SEQUENCE LISTING

<110> NOVARTIS AG

<120> SOLUBILIZED APYRASES, METHODS AND USE

<130> PAT057510-EP-EPA

<140> EP 18184269.1
<141> 2018-07-18

<160> 253

<170> PatentIn version 3.5

<210> 1
<211> 510
<212> PRT
<213> Homo sapiens

<400> 1
Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn
1   5   10   15

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

Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
        35   40   45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
    50   55   60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
65   70   75   80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
                85   90   95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
            100   105   110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
        115   120   125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
    130   135   140

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Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
145                 150                 155                 160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
                165                 170                 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
            180                 185                 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
        195                 200                 205

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

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225                 230                 235                 240

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

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
            260                 265                 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
        275                 280                 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
    290                 295                 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
305                 310                 315                 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
                325                 330                 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
            340                 345                 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
        355                 360                 365
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Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
    370                 375                 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385                 390                 395                 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
                405                 410                 415

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

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
        435                 440                 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
    450                 455                 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
465                 470                 475                 480

Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
                485                 490                 495

Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
            500                 505                 510
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<210> 2
<211> 511
<212> PRT
<213> Rattus norvegicus

<400> 2

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Met Glu Asp Ile Lys Asp Ser Lys Val Lys Arg Phe Cys Ser Lys Asn
1               5                   10                  15

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

Ile Ala Val Gly Leu Thr His Asn Lys Pro Leu Pro Glu Asn Val Lys
        35                  40                  45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Asn Leu Tyr Ile
```

```
    50                  55                  60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val Gln Leu
65                  70                  75                  80

Leu Glu Glu Cys Gln Val Lys Gly Pro Gly Ile Ser Lys Tyr Ala Gln
                85                  90                  95

Lys Thr Asp Glu Ile Ala Ala Tyr Leu Ala Glu Cys Met Lys Met Ser
            100                 105                 110

Thr Glu Arg Ile Pro Ala Ser Lys Gln His Gln Thr Pro Val Tyr Leu
        115                 120                 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Lys Gln Ser
    130                 135                 140

Ala Asp Glu Val Leu Ala Ala Val Ser Arg Ser Leu Lys Ser Tyr Pro
145                 150                 155                 160

Phe Asp Phe Gln Gly Ala Lys Ile Ile Thr Gly Gln Glu Glu Gly Ala
                165                 170                 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Arg Phe Thr Gln Glu
            180                 185                 190

Gln Ser Trp Leu Asn Phe Ile Ser Asp Ser Gln Lys Gln Ala Thr Phe
        195                 200                 205

Gly Ala Leu Asp Leu Gly Gly Ser Ser Thr Gln Val Thr Phe Val Pro
    210                 215                 220

Leu Asn Gln Thr Leu Glu Ala Pro Glu Thr Ser Leu Gln Phe Arg Leu
225                 230                 235                 240

Tyr Gly Thr Asp Tyr Thr Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
                245                 250                 255

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Gln Asp Ile Gln Val Ser
            260                 265                 270

Ser Gly Gly Ile Leu Lys Asp Pro Cys Phe Tyr Pro Gly Tyr Lys Lys
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        275                 280                 285

Val Val Asn Val Ser Glu Leu Tyr Gly Thr Pro Cys Thr Lys Arg Phe
    290                 295                 300

Glu Lys Lys Leu Pro Phe Asn Gln Phe Gln Val Gln Gly Thr Gly Asp
305                 310                 315                 320

Tyr Glu Gln Cys His Gln Ser Ile Leu Lys Phe Phe Asn Asn Ser His
                325                 330                 335

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Val Phe Leu Pro Pro Leu
            340                 345                 350

Gln Gly Ser Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Asp Phe
        355                 360                 365

Phe Lys Lys Met Ala Asn Asp Ser Val Ser Ser Gln Glu Lys Met Thr
    370                 375                 380

Glu Ile Thr Lys Asn Phe Cys Ser Lys Pro Trp Glu Glu Val Lys Ala
385                 390                 395                 400

Ser Tyr Pro Thr Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser
                405                 410                 415

Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr Asn Phe Thr Gly
            420                 425                 430

Thr Ser Trp Asp Gln Ile His Phe Met Gly Lys Ile Lys Asp Ser Asn
        435                 440                 445

Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro
    450                 455                 460

Ala Glu Gln Pro Leu Ser Pro Pro Leu Pro His Ser Thr Tyr Ile Ser
465                 470                 475                 480

Leu Met Val Leu Phe Ser Leu Val Leu Val Ala Met Val Ile Thr Gly
                485                 490                 495

Leu Phe Ile Phe Ser Lys Pro Ser Tyr Phe Trp Lys Glu Ala Val
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            500                 505                 510


<210> 3
<211> 441
<212> PRT
<213> Homo sapiens

<400> 3
Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly Ile
1               5                   10                  15


Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln Trp
            20                  25                  30


Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe Lys
        35                  40                  45


Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro Gln
    50                  55                  60


Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly Gln
65                  70                  75                  80


Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala Thr
                85                  90                  95


Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn Glu
            100                 105                 110


Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp Phe
        115                 120                 125


Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly Trp
    130                 135                 140


Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu Trp
145                 150                 155                 160


His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu Asp
                165                 170                 175


Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys Met
            180                 185                 190
```

```
Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr Val
        195                 200                 205

Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu Ala
    210                 215                 220

Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys Asn
225                 230                 235                 240

His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe Thr
                245                 250                 255

Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro Glu
            260                 265                 270

Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp Pro
        275                 280                 285

Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala Cys
    290                 295                 300

His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys Ile
305                 310                 315                 320

Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser Ala
                325                 330                 335

Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser Thr
            340                 345                 350

Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu Pro
        355                 360                 365

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

Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr Trp
385                 390                 395                 400

Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala Trp
                405                 410                 415
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Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu Ser
420 425 430

Pro Leu Ile Arg Leu Pro Ile Glu Pro
435 440

<210> 4
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 4
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

```
Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365
```

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370   375   380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385   390   395   400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405   410   415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420   425

<210> 5
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 5
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc   60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg   120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa   180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc   240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg   300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc   360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac   420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc   480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc   540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac   600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac   660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa   720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg   780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc   840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc   900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 6
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 6
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly

```
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
```

340 345 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 7
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 7
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccatgga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 8
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 8
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

```
Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Met
            100                 105                 110

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe
305                 310                 315                 320
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```
Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425
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<210> 9
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 9
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccatgga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgatggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccaaggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 10
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 10
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

```
Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

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

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285
```

```
Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Arg Thr Pro Leu Ser His Ser Thr
            420                 425
```

<210> 11
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 11
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccatgga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agggattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgcgc 1260

acacctctga gccacagcac c 1281

<210> 12
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 12
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

```
Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Ala Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255
```

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Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Arg Thr Pro Leu Ser His Ser Thr
            420                 425
```

<210> 13
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 13
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgcgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccatgga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagg 1260

acacctctga gccacagcac c 1281

<210> 14
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 14
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu

```
1               5                   10                  15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
            20                  25                  30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
```

225 230 235 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
245 250 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
260 265 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
275 280 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
290 295 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
325 330 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
340 345 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Asp Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 15
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 15
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgatggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcgacaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 16
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 16
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Ser Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145 150 155 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
180 185 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
195 200 205

```
Lys Asp Gln Ala Leu Arg Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425
```

<210> 17
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 17
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatctc cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgatggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgc ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 18
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 18
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Glu Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

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

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Ala Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145 150 155 160

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

```
Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Thr Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400
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Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 19
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 19
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgagg aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgtccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg cggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcacc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 20
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 20
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Ala Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

```
Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365
```

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 21
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 21
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgattccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg cggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggt aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtagtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

ccattccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 22
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 22
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly

```
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Arg Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
```

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            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425
```

<210> 23
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 23
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctga ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 24
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 24
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

```
Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
            100                 105                 110

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Thr Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

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Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425
```

<210> 25
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 25
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta tggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcacc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcctttgagc 1260

acacctctga gccacagcac c 1281

<210> 26
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 26
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

```
Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Thr Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285
```

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
290 295 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
325 330 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
340 345 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 27
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 27
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccatgga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcacc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ctagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 28
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 28
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

```
Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Asp Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255
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Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Thr Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425
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<210> 29
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 29
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga tatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcacc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 30
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 30
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu

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1               5                   10                  15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
            20                  25                  30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
```

225 230 235 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
245 250 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
260 265 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
275 280 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
290 295 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
325 330 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
340 345 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Pro Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 31
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 31
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgccgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 32
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 32
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145 150 155 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
180 185 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
195 200 205

```
Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425
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<210> 33
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 33
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccttgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gttacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 34
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 34
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145 150 155 160

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

```
Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Lys Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Pro Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400
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Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Ser Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 35
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 35
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggcgctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaagg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgccca tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgccgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatct ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 36
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 36
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

```
Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Asn Glu Lys Tyr Leu Ser Glu Phe Cys Phe Ser Gly Thr
        355                 360                 365
```

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 37
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 37
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccaac cctgggagga aatcaagacc tcctacgctg gcgtgaacga gaagtacctg 1080

agcgagtttt gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 38
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 38
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly

```
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
```

340 345 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Phe Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 39
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 39
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtttt gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 40
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 40
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Asp Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

```
Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
            100                 105                 110

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

```
Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425
```

<210> 41
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 41
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcgacatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgcagcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 42
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 42
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

```
Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285
```

```
Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu Asp Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425


<210> 43
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 43
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc       60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg      120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa      180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc      240
```

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgcagcaggg ctaccacttc 1140

accgccgata gctgggagga catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 44
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 44
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

```
Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Gly Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255
```

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
260 265 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
275 280 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
290 295 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
325 330 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
340 345 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Ser Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 45
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 45
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacgg gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccactcc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 46
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 46
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu

```
1               5                   10                  15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
            20                  25                  30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
```

225 230 235 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
245 250 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
260 265 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
275 280 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
290 295 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
325 330 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
340 345 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Arg Thr Pro Leu Ser His Ser Thr
420 425

<210> 47
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 47
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccatgga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgcgc 1260

acacctctga gccacagcac c 1281

<210> 48
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 48
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145 150 155 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
180 185 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
195 200 205

```
Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Gly Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Gly Thr Pro Leu Ser His Ser Thr
            420                 425
```

<210> 49
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 49
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacgg gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgtt gaatctgacc aacatgatcc ccgccgagca gcccctgggc 1260

acacctctga gccacagcac c 1281

<210> 50
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 50
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145 150 155 160

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

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Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Met Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Arg Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Ser Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400
```

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Arg Thr Pro Leu Ser His Ser Thr
420 425

<210> 51
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 51
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttatgtgcta cggaaaggac caggctctga ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgtacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccactcc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgaga 1260

acacctctga gccacagcac c 1281

<210> 52
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 52
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Lys Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

```
Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365
```

Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Asn His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 53
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 53
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaagga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgcagcaggg ctaccacttc 1140

accgccgata gctgggagca caaccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 54
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 54
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly

```
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
```

340 345 350

Ala Gly Val Asn Glu Lys Tyr Leu Ser Glu Phe Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 55
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 55
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccatgga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccaac cctgggagga aatcaagacc tcctacgctg gcgtgaacga gaagtacctg 1080

agcgagtttt gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 56
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 56
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

```
Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
            100                 105                 110

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe
305                 310                 315                 320
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```
Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Phe Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425
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<210> 57
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 57
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccatgga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtttt gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 58
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 58
Ala Pro Thr Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
1 5 10 15

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
20 25 30

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
35 40 45

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
50 55 60

```
Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu
65                  70                  75                  80

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
                85                  90                  95

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

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
        115                 120                 125

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
    130                 135                 140

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln
145                 150                 155                 160

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
                165                 170                 175

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
            180                 185                 190

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
        195                 200                 205

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
    210                 215                 220

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
225                 230                 235                 240

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
                245                 250                 255

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

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
        275                 280                 285
```

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
290 295 300

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

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
325 330 335

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
340 345 350

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
355 360 365

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
370 375 380

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
385 390 395 400

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
405 410 415

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425 430

<210> 59
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 59
gcccctacca cccagaacaa ggccctgccc gagaacgtga agtacggcat cgtgctggac 60

gccggctcct cccacacctc cctgtacatc tacaagtggc ctgccgagaa agaaaacgac 120

accggcgtgg tgcaccaagt ggaagagtgc agagtgaagg gccccggcat ctccaagttc 180

gtgcagaaag tgaacgagat cggcatctac ctgaccgact gcatggaacg ggccagagaa 240

gtgatccctc ggtcccagca ccaggaaacc cctgtctacc tgggcgccac cgccggcatg 300

cggctgctgc ggatggaatc cgaggaactg gccgaccggg tgctggacgt ggtggaacgg 360

tccctgtcca actacccatt cgattttcaa ggcgccagaa tcatcaccgg ccaggaagag 420

ggcgcctacg gctggatcac catcaactac ctgctgggca agttctccca gaagaatcag 480

gaaaccttcg gcgccctgga cctgggcgga gccagcaccc aagtcacatt cgtgccccag 540

aaccagacca tcgagagccc cgacaacgcc ctgcagttcc ggctgtacgg caaggactac 600

aacgtgtaca cccacagctt tctgtgctac ggcaaggacc aggccctgtg gcagaagctg 660

gccaaggaca tccaagtggc ctccaacgag atcctgcggg acccctgctt ccaccccggc 720

tacaagaaag tggtcaacgt gtccgacctg tacaagaccc cttgcaccaa gagattcgag 780

atgaccctgc ccttccagca gttcgagatc cagggcatcg gcaactacca gcagtgccac 840

cagtccatcc tggaactgtt caacacctcc tactgcccct actcccagtg cgccttcaac 900

ggcatcttcc tgcctccact gcagggcgac ttcggcgcct tctccgcctt ctacttcgtg 960

atgaagttcc tgaacctgac ctccgagaaa gtgtcccagg aaaaagtgac cgagatgatg 1020

aagaagttct gcgcccagcc ctgggaggaa atcaagacct cctacgctgg cgtgaaagag 1080

aagtacctgt ccgagtactg cttctccggc acctacatcc tgtccctgct gctgcagggc 1140

taccacttca ccgccgacag ctgggagcac atccacttca tcggcaagat ccagggatcc 1200

gacgctggct ggaccctggg ctacatgctg aatctgacca acatgatccc cgccgagcag 1260

cccctgtcca cccctctgtc tcactccacc 1290

<210> 60
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 60
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

```
Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255
```

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Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Phe Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425
```

<210> 61
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 61
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccttgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtttt gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gttacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 62
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 62
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu

```
1               5                   10                  15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
            20                  25                  30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
```

225 230 235 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
245 250 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Thr Gly Asn
260 265 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
275 280 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
290 295 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
325 330 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
340 345 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu Asp Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 63
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 63
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcacc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgcagcaggg ctaccacttc 1140

accgccgata gctgggagga catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 64
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 64
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145 150 155 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
180 185 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
195 200 205

```
Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425
```

<210> 65
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 65
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccttgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgcagcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gttacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 66
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 66
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr
1 5 10 15

Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20 25 30

Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
35 40 45

Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
50 55 60

Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
65 70 75 80

Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg
85 90 95

Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
100 105 110

Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp
115 120 125

Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
130 135 140

Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile
145 150 155 160

Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe Gly
165 170 175

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

Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr
        195                 200                 205

Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys
    210                 215                 220

Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser
225                 230                 235                 240

Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val
                245                 250                 255

Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu
            260                 265                 270

Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr
        275                 280                 285

Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys
    290                 295                 300

Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln
305                 310                 315                 320

Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu
                325                 330                 335

Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met
            340                 345                 350

Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala
        355                 360                 365

Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr
    370                 375                 380

Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp
385                 390                 395                 400
```

Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp
405 410 415

Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln
420 425 430

Pro Leu Ser Thr Pro Leu Ser His Ser Thr
435 440

<210> 67
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 67
gcccctacca gcagcagcac caagaaaacc cagctgacca gcagcaccca gaacaaggcc 60

ctgcccgaga acgtgaagta cggcatcgtg ctggatgccg gcagcagcca caccagcctg 120

tacatctaca agtggcctgc cgagaaagaa aacgacaccg gcgtggtgca tcaggtggaa 180

gagtgcagag tgaagggccc tggcatcagc aagttcgtgc agaaagtgaa cgagatcggc 240

atctacctga ccgactgcat ggaacgggcc agggaagtga tccccagaag ccagcaccag 300

gaaaccccg tgtatctggg agccaccgcc ggcatgagac tgctgagaat ggaaagcgag 360

gaactggccg accgggtgct ggacgtggtg gaaagaagcc tgagcaacta cccattcgat 420

tttcaaggcg ccagaatcat caccggccag gaagaaggcg cctacggctg gatcaccatc 480

aactacctgc tgggcaagtt cagccagaag aatcaggaaa ccttcggcgc cctggacctg 540

ggcggagctt ctacccaagt gaccttcgtg ccccagaatc agaccatcga gagccccgac 600

aacgccctgc agttccggct gtacggcaag gactacaatg tgtacaccca cagctttctg 660

tgctacggaa aggaccaggc tctgtggcag aagctggcca aggacatcca ggtggccagc 720

aacgagatcc tgcgggaccc ttgcttccac cccggctaca agaaagtcgt gaacgtgtcc 780

gacctgtaca agacccccctg caccaagaga ttcgagatga ccctgccctt ccagcagttc 840

gagatccagg gcatcggcaa ttaccagcag tgccaccaga gcatcctgga actgttcaac 900

accagctact gcccctacag ccagtgcgcc ttcaacggca tcttcctgcc acctctgcag 960

ggggatttcg gcgccttcag cgccttctac ttcgtgatga agttcctgaa cctgaccagc 1020

gagaaggtgt cccaggaaaa agtgacagag atgatgaaga agttctgcgc ccagccctgg 1080

gaggaaatca agacctccta cgctggcgtg aaagagaagt acctgagcga gtactgcttc 1140

agcggcacct acatcctgag cctgctgctg cagggctacc acttcaccgc cgatagctgg 1200

gagcacatcc acttcatcgg caagattcag ggcagcgacg ccggctggac actgggctac 1260

atgctgaatc tgaccaacat gatccccgcc gagcagcccc tgagcacacc tctgagccac 1320

agcacc 1326

<210> 68
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 68
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

```
Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350
```

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Phe Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu Asp Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 69
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 69
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtttt gcttcagcgg cacctacatc ctgagcctgc tgcagcaggg ctaccacttc 1140

accgccgata gctgggagga catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 70
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 70
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

```
Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
            100                 105                 110

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
325 330 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
340 345 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Phe Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 71
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 71
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtttt gcttcagcgg cacctacatc ctgagcctgc tgcagcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 72
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 72
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Gly
1 5 10 15

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

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
35 40 45

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
50 55 60

```
Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
65                  70                  75                  80

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
                85                  90                  95

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
            100                 105                 110

Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
        115                 120                 125

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
    130                 135                 140

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
145                 150                 155                 160

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

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
        195                 200                 205

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
    210                 215                 220

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
225                 230                 235                 240

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
                245                 250                 255

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
            260                 265                 270

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
        275                 280                 285
```

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
290 295 300

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
305 310 315 320

Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe
325 330 335

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
340 345 350

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
355 360 365

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
370 375 380

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
385 390 395 400

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
405 410 415

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
420 425 430

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
435 440

<210> 73
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 73
gcccctacct cctccagcac caagaaaacc cagctgacct ccagcggcac ccagaacaag 60

gccctgcccg agaacgtgaa gtacggcatc gtgctggacg ccggctcctc ccacacctcc 120

ctgtacatct acaagtggcc tgccgagaaa gaaaacgaca ccggcgtggt gcaccaagtg 180

gaagagtgca gagtgaaggg ccccggcatc tccaagttcg tgcagaaagt gaacgagatc 240

ggcatctacc tgaccgactg catggaacgg gccagagaag tgatccctcg gtcccagcac 300

caggaaaccc ctgtctacct gggcgccacc gccggcatgc ggctgctgcg gatggaatcc 360

gaggaactgg ccgaccgggt gctggacgtg gtggaacggt ccctgtccaa ctacccattc 420

gattttcaag gcgccagaat catcaccggc caggaagagg gcgcctacgg ctggatcacc 480

atcaactacc tgctgggcaa gttctcccag aagaatcagg aaaccttcgg cgccctggac 540

ctgggcggag ccagcaccca agtcacattc gtgccccaga accagaccat cgagagcccc 600

gacaacgccc tgcagttccg gctgtacggc aaggactaca acgtgtacac ccacagcttt 660

ctgtgctacg gcaaggacca ggccctgtgg cagaagctgg ccaaggacat ccaagtggcc 720

tccaacgaga tcctgcggga cccctgcttc caccccggct acaagaaagt ggtcaacgtg 780

tccgacctgt acaagacccc ttgcaccaag agattcgaga tgaccctgcc cttccagcag 840

ttcgagatcc agggcatcgg caactaccag cagtgccacc agtccatcct ggaactgttc 900

aacacctcct actgccccta ctcccagtgc gccttcaacg gcatcttcct gcctccactg 960

cagggcgact tcggcgcctt ctccgccttc tacttcgtga tgaagttcct gaacctgacc 1020

tccgagaaag tgtcccagga aaaagtgacc gagatgatga agaagttctg cgcccagccc 1080

tgggaggaaa tcaagacctc ctacgctggc gtgaaagaga agtacctgtc cgagtactgc 1140

ttctccggca cctacatcct gtccctgctg ctgcagggct accacttcac cgccgacagc 1200

tgggagcaca tccacttcat cggcaagatc cagggatccg acgctggctg gaccctgggc 1260

tacatgctga atctgaccaa catgatcccc gccgagcagc ccctgtccac ccctctgtct 1320

cactccacc 1329

<210> 74
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 74
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

```
Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
            20                  25                  30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240
```

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Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425
```

<210> 75
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 75
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccatgga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgcagcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 76
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 76
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1   5   10   15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
            20   25   30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35   40   45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50   55   60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu Val Ile Pro
65   70   75   80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85   90   95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115   120   125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130   135   140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145   150   155   160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180   185   190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195   200   205

```
Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Phe Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425
```

<210> 77
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 77
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccatgga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagttct gcttcagcgg cacctacatc ctgagcctgc tgcagcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 78
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 78
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145 150 155 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu

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            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
```

405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 79
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 79
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccatgga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccttgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gttacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 80
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 80
Ala Pro Thr Ser Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val
1 5 10 15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
20 25 30

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
35 40 45

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
50 55 60

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
65 70 75 80

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
85 90 95

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
100 105 110

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
115 120 125

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
130 135 140

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
145 150 155 160

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Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr
                165                 170                 175

Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn
            180                 185                 190

Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His
        195                 200                 205

Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala
    210                 215                 220

Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe
225                 230                 235                 240

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

Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu
            260                 265                 270

Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu
        275                 280                 285

Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly
    290                 295                 300

Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe
305                 310                 315                 320

Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln
                325                 330                 335

Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu
            340                 345                 350

Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu
        355                 360                 365

Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr
    370                 375                 380
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His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile
385                 390                 395                 400


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


Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser
            420                 425                 430


Thr
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<210> 81
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 81
gcccctacca gcagcagcac ccagaacaag gccctgcccg agaacgtgaa gtacggcatc 60

gtgctggatg ccggcagcag ccacaccagc ctgtacatct acaagtggcc tgccgagaaa 120

gaaaacgaca ccggcgtggt gcatcaggtg gaagagtgca gagtgaaggg ccctggcatc 180

agcaagttcg tgcagaaagt gaacgagatc ggcatctacc tgaccgactg catggaacgg 240

gccagggaag tgatccccag aagccagcac caggaaaccc ccgtgtatct gggagccacc 300

gccggcatga gactgctgag aatggaaagc gaggaactgg ccgaccgggt gctggacgtg 360

gtggaaagaa gcctgagcaa ctacccattc gattttcaag gcgccagaat catcaccggc 420

caggaagaag gcgcctacgg ctggatcacc atcaactacc tgctgggcaa gttcagccag 480

aagaatcagg aaaccttcgg cgccctggac ctgggcggag cttctaccca agtgaccttc 540

gtgccccaga atcagaccat cgagagcccc gacaacgccc tgcagttccg gctgtacggc 600

aaggactaca atgtgtacac ccacagcttt ctgtgctacg gaaaggacca ggctctgtgg 660

cagaagctgg ccaaggacat ccaggtggcc agcaacgaga tcctgcggga cccttgcttc 720

caccccggct acaagaaagt cgtgaacgtg tccgacctgt acaagacccc ctgcaccaag 780

agattcgaga tgaccctgcc cttccagcag ttcgagatcc agggcatcgg caattaccag 840

cagtgccacc agagcatcct ggaactgttc aacaccagct actgccccta cagccagtgc 900

gccttcaacg gcatcttcct gccacctctg caggggggatt tcggcgcctt cagcgccttc 960

tacttcgtga tgaagttcct gaacctgacc agcgagaagg tgtcccagga aaaagtgaca 1020

gagatgatga agaagttctg cgcccagccc tgggaggaaa tcaagacctc ctacgctggc 1080

gtgaaagaga agtacctgag cgagtactgc ttcagcggca cctacatcct gagcctgctg 1140

ctgcagggct accacttcac cgccgatagc tgggagcaca tccacttcat cggcaagatt 1200

cagggcagcg acgccggctg gacactgggc tacatgctga atctgaccaa catgatcccc 1260

gccgagcagc ccctgagcac acctctgagc cacagcacc 1299

<210> 82
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 82
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

```
Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Ala Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335
```

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
340 345 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 83
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 83
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaagc cggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 84
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 84
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

```
Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Ala Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

Gly Ala Leu Asp Leu Gly Gly Ala Ala Thr Gln Val Thr Phe Val Pro
                165                 170                 175

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300
```

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
325 330 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
340 345 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 85
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 85
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaagc cggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agctgctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctacttcgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 86
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 86
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Gln Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile

```
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
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        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425


<210> 87
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 87
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc       60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaacagga caccggcgtg      120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa      180
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gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 88
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 88
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

```
Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Ala Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255
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Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425


<210> 89
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"
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<400> 89
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcaggcc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 90
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 90

```
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1               5                  10                  15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
            20                  25                  30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220
```

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225 230 235 240

Val Val Gln Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
245 250 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
260 265 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
275 280 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
290 295 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
325 330 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
340 345 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
355 360 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 91
<211> 1281
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 91
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgcagg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 92
<211> 427
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 92
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145 150 155 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
180 185 190

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Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Gln Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385                 390                 395                 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
                405                 410                 415
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Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 93
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 93
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tccagaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 94
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 94
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145 150 155 160

Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro

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                165                 170                 175

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Gln Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
    370                 375                 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
```

385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 95
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 95
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgcagctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gaatctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 96
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 96
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

```
Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
                325                 330                 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
            340                 345                 350

Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr
        355                 360                 365
```

Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser
370 375 380

Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly
385 390 395 400

Trp Thr Leu Gly Tyr Met Leu Gln Leu Thr Asn Met Ile Pro Ala Glu
405 410 415

Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 97
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 97
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggaaaggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaattacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcgcct tctactccgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcctacgctg gcgtgaaaga gaagtacctg 1080

agcgagtact gcttcagcgg cacctacatc ctgagcctgc tgctgcaggg ctaccacttc 1140

accgccgata gctgggagca catccacttc atcggcaaga ttcagggcag cgacgccggc 1200

tggacactgg gctacatgct gcagctgacc aacatgatcc ccgccgagca gcccctgagc 1260

acacctctga gccacagcac c 1281

<210> 98
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 98
tgccctacga gacaaacaat caggaaacct tcggcgccct ggacctgggc ggagcttcta 60

cccaagtga 69

<210> 99
<211> 431
<212> PRT
<213> Homo sapiens

<400> 99
Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
1 5 10 15

Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
20 25 30

Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
35 40 45

Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
50 55 60

```
Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg
65                  70                  75                  80

Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
                85                  90                  95

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

Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
        115                 120                 125

Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile
    130                 135                 140

Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile
145                 150                 155                 160

Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu
                165                 170                 175

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

Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr
        195                 200                 205

Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu
    210                 215                 220

Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu
225                 230                 235                 240

Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser
                245                 250                 255

Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro
            260                 265                 270

Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His
        275                 280                 285
```

```
Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln
    290                 295                 300

Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly
305                 310                 315                 320

Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser
                325                 330                 335

Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys
            340                 345                 350

Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu
        355                 360                 365

Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu
    370                 375                 380

Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His
385                 390                 395                 400

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

Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser
            420                 425                 430
```

<210> 100
<211> 1293
<212> DNA
<213> Homo sapiens

<400> 100
cagaacaaag ccctgcccga gaacgtgaag tacggcatcg tgctggatgc cggcagcagc 60

cacaccagcc tgtacatcta caagtggcct gccgagaaag aaaacgatac cggtgtcgtg 120

caccaggtgg aagagtgcag agtgaagggc cctggcatca gcaagttcgt gcagaaagtg 180

aacgagatcg gcatctacct gaccgactgc atggaacggg ccagagaagt gatccccaga 240

agccagcacc aggaaacccc cgtgtacctg ggagccacag ccggcatgag actgctgcgg 300

atggaaagcg aggaactggc cgacagagtg ctggacgtgg tggaaagaag cctgagcaac 360

tacccattcg attttcaagg ggccagaatc atcaccggcc aggaagaggg cgcttacggc 420

tggatcacca tcaactacct gctgggcaag ttcagccaga aaacccggtg gttcagcatc 480

gtgccctacg agacaaacaa tcaggaaacc ttcggagccc tggacctggg cggagcctct 540

acccaagtga ccttcgtgcc ccagaatcag accatcgaga gccccgacaa cgccctgcag 600

ttccggctgt acggcaagga ctacaatgtg tacacccaca gctttctgtg ctacggaaag 660

gaccaggccc tgtggcagaa gctggccaag gacatccagg tggccagcaa cgagatcctg 720

cgggaccctt gcttccaccc cggctacaag aaagtcgtga acgtgtccga cctgtacaag 780

acccccctgca ccaagagatt cgagatgacc ctgcccttcc agcagttcga gatccagggc 840

atcggcaact accagcagtg ccaccagagc atcctggaac tgttcaacac cagctactgc 900

ccctacagcc agtgcgcctt caacggcatc ttcctgccac ctctgcaggg ggacttcggc 960

gctttcagcg ccttctactt cgtgatgaag ttcctgaacc tgaccagcga gaaggtgtcc 1020

caggaaaaag tgacagagat gatgaagaag ttctgcgccc agccctggga ggaaatcaag 1080

acctcctacg ctggcgtgaa agagaagtac ctgagcgagt actgcttcag cggtacctac 1140

atcctgagcc tgctgctgca gggctaccac ttcaccgccg atagctggga gcacatccac 1200

ttcatcggca agattcaggg cagcgacgcc ggctggacac tgggctacat gctgaatctg 1260

accaacatga tccccgccga gcagcccctg agc 1293

<210> 101
<211> 431
<212> PRT
<213> Homo sapiens

<400> 101
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
50 55 60

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
65 70 75 80

```
Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
                85                  90                  95

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
            100                 105                 110

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn
145                 150                 155                 160

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val
                165                 170                 175

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu
            180                 185                 190

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe
        195                 200                 205

Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp
    210                 215                 220

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro
225                 230                 235                 240

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

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln
            260                 265                 270

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe
        275                 280                 285

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe
    290                 295                 300
```

```
Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe
305                 310                 315                 320

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
                325                 330                 335

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile
            340                 345                 350

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys
        355                 360                 365

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe
    370                 375                 380

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
385                 390                 395                 400

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

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425                 430
```

<210> 102
<211> 1293
<212> DNA
<213> Homo sapiens

<400> 102
aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac 60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agagtgcaga 120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg 180

accgactgca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc 240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc 300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg 360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg 420

ctgggcaagt tcagccagaa aacccggtgg ttcagcatcg tgccctacga gacaaacaat 480

caggaaacct tcggagccct ggacctgggc ggagcctcta cccaagtgac cttcgtgccc 540

cagaatcaga ccatcgagag ccccgacaac gccctgcagt tccggctgta cggcaaggac 600

tacaatgtgt acacccacag ctttctgtgc tacggaaagg accaggccct gtggcagaag 660

ctggccaagg acatccaggt ggccagcaac gagatcctgc gggacccttg cttccacccc 720

ggctacaaga aagtcgtgaa cgtgtccgac ctgtacaaga ccccctgcac caagagattc 780

gagatgaccc tgcccttcca gcagttcgag atccagggca tcggcaacta ccagcagtgc 840

caccagagca tcctggaact gttcaacacc agctactgcc cctacagcca gtgcgccttc 900

aacggcatct tcctgccacc tctgcagggg gacttcggcg ctttcagcgc cttctacttc 960

gtgatgaagt tcctgaacct gaccagcgag aaggtgtccc aggaaaaagt gacagagatg 1020

atgaagaagt tctgcgccca gccctgggag gaaatcaaga cctcctacgc tggcgtgaaa 1080

gagaagtacc tgagcgagta ctgcttcagc ggtacctaca tcctgagcct gctgctgcag 1140

ggctaccact tcaccgccga tagctgggag cacatccact tcatcggcaa gattcagggc 1200

agcgacgccg gctggacact gggctacatg ctgaatctga ccaacatgat ccccgccgag 1260

cagcccctga gcacacctct gtctcacagc acc 1293

<210> 103
<211> 416
<212> PRT
<213> Homo sapiens

<400> 103
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
50 55 60

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
65 70 75 80

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
85 90 95

```
Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
            100                 105                 110

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn
145                 150                 155                 160

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val
                165                 170                 175

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu
            180                 185                 190

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe
        195                 200                 205

Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp
    210                 215                 220

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro
225                 230                 235                 240

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

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln
            260                 265                 270

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe
        275                 280                 285

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe
    290                 295                 300

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe
305                 310                 315                 320
```

```
Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
                325                 330                 335

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile
            340                 345                 350

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys
        355                 360                 365

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe
    370                 375                 380

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
385                 390                 395                 400

Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met
                405                 410                 415
```

<210> 104
<211> 1248
<212> DNA
<213> Homo sapiens

<400> 104
aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac 60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agagtgcaga 120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg 180

accgactgca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc 240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc 300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg 360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg 420

ctgggcaagt tcagccagaa aacccggtgg ttcagcatcg tgccctacga gacaaacaat 480

caggaaacct tcggagccct ggacctgggc ggagcctcta cccaagtgