thr Trp Ser Thr Pro
        515                 520                 525

Val Gln Pro Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
    530                 535                 540

Pro Thr Glu Pro Ser Ser Lys Thr Gly Asn Pro Arg His Leu His Val
545                 550                 555                 560

Leu Ile Gly Thr Ser Val Val Lys Ile Pro Phe Thr Ile Leu Leu Phe
                565                 570                 575

Phe Leu Leu His Arg Trp Cys Ser Asn Lys Lys Asn Ala Ala Val Met
            580                 585                 590

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

Glu Gln Asp His Gln Glu Val Ser Tyr Ala Glx
    610                 615
```

<210> 32
<211> 1857
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 32
atgggggac ttgaaccctg cagcaggttc ctgctcctgc ctctcctgct ggctgtaagt 60

ggtctccgtc ctgtccaggt ccaggcccag agcgattgca gttgctctac ggtgagcccg 120

ggcgtgctgg cagggatcgt gatgggagac ctggtgctga cagtgctcat tgccctggcc 180

gtgtacttcc tgggccggct ggtccctcgg gggcgagggg ctgcggaggc agcgacccgg 240

aaacagcgta tcactgagac cgagtcgcct tatcaggagc tccagggtca gaggtcggat 300

gtctacagcg acctcaacac acagaggccg tattacaaag tcgagggcgg cggagagggc 360

agaggaagtc ttctaacatg cggtgacgtg gaggagaatc ccggccctag gatggctctg 420

cctgtgacag ctctgctgct gcctctggcc ctgctgctgc atgctgccag acctggatcc 480

aagaaagtgg tgcttggcaa gaagggcgac accgtggaac tgacctgcac cgccagccag 540

aagaagtcca tccagttcca ctggaagaac agcaaccaga tcaagatcct gggcaaccag 600

ggcagcttcc tgaccaaggg ccccagcaag ctgaacgaca gagccgactc tcggcggagc 660

ctgtgggacc agggcaattt cccactgatc atcaagaacc tgaagatcga ggacagcgac 720

acctacatct gcgaggtgga agatcagaaa gaagaggtgc agctgctggt gttcggcctg 780

accgccaact ccgacaccca tctgctgcag ggccagagcc tgaccctgac actggaaagc 840

cctccaggca gcagcccgag cgtgcagtgt agaagcccca gaggcaagaa catccagggc 900

ggcaagaccc tgagcgtgtc ccagcttgaa ctgcaggata gcggcacctg gacctgtacc 960

gtgctgcaga accagaagaa agtggaattc aagatcgaca tcgtcgtgct cgccttccag 1020

aaagccagct ccatcgtgta caagaaggag ggcgaacagg tggaattttc cttccccctg 1080

gccttcactg tggaaaagct gaccggcagc ggcgagctgt ggtggcaggc tgaaagagcc 1140

agctccagca agtcctggat caccttcgac ctgaagaaca aagaggtgtc cgtgaagaga 1200

gtgacccagg accccaagct gcagatgggc aagaagctgc ccctgcatct gacactgcca 1260

caggcccttc cacagtatgc cggctctggc aatctcactc ttgctcttga agccaagacc 1320

ggcaagctgc accaggaagt gaacctggtc gtgatgcggg ccacccagct gcagaagaat 1380

ctgacctgcg aagtgtgggg ccctaccagc cctaagctga tgctgagcct gaagctggaa 1440

aacaaagaag ccaaggtgtc caagcgcgag aaggccgtgt gggtgctgaa tcctgaggcc 1500

ggcatgtggc agtgtctgct gagcgattct ggccaggtgc tgctcgaaag caacatcaag 1560

gtgctgccca cctggtccac tccagtgcag cctgctagcg gcggaggggg atctggaggt 1620

gggggttcct cacccactga accaagctcc aaaaccggta accccagaca cctgcatgtt 1680

ctgattggga cctcagtggt caaaatccct ttcaccatcc tcctcttctt tctccttcat 1740

cgctggtgct ccaacaaaaa aaatgctgct gtaatggacc aagagcctgc agggaacaga 1800

acagtgaaca gcgaggattc tgatgaacaa gaccatcagg aggtgtcata cgcataa 1857

<210> 33
<211> 619
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 33

Met Gly Gly Leu Glu Pro Cys Ser Arg Phe Leu Leu Leu Pro Leu Leu
1 5 10 15

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Val Gln Ala Gln Ser Asp
20 25 30

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
35 40 45

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
50 55 60

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg
65 70 75 80

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

Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr

```
            100                 105                 110

Lys Val Glu Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
        115                 120                 125

Asp Val Glu Glu Asn Pro Gly Pro Arg Met Ala Leu Pro Val Thr Ala
    130                 135                 140

Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Gly Ser
145                 150                 155                 160

Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys
                165                 170                 175

Thr Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn
            180                 185                 190

Gln Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro
        195                 200                 205

Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln
    210                 215                 220

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

Thr Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu
                245                 250                 255

Val Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln
            260                 265                 270

Ser Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val
        275                 280                 285

Gln Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu
```

```
    290                 295                 300

Ser Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr
305                 310                 315                 320

Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val
                325                 330                 335

Leu Ala Phe Gln Lys Ala Ser Ser Ile Val Tyr Lys Lys Glu Gly Glu
            340                 345                 350

Gln Val Glu Phe Ser Phe Pro Leu Ala Phe Thr Val Glu Lys Leu Thr
        355                 360                 365

Gly Ser Gly Glu Leu Trp Trp Gln Ala Glu Arg Ala Ser Ser Ser Lys
    370                 375                 380

Ser Trp Ile Thr Phe Asp Leu Lys Asn Lys Glu Val Ser Val Lys Arg
385                 390                 395                 400

Val Thr Gln Asp Pro Lys Leu Gln Met Gly Lys Lys Leu Pro Leu His
                405                 410                 415

Leu Thr Leu Pro Gln Ala Leu Pro Gln Tyr Ala Gly Ser Gly Asn Leu
            420                 425                 430

Thr Leu Ala Leu Glu Ala Lys Thr Gly Lys Leu His Gln Glu Val Asn
        435                 440                 445

Leu Val Val Met Arg Ala Thr Gln Leu Gln Lys Asn Leu Thr Cys Glu
    450                 455                 460

Val Trp Gly Pro Thr Ser Pro Lys Leu Met Leu Ser Leu Lys Leu Glu
465                 470                 475                 480

Asn Lys Glu Ala Lys Val Ser Lys Arg Glu Lys Ala Val Trp Val Leu
```

485 490 495

Asn Pro Glu Ala Gly Met Trp Gln Cys Leu Leu Ser Asp Ser Gly Gln
500 505 510

Val Leu Leu Glu Ser Asn Ile Lys Val Leu Pro Thr Trp Ser Thr Pro
515 520 525

Val Gln Pro Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
530 535 540

Pro Thr Glu Pro Ser Ser Lys Thr Gly Asn Pro Arg His Leu His Val
545 550 555 560

Leu Ile Gly Thr Ser Val Val Lys Ile Pro Phe Thr Ile Leu Leu Phe
565 570 575

Phe Leu Leu His Arg Trp Cys Ser Asn Lys Lys Asn Ala Ala Val Met
580 585 590

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

Glu Gln Asp His Gln Glu Val Ser Tyr Ala Glx
610 615

<210> 34
<211> 1923
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 34
atggctctgc ctgtgacagc tctgctgctg cctctggccc tgctgctgca tgctgccaga 60

cctggatccg agatcgtgct gacacagagc cctggcaccc tgagcctgtc tccaggcgag 120

acagccatca tcagctgccg gacaagccag tacggcagcc tggcctggta tcagcagagg 180

cctggacagg cccccagact cgtgatctac agcggcagca caagagccgc cggaatcccc 240

gatagattca gcggctctag atggggccct gactacaacc tgaccatcag caacctggaa 300

agcggcgact tcggcgtgta ctactgccag cagtacgagt tcttcggcca gggcaccaag 360

gtgcaggtgg acatcaagag aggcggcagc tccagaagct ccagctctgg cggcggagga 420

tctggcggag gcggacaggt gcagctggtg cagtctggcg gccagatgaa gaaacccggc 480

gagagcatgc ggatcagctg cagagcctcc ggctacgagt tcatcgactg caccctgaac 540

tggattcggc tggcccctgg caaaagaccc gagtggatgg gctggctgaa gcccagaggc 600

ggagccgtga attacgccag acctctgcag ggcagagtga ccatgacccg ggacgtgtac 660

agcgataccg ccttcctgga actgcggagc ctgaccgtgg atgataccgc cgtgtacttc 720

tgcacccggg gcaagaactg cgactacaac tgggacttcg agcactgggg cagaggcacc 780

cctgtgatcg tgtctagcgc tagcgagagc aagtacggcc ctccctgccc cccttgccct 840

gcccccgagt tcctgggcgg acccagcgtg ttcctgttcc cccccaagcc caaggacacc 900

ctgatgatca gccggacccc cgaggtgacc tgtgtggtgg tggacgtgtc ccaggaggac 960

cccgaggtcc agttcaactg gtacgtggac ggcgtggagg tgcacaacgc caagaccaag 1020

ccccgggagg agcagttcaa tagcacctac cgggtggtgt ccgtgctgac cgtgctgcac 1080

caggactggc tgaacggcaa ggaatacaag tgtaaggtgt ccaacaaggg cctgcccagc 1140

agcatcgaga aaaccatcag caaggccaag ggccagcctc gggagcccca ggtgtacacc 1200

ctgccccta gccaagagga gatgaccaag aaccaggtgt ccctgacctg cctggtgaag 1260

ggcttctacc ccagcgacat cgccgtggag tgggagagca acggccagcc cgagaacaac 1320

tacaagacca ccccccctgt gctggacagc gacggcagct tcttcctgta cagccggctg 1380

accgtggaca agagccggtg gcaggagggc aacgtcttta gctgctccgt gatgcacgag 1440

gccctgcaca accactacac ccagaagagc ctgagcctgt ccctgggcaa gatgtccgga 1500

atctacatct gggcgccctt ggccgggact tgtggggtcc ttctcctgtc actggttatc 1560

acccttttact gcaaacgggg cagaaagaaa ctcctgtata tattcaaaca accatttatg 1620

agaccagtac aaactactca agaggaagat ggctgtagct gccgatttcc agaagaagaa 1680

gaaggaggat gtgaactgcg tggccgggac cctgagatgg ggggaaagcc gagaaggaag 1740

aaccctcagg aaggcctgta caatgaactg cagaaagata agatggcgga ggcctacagt 1800

gagattggga tgaaaggcga gcgccggagg ggcaaggggc acgatggcct ttaccagggt 1860

ctcagtacag ccaccaagga cacctacgac gcccttcaca tgcaggccct gccccctcgc 1920

taa 1923

<210> 35
<211> 679
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 35

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

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

Thr Leu Ser Leu Ser Pro Gly Glu Thr Ala Ile Ile Ser Cys Arg Thr
35 40 45

Ser Gln Tyr Gly Ser Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala
50 55 60

Pro Arg Leu Val Ile Tyr Ser Gly Ser Thr Arg Ala Ala Gly Ile Pro
65 70 75 80

Asp Arg Phe Ser Gly Ser Arg Trp Gly Pro Asp Tyr Asn Leu Thr Ile
85 90 95

```
Ser Asn Leu Glu Ser Gly Asp Phe Gly Val Tyr Tyr Cys Gln Gln Tyr
            100                 105                 110


Glu Phe Phe Gly Gln Gly Thr Lys Val Gln Val Asp Ile Lys Arg Gly
        115                 120                 125


Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140


Gly Gln Val Gln Leu Val Gln Ser Gly Gly Gln Met Lys Lys Pro Gly
145                 150                 155                 160


Glu Ser Met Arg Ile Ser Cys Arg Ala Ser Gly Tyr Glu Phe Ile Asp
                165                 170                 175


Cys Thr Leu Asn Trp Ile Arg Leu Ala Pro Gly Lys Arg Pro Glu Trp
            180                 185                 190


Met Gly Trp Leu Lys Pro Arg Gly Gly Ala Val Asn Tyr Ala Arg Pro
        195                 200                 205


Leu Gln Gly Arg Val Thr Met Thr Arg Asp Val Tyr Ser Asp Thr Ala
    210                 215                 220


Phe Leu Glu Leu Arg Ser Leu Thr Val Asp Asp Thr Ala Val Tyr Phe
225                 230                 235                 240


Cys Thr Arg Gly Lys Asn Cys Asp Tyr Asn Trp Asp Phe Glu His Trp
                245                 250                 255


Gly Arg Gly Thr Pro Val Ile Val Ser Ser Ala Ser Glu Ser Lys Tyr
            260                 265                 270


Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
        275                 280                 285
```

```
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
    290                 295                 300

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
305                 310                 315                 320

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                325                 330                 335

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
            340                 345                 350

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
        355                 360                 365

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
    370                 375                 380

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
385                 390                 395                 400

Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
                405                 410                 415

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
            420                 425                 430

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
        435                 440                 445

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
    450                 455                 460

Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
465                 470                 475                 480
```

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

Lys Met Ser Gly Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
            500                 505                 510

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
        515                 520                 525

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
    530                 535                 540

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
545                 550                 555                 560

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
                565                 570                 575

Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
            580                 585                 590

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
        595                 600                 605

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
    610                 615                 620

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

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
                645                 650                 655

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
            660                 665                 670
```

Gln Ala Leu Pro Pro Arg Glx
675

<210> 36
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 36

Thr Thr Ala Ala Thr Gly Gly Gly Ala Thr Cys Cys Ala Thr Gly Ala
1 5 10 15

Ala Cys Cys Gly Gly Gly Gly Ala Gly Thr Cys Cys Cys Thr Thr Thr
20 25 30

<210> 37
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 37
aaggacttcc ggatggctgc accggggtgg accatg 36

<210> 38
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 38
gggacactcc ggaaccacga cgccagcgcc gcg 33

<210> 39

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 39
gggacacgtc gacttagcga gggggca 27

<210> 40
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 40
gtatcgatca cgagactagc 20

<210> 41
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 41
ttaaaccggt gtctggcctt tgagtggtga 30

<210> 42
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 42

Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe
1 5 10

<210> 43
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 43

Gly Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly Ser Gly Gly
1 5 10 15

Gly Gly

<210> 44
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 44

Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
1 5 10 15

Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
20 25 30

Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
35 40 45

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

Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
65 70 75 80

```
Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
                85                  90                  95

Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
            100                 105                 110

Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
        115                 120                 125

Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
    130                 135                 140

Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
145                 150                 155                 160

Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
                165                 170                 175

Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
            180                 185                 190

Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
        195                 200                 205

Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro
    210                 215                 220

Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
225                 230                 235                 240

Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
                245                 250                 255

Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
            260                 265                 270
```

```
Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
        275                 280                 285

Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
    290                 295                 300

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

Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
                325                 330                 335

Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
            340                 345                 350

Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
        355                 360                 365

Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
    370                 375                 380

Lys Val Leu Pro Thr Trp Ser Thr Pro Val Gln Pro Ser Gly Thr Thr
385                 390                 395                 400

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
                405                 410                 415

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
            420                 425                 430

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val
        435                 440                 445

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
    450                 455                 460
```

```
Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
465                 470                 475                 480


Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
                485                 490                 495


Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Ile
            500                 505                 510


Asp Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
        515                 520                 525


Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
    530                 535                 540


Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
545                 550                 555                 560


Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
                565                 570                 575


Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
            580                 585                 590


Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
        595                 600                 605


Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
    610                 615                 620


Arg
625


<210>  45
<211>  621
<212>  PRT
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<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 45

```
Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
1               5                  10                  15


Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
            20                  25                  30


Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
        35                  40                  45


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


Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
65                  70                  75                  80


Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
                85                  90                  95


Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
            100                 105                 110


Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
        115                 120                 125


Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
    130                 135                 140


Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
145                 150                 155                 160


Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
```

```
                165                 170                 175

Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
            180                 185                 190

Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
        195                 200                 205

Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro
    210                 215                 220

Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
225                 230                 235                 240

Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
                245                 250                 255

Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
            260                 265                 270

Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
        275                 280                 285

Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
    290                 295                 300

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

Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
                325                 330                 335

Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
            340                 345                 350

Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
```

```
        355                 360                 365

Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
    370                 375                 380

Lys Val Leu Pro Thr Trp Ser Thr Pro Val Gln Pro Ser Gly Thr Thr
385                 390                 395                 400

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
                405                 410                 415

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
            420                 425                 430

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
        435                 440                 445

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
    450                 455                 460

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
465                 470                 475                 480

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
                485                 490                 495

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
            500                 505                 510

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
        515                 520                 525

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
    530                 535                 540

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
```

545 550 555 560

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
565 570 575

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
580 585 590

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
595 600 605

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
610 615 620

<210> 46
<211> 396
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 46

Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
1 5 10 15

Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
20 25 30

Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
35 40 45

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

Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
65 70 75 80

```
Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
                85                  90                  95

Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
            100                 105                 110

Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
        115                 120                 125

Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
    130                 135                 140

Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
145                 150                 155                 160

Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
                165                 170                 175

Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
            180                 185                 190

Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
        195                 200                 205

Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro
    210                 215                 220

Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
225                 230                 235                 240

Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
                245                 250                 255

Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
            260                 265                 270
```

```
Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
        275                 280                 285


Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
    290                 295                 300


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


Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
                325                 330                 335


Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
            340                 345                 350


Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
        355                 360                 365


Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
    370                 375                 380


Lys Val Leu Pro Thr Trp Ser Thr Pro Val Gln Pro
385                 390                 395


<210>  47
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Artificially Synthesized

<400>  47

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1               5                   10                  15


Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
```

20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 48
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 48

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr Leu Tyr Cys
20

<210> 49
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 49

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
20 25 30

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
35 40 45

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala

50 55 60

Ala Tyr Arg Ser
65

<210> 50
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 50

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 51
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 51

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys

35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

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

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 52
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 52

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

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Gln Gly
20 25 30

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

Phe Ile Lys Tyr Asp Gly Ser Glu Lys Tyr His Ala Asp Ser Val Trp
50 55 60

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

```
Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Thr Tyr Phe Cys Val
                85                  90                  95


Arg Glu Ala Gly Gly Pro Asp Tyr Arg Asn Gly Tyr Asn Tyr Tyr Asp
            100                 105                 110


Phe Tyr Asp Gly Tyr Tyr Asn Tyr His Tyr Met Asp Val Trp Gly Lys
        115                 120                 125


Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140


Gly Ser Gly Gly Gly Gly Ser Gln Ser Ala Leu Thr Gln Pro Ala Ser
145                 150                 155                 160


Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Asn Gly Thr
                165                 170                 175


Ser Asn Asp Val Gly Gly Tyr Glu Ser Val Ser Trp Tyr Gln Gln His
            180                 185                 190


Pro Gly Lys Ala Pro Lys Val Val Ile Tyr Asp Val Ser Lys Arg Pro
        195                 200                 205


Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala
    210                 215                 220


Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Gly Asp Tyr Tyr
225                 230                 235                 240


Cys Lys Ser Leu Thr Ser Thr Arg Arg Arg Val Phe Gly Thr Gly Thr
                245                 250                 255


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

```
Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
        275                 280                 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
    290                 295                 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305                 310                 315                 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Val Lys Phe
                325                 330                 335

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
            340                 345                 350

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
        355                 360                 365

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
    370                 375                 380

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

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
                405                 410                 415

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
            420                 425                 430

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
        435                 440
```

<210> 53
<211> 442
<212> PRT

<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 53

```
Gln Ser Ala Leu Thr Gln Pro Pro Ser Ala Ser Gly Ser Pro Gly Gln
1               5                  10                  15


Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Asn Asn Phe Val Ser Trp
            20                  25                  30


Tyr Gln Gln His Ala Gly Lys Ala Pro Lys Leu Val Ile Tyr Asp Val
        35                  40                  45


Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser
    50                  55                  60


Gly Asn Thr Ala Ser Leu Thr Val Ser Gly Leu Gln Thr Asp Asp Glu
65                  70                  75                  80


Ala Val Tyr Tyr Cys Gly Ser Leu Val Gly Asn Trp Asp Val Ile Phe
                85                  90                  95


Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Ser Ser Arg Ser Ser
            100                 105                 110


Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gln Pro Gln Leu Gln
        115                 120                 125


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


Cys Ala Val Ser Gly Asp Ser Thr Ala Ala Cys Asn Ser Phe Trp Gly
145                 150                 155                 160


Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Val Gly Ser Leu
```

165 170 175

Ser His Cys Ala Ser Tyr Trp Asn Arg Gly Trp Thr Tyr His Asn Pro
180 185 190

Ser Leu Lys Ser Arg Leu Thr Leu Ala Leu Asp Thr Pro Lys Asn Leu
195 200 205

Val Phe Leu Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr
210 215 220

Tyr Cys Ala Arg Phe Gly Gly Glu Val Leu Arg Tyr Thr Asp Trp Pro
225 230 235 240

Lys Pro Ala Trp Val Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val
245 250 255

Ser Ser Ser Gly Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
260 265 270

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
275 280 285

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
290 295 300

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
305 310 315 320

Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Val Lys Phe Ser Arg Ser
325 330 335

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
340 345 350

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg

355 360 365

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
370 375 380

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
385 390 395 400

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
405 410 415

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
420 425 430

Leu His Met Gln Ala Leu Pro Pro Arg Arg
435 440

<210> 54
<211> 426
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 54

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

Glu Thr Ala Ile Ile Ser Cys Arg Thr Ser Gln Tyr Gly Ser Leu Ala
20 25 30

Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Val Ile Tyr Ser
35 40 45

Gly Ser Thr Arg Ala Ala Gly Ile Pro Asp Arg Phe Ser Gly Ser Arg
50 55 60

```
Trp Gly Pro Asp Tyr Asn Leu Thr Ile Ser Asn Leu Glu Ser Gly Asp
65                  70                  75                  80

Phe Gly Val Tyr Tyr Cys Gln Gln Tyr Glu Phe Phe Gly Gln Gly Thr
                85                  90                  95

Lys Val Gln Val Asp Ile Lys Arg Gly Gly Ser Ser Arg Ser Ser Ser
            100                 105                 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln
        115                 120                 125

Ser Gly Gly Gln Met Lys Lys Pro Gly Glu Ser Met Arg Ile Ser Cys
    130                 135                 140

Arg Ala Ser Gly Tyr Glu Phe Ile Asp Cys Thr Leu Asn Trp Ile Arg
145                 150                 155                 160

Leu Ala Pro Gly Lys Arg Pro Glu Trp Met Gly Trp Leu Lys Pro Arg
                165                 170                 175

Gly Gly Ala Val Asn Tyr Ala Arg Pro Leu Gln Gly Arg Val Thr Met
            180                 185                 190

Thr Arg Asp Val Tyr Ser Asp Thr Ala Phe Leu Glu Leu Arg Ser Leu
        195                 200                 205

Thr Val Asp Asp Thr Ala Val Tyr Phe Cys Thr Arg Gly Lys Asn Cys
    210                 215                 220

Asp Tyr Asn Trp Asp Phe Glu His Trp Gly Arg Gly Thr Pro Val Ile
225                 230                 235                 240

Val Ser Ser Ser Gly Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255
```

```
Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
            260                 265                 270


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


Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
    290                 295                 300


Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Val Lys Phe Ser Arg
305                 310                 315                 320


Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
                325                 330                 335


Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
            340                 345                 350


Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
        355                 360                 365


Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
    370                 375                 380


Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
385                 390                 395                 400


Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
                405                 410                 415


Ala Leu His Met Gln Ala Leu Pro Pro Arg
            420                 425


<210>  55
<211>  423
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 55

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


Asp Thr Val Thr Ile Thr Cys Gln Ala Asn Gly Tyr Leu Asn Trp Tyr
            20                  25                  30


Gln Gln Arg Arg Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Gly Ser
        35                  40                  45


Lys Leu Glu Arg Gly Val Pro Ala Arg Phe Ser Gly Arg Arg Trp Gly
    50                  55                  60


Gln Glu Tyr Asn Leu Thr Ile Asn Asn Leu Gln Pro Glu Asp Val Ala
65                  70                  75                  80


Thr Tyr Phe Cys Gln Val Tyr Glu Phe Ile Val Pro Gly Thr Arg Leu
                85                  90                  95


Asp Leu Lys Gly Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly
            100                 105                 110


Ser Gly Gly Gly Gly Gln Val His Leu Ser Gln Ser Gly Ala Ala Val
        115                 120                 125


Thr Lys Pro Gly Ala Ser Val Arg Val Ser Cys Glu Ala Ser Gly Tyr
    130                 135                 140


Lys Ile Ser Asp His Phe Ile His Trp Trp Arg Gln Ala Pro Gly Gln
145                 150                 155                 160


Gly Leu Gln Trp Val Gly Trp Ile Asn Pro Lys Thr Gly Gln Pro Asn
```

```
                165                 170                 175

Asn Pro Arg Gln Phe Gln Gly Arg Val Ser Leu Thr Arg Gln Ala Ser
            180                 185                 190

Trp Asp Phe Asp Thr Tyr Ser Phe Tyr Met Asp Leu Lys Ala Val Arg
        195                 200                 205

Ser Asp Asp Thr Ala Ile Tyr Phe Cys Ala Arg Gln Arg Ser Asp Phe
    210                 215                 220

Trp Asp Phe Asp Val Trp Gly Ser Gly Thr Gln Val Thr Val Ser Ser
225                 230                 235                 240

Ser Gly Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
        275                 280                 285

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
    290                 295                 300

Leu Val Ile Thr Leu Tyr Cys Arg Val Lys Phe Ser Arg Ser Ala Asp
305                 310                 315                 320

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                325                 330                 335

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            340                 345                 350

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
```

355 360 365

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
370 375 380

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
385 390 395 400

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
405 410 415

Met Gln Ala Leu Pro Pro Arg
420

<210> 56
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 56

Asp Phe Val Leu Thr Gln Ser Pro His Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Glu Ser Ala Ser Ile Ser Cys Lys Ser Ser His Ser Leu Ile His Gly
20 25 30

Asp Arg Asn Asn Tyr Leu Ala Trp Tyr Val Gln Lys Pro Gly Arg Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Ala Ser Ser Arg Ala Ser Gly Val Pro
50 55 60

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

```
Ser Arg Val Glu Thr Glu Asp Val Gly Thr Tyr Tyr Cys Met Gln Gly
                85                  90                  95

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

Gly Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Gln Ala Gln Leu Val Gln Ser Gly Pro Glu Val Arg Lys Pro
    130                 135                 140

Gly Thr Ser Val Lys Val Ser Cys Lys Ala Pro Gly Asn Thr Leu Lys
145                 150                 155                 160

Thr Tyr Asp Leu His Trp Val Arg Ser Val Pro Gly Gln Gly Leu Gln
                165                 170                 175

Trp Met Gly Trp Ile Ser His Glu Gly Asp Lys Lys Val Ile Val Glu
            180                 185                 190

Arg Phe Lys Ala Lys Val Thr Ile Asp Trp Asp Arg Ser Thr Asn Thr
        195                 200                 205

Ala Tyr Leu Gln Leu Ser Gly Leu Thr Ser Gly Asp Thr Ala Val Tyr
    210                 215                 220

Tyr Cys Ala Lys Gly Ser Lys His Arg Leu Arg Asp Tyr Ala Leu Tyr
225                 230                 235                 240

Asp Asp Asp Gly Ala Leu Asn Trp Ala Val Asp Val Asp Tyr Leu Ser
                245                 250                 255

Asn Leu Glu Phe Trp Gly Gln Gly Thr Ala Val Thr Val Ser Ser Ser
            260                 265                 270
```

```
Gly Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
        275                 280                 285


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


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


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


Val Ile Thr Leu Tyr Cys Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
            340                 345                 350


Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
        355                 360                 365


Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
    370                 375                 380


Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
385                 390                 395                 400


Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
                405                 410                 415


Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
            420                 425                 430


Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
        435                 440                 445


Gln Ala Leu Pro Pro Arg
    450
```

<210> 57
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 57

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


Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Gln Gly
            20                  25                  30


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


Phe Ile Lys Tyr Asp Gly Ser Glu Lys Tyr His Ala Asp Ser Val Trp
    50                  55                  60


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


Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Thr Tyr Phe Cys Val
                85                  90                  95


Arg Glu Ala Gly Gly Pro Asp Tyr Arg Asn Gly Tyr Asn Tyr Tyr Asp
            100                 105                 110


Phe Tyr Asp Gly Tyr Tyr Asn Tyr His Tyr Met Asp Val Trp Gly Lys
        115                 120                 125


Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140


Gly Ser Gly Gly Gly Gly Ser Gln Ser Ala Leu Thr Gln Pro Ala Ser
```

```
145                 150                 155                 160

Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Asn Gly Thr
                165                 170                 175

Ser Asn Asp Val Gly Gly Tyr Glu Ser Val Ser Trp Tyr Gln Gln His
            180                 185                 190

Pro Gly Lys Ala Pro Lys Val Val Ile Tyr Asp Val Ser Lys Arg Pro
        195                 200                 205

Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala
    210                 215                 220

Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Gly Asp Tyr Tyr
225                 230                 235                 240

Cys Lys Ser Leu Thr Ser Thr Arg Arg Arg Val Phe Gly Thr Gly Thr
                245                 250                 255

Lys Leu Thr Val Leu
            260
```

<210> 58
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 58

```
Gln Ser Ala Leu Thr Gln Pro Pro Ser Ala Ser Gly Ser Pro Gly Gln
1               5                   10                  15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Asn Asn Phe Val Ser Trp
            20                  25                  30
```

```
Tyr Gln Gln His Ala Gly Lys Ala Pro Lys Leu Val Ile Tyr Asp Val
        35                  40                  45

Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser
    50                  55                  60

Gly Asn Thr Ala Ser Leu Thr Val Ser Gly Leu Gln Thr Asp Asp Glu
65                  70                  75                  80

Ala Val Tyr Tyr Cys Gly Ser Leu Val Gly Asn Trp Asp Val Ile Phe
                85                  90                  95

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Ser Ser Arg Ser Ser
            100                 105                 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gln Pro Gln Leu Gln
        115                 120                 125

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

Cys Ala Val Ser Gly Asp Ser Thr Ala Ala Cys Asn Ser Phe Trp Gly
145                 150                 155                 160

Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Val Gly Ser Leu
                165                 170                 175

Ser His Cys Ala Ser Tyr Trp Asn Arg Gly Trp Thr Tyr His Asn Pro
            180                 185                 190

Ser Leu Lys Ser Arg Leu Thr Leu Ala Leu Asp Thr Pro Lys Asn Leu
        195                 200                 205

Val Phe Leu Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr
    210                 215                 220
```

Tyr Cys Ala Arg Phe Gly Gly Glu Val Leu Arg Tyr Thr Asp Trp Pro
225 230 235 240

Lys Pro Ala Trp Val Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val
245 250 255

Ser Ser

<210> 59
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 59

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

Glu Thr Ala Ile Ile Ser Cys Arg Thr Ser Gln Tyr Gly Ser Leu Ala
20 25 30

Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Val Ile Tyr Ser
35 40 45

Gly Ser Thr Arg Ala Ala Gly Ile Pro Asp Arg Phe Ser Gly Ser Arg
50 55 60

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

Phe Gly Val Tyr Tyr Cys Gln Gln Tyr Glu Phe Phe Gly Gln Gly Thr
85 90 95

Lys Val Gln Val Asp Ile Lys Arg Gly Gly Ser Ser Arg Ser Ser Ser

100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln
115 120 125

Ser Gly Gly Gln Met Lys Lys Pro Gly Glu Ser Met Arg Ile Ser Cys
130 135 140

Arg Ala Ser Gly Tyr Glu Phe Ile Asp Cys Thr Leu Asn Trp Ile Arg
145 150 155 160

Leu Ala Pro Gly Lys Arg Pro Glu Trp Met Gly Trp Leu Lys Pro Arg
165 170 175

Gly Gly Ala Val Asn Tyr Ala Arg Pro Leu Gln Gly Arg Val Thr Met
180 185 190

Thr Arg Asp Val Tyr Ser Asp Thr Ala Phe Leu Glu Leu Arg Ser Leu
195 200 205

Thr Val Asp Asp Thr Ala Val Tyr Phe Cys Thr Arg Gly Lys Asn Cys
210 215 220

Asp Tyr Asn Trp Asp Phe Glu His Trp Gly Arg Gly Thr Pro Val Ile
225 230 235 240

Val Ser Ser

<210> 60
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 60

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

Asp Thr Val Thr Ile Thr Cys Gln Ala Asn Gly Tyr Leu Asn Trp Tyr
            20                  25                  30

Gln Gln Arg Arg Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Gly Ser
        35                  40                  45

Lys Leu Glu Arg Gly Val Pro Ala Arg Phe Ser Gly Arg Arg Trp Gly
    50                  55                  60

Gln Glu Tyr Asn Leu Thr Ile Asn Asn Leu Gln Pro Glu Asp Val Ala
65                  70                  75                  80

Thr Tyr Phe Cys Gln Val Tyr Glu Phe Ile Val Pro Gly Thr Arg Leu
                85                  90                  95

Asp Leu Lys Gly Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly
            100                 105                 110

Ser Gly Gly Gly Gly Gln Val His Leu Ser Gln Ser Gly Ala Ala Val
        115                 120                 125

Thr Lys Pro Gly Ala Ser Val Arg Val Ser Cys Glu Ala Ser Gly Tyr
    130                 135                 140

Lys Ile Ser Asp His Phe Ile His Trp Trp Arg Gln Ala Pro Gly Gln
145                 150                 155                 160

Gly Leu Gln Trp Val Gly Trp Ile Asn Pro Lys Thr Gly Gln Pro Asn
                165                 170                 175

Asn Pro Arg Gln Phe Gln Gly Arg Val Ser Leu Thr Arg Gln Ala Ser
            180                 185                 190
```

```
Trp Asp Phe Asp Thr Tyr Ser Phe Tyr Met Asp Leu Lys Ala Val Arg
        195                 200                 205


Ser Asp Asp Thr Ala Ile Tyr Phe Cys Ala Arg Gln Arg Ser Asp Phe
    210                 215                 220


Trp Asp Phe Asp Val Trp Gly Ser Gly Thr Gln Val Thr Val Ser Ser
225                 230                 235                 240


<210>  61
<211>  271
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Artificially Synthesized

<400>  61

Asp Phe Val Leu Thr Gln Ser Pro His Ser Leu Ser Val Thr Pro Gly
1               5                   10                  15


Glu Ser Ala Ser Ile Ser Cys Lys Ser Ser His Ser Leu Ile His Gly
            20                  25                  30


Asp Arg Asn Asn Tyr Leu Ala Trp Tyr Val Gln Lys Pro Gly Arg Ser
        35                  40                  45


Pro Gln Leu Leu Ile Tyr Leu Ala Ser Ser Arg Ala Ser Gly Val Pro
    50                  55                  60


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


Ser Arg Val Glu Thr Glu Asp Val Gly Thr Tyr Tyr Cys Met Gln Gly
                85                  90                  95


Arg Glu Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
```

100 105 110

Gly Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Gln Ala Gln Leu Val Gln Ser Gly Pro Glu Val Arg Lys Pro
130 135 140

Gly Thr Ser Val Lys Val Ser Cys Lys Ala Pro Gly Asn Thr Leu Lys
145 150 155 160

Thr Tyr Asp Leu His Trp Val Arg Ser Val Pro Gly Gln Gly Leu Gln
165 170 175

Trp Met Gly Trp Ile Ser His Glu Gly Asp Lys Lys Val Ile Val Glu
180 185 190

Arg Phe Lys Ala Lys Val Thr Ile Asp Trp Asp Arg Ser Thr Asn Thr
195 200 205

Ala Tyr Leu Gln Leu Ser Gly Leu Thr Ser Gly Asp Thr Ala Val Tyr
210 215 220

Tyr Cys Ala Lys Gly Ser Lys His Arg Leu Arg Asp Tyr Ala Leu Tyr
225 230 235 240

Asp Asp Asp Gly Ala Leu Asn Trp Ala Val Asp Val Asp Tyr Leu Ser
245 250 255

Asn Leu Glu Phe Trp Gly Gln Gly Thr Ala Val Thr Val Ser Ser
260 265 270

<210> 62
<211> 1863
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 62
atgaaccggg gagtcccttt taggcacttg cttctggtgc tgcaactggc gctcctccca 60

gcagccactc agggaaagaa agtggtgctg ggcaaaaaag gggatacagt ggaactgacc 120

tgtacagctt cccagaagaa gagcatacaa ttccactgga aaaactccaa ccagataaag 180

attctgggaa atcagggctc cttcttaact aaaggtccat ccaagctgaa tgatcgcgct 240

gactcaagaa gaagcctttg ggaccaagga aacttccccc tgatcatcaa gaatcttaag 300

atagaagact cagatactta catctgtgaa gtggaggacc agaaggagga ggtgcaattg 360

ctagtgttcg gattgactgc caactctgac acccacctgc ttcaggggca gagcctgacc 420

ctgaccttgg agagcccccc tggtagtagc ccctcagtgc aatgtaggag tccaaggggt 480

aaaaacatac agggggggaa gaccctctcc gtgtctcagc tggagctcca ggatagtggc 540

acctggacat gcactgtctt gcagaaccag aagaaggtgg agttcaaaat agacatcgtg 600

gtgctagctt tccagaaggc ctccagcata gtctataaga aagaggggga acaggtggag 660

ttctccttcc cactcgcctt tacagttgaa aagctgacgg gcagtggcga gctgtggtgg 720

caggcggaga gggcttcctc ctccaagtct tggatcacct ttgacctgaa gaacaaggaa 780

gtgtctgtaa aacgggttac ccaggaccct aagctccaga tgggcaagaa gctcccgctc 840

cacctcaccc tgccccaggc cttgcctcag tatgctggct ctggaaacct caccctggcc 900

cttgaagcga aaacaggaaa gttgcatcag gaagtgaacc tggtggtgat gagagccact 960

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ccacgcgact tcgcagccta tcgctccaga gtgaagttca gcaggagcgc agacgccccc 1560

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cgc 1863

<210> 63
<211> 1857
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 63
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tgtacagctt cccagaagaa gagcatacaa ttccactgga aaaactccaa ccagataaag 180

attctgggaa atcagggctc cttcttaact aaaggtccat ccaagctgaa tgatcgcgct 240

gactcaagaa gaagcctttg ggaccaagga aacttccccc tgatcatcaa gaatcttaag 300

atagaagact cagatactta catctgtgaa gtggaggacc agaaggagga ggtgcaattg 360

ctagtgttcg gattgactgc caactctgac acccacctgc ttcaggggca gagcctgacc 420

ctgaccttgg agagcccccc tggtagtagc ccctcagtgc aatgtaggag tccaaggggt 480

aaaaacatac agggggggaa gaccctctcc gtgtctcagc tggagctcca ggatagtggc 540

acctggacat gcactgtctt gcagaaccag aagaaggtgg agttcaaaat agacatcgtg 600

gtgctagctt tccagaaggc ctccagcata gtctataaga aagaggggga acaggtggag 660

ttctccttcc cactcgcctt tacagttgaa aagctgacgg gcagtggcga gctgtggtgg 720

caggcggaga gggcttcctc ctccaagtct tggatcacct ttgacctgaa gaacaaggaa 780

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gaagaaggag gatgtgaact gagagtgaag ttcagcagga gcgcagacgc ccccgcgtac 1560

cagcagggcc agaaccagct ctataacgag ctcaatctag gacgaagaga ggagtacgat 1620

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agtacagcca ccaaggacac ctacgacgcc cttcacatgc aggccctgcc ccctcgc 1857

<210> 64
<211> 1188
<212> DNA

<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 64
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tgtacagctt cccagaagaa gagcatacaa ttccactgga aaaactccaa ccagataaag 180

attctgggaa atcagggctc cttcttaact aaaggtccat ccaagctgaa tgatcgcgct 240

gactcaagaa gaagcctttg ggaccaagga aacttccccc tgatcatcaa gaatcttaag 300

atagaagact cagatactta catctgtgaa gtggaggacc agaaggagga ggtgcaattg 360

ctagtgttcg gattgactgc caactctgac acccacctgc ttcaggggca gagcctgacc 420

ctgaccttgg agagcccccc tggtagtagc ccctcagtgc aatgtaggag tccaaggggt 480

aaaaacatac agggggggaa gaccctctcc gtgtctcagc tggagctcca ggatagtggc 540

acctggacat gcactgtctt gcagaaccag aagaaggtgg agttcaaaat agacatcgtg 600

gtgctagctt tccagaaggc ctccagcata gtctataaga aagaggggga acaggtggag 660

ttctccttcc cactcgcctt tacagttgaa aagctgacgg gcagtggcga gctgtggtgg 720

caggcggaga gggcttcctc ctccaagtct tggatcacct ttgacctgaa gaacaaggaa 780

gtgtctgtaa aacgggttac ccaggaccct aagctccaga tgggcaagaa gctcccgctc 840

cacctcaccc tgccccaggc cttgcctcag tatgctggct ctggaaacct caccctggcc 900

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ctgaaccctg aggcggggat gtggcagtgt ctgctgagtg actcgggaca ggtcctgctg 1140

gaatccaaca tcaaggttct gcccacatgg tccaccccgg tgcagcca 1188

<210> 65

<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 65
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tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg cagtgcacac gagggggctg 120

gacttcgcct gtgat 135

<210> 66
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 66
atctacatct gggcgccctt ggccgggact tgtggggtcc ttctcctgtc actggttatc 60

acccttact gc 72

<210> 67
<211> 204
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 67
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gcctttatta ttttctgggt gaggagtaag aggagcaggc tcctgcacag tgactacatg 120

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cgcgacttcg cagcctatcg ctcc 204

<210> 68

<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 68
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actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120

gaactg 126

<210> 69
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 69
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tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 70
<211> 1325
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 70
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tgcgccgctt ccggcttcga cttcagccgg cagggcatgc attgggtgcg ccaggctcca 120

ggacagggac tggaatgggt ggccttcatc aagtacgacg gcagcgagaa gtaccacgcc 180

gacagcgtgt ggggtagact gtctatcagc cgggacaaca gcaaggacac cctgtacctg 240

cagatgaaca gcctgcgggt ggaggacacc gccacatact tttgcgtgcg ggaggctggt 300

ggacctgact accggaacgg ctacaactac tacgacttct acgacggcta ctacaactac 360

cactacatgg atgtgtgggg caagggcacc accgtgaccg tgtctagcgg aggcggagga 420

tctggcggcg gaggaagtgg aggcggcgga agccagtctg ccctgaccca gcctgcctct 480

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agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga aagccgagaa 1140

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acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat ggcctttacc 1260

agggtctcag tacagccacc aaggacacct acgacgccct tcacatgcag gccctgcccc 1320

ctcgc 1325

<210> 71
<211> 1328
<212> DNA

<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 71
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accatcagct gtaccggcac cagcaacaac ttcgtgtcct ggtatcagca gcacgccggc 120

aaggccccca agctcgtgat ctacgacgtg aacaagcggc ccagcggcgt gcccgataga 180

ttcagcggca gcaagagcgg caacaccgcc agcctgacag tgtctggcct gcagaccgat 240

gacgaggccg tgtactactg cggcagcctc gtgggcaact gggacgtgat ctttggcgga 300

ggcaccaagc tgaccgtgct gggcggaagc agcagaagct ctagttctgg cggcggagga 360

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cctacagtga gattgggatg aaaggcgagc gccggagggg caaggggcac gatggccttt 1260

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cccctcgc 1328

<210> 72
<211> 1283
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 72
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gccatcatca gctgccggac aagccagtac ggcagcctgg cctggtatca gcagaggcct 120

ggacaggccc ccagactcgt gatctacagc ggcagcacaa gagccgccgg aatccccgat 180

agattcagcg gctctagatg gggccctgac tacaacctga ccatcagcaa cctggaaagc 240

ggcgacttcg gcgtgtacta ctgccagcag tacgagttct tcggccaggg caccaaggtg 300

caggtggaca tcaagagagg cggcagctcc agaagctcca gctctggcgg cggaggatct 360

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agcatgcgga tcagctgcag agcctccggc tacgagttca tcgactgcac cctgaactgg 480

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gataccgcct tcctggaact gcggagcctg accgtggatg ataccgccgt gtacttctgc 660

acccggggca agaactgcga ctacaactgg gacttcgagc actggggcag aggcacccct 720

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ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg aggggcaagg 1200

ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac gacgcccttc 1260

acatgcaggc cctgcccccc cgc 1283

<210> 73
<211> 1262
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 73
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atcacctgtc aggccaacgg ctacctgaac tggtatcagc agcggagagg caaggccccc 120

aagctgctga tctacgacgg cagcaagctg gaaagaggcg tgcccgccag attcagcggc 180

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gc 1262

<210> 74
<211> 1355
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 74
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atcagctgca agagcagcca ctccctgatc cacggcgacc ggaacaacta cctggcttgg 120

tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180

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tggacctttg gccagggcac caaggtggac atcaagggcg gcagctccag aagcagctct 360

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gacgatgacg gcgccctgaa ctgggccgtg gatgtggact acctgagcaa cctggaattc 780

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gagtgaagtt cagcaggagc gcagacgccc ccgcgtacaa gcagggccag aaccagctct 1080

ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag agacgtggcc 1140

gggaccctga gatgggggga aagccgagaa ggaagaaccc tcaggaaggc ctgtacaatg 1200

aactgcagaa agataagatg gcggaggcct acagtgagat tgggatgaaa ggcgagcgcc 1260

ggaggggcaa ggggcacgat ggcctttacc agggtctcag tacagccacc aaggacacct 1320

acgacgccct tcacatgcag gccctgcccc ctcgc 1355

<210> 75
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 75
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tgcgccgctt ccggcttcga cttcagccgg cagggcatgc attgggtgcg ccaggctcca 120

ggacagggac tggaatgggt ggccttcatc aagtacgacg gcagcgagaa gtaccacgcc 180

gacagcgtgt ggggtagact gtctatcagc cgggacaaca gcaaggacac cctgtacctg 240

cagatgaaca gcctgcgggt ggaggacacc gccacatact tttgcgtgcg ggaggctggt 300

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ctg 783

<210> 76
<211> 786
<212> DNA
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<220>
<223> Artificially Synthesized

<400> 76
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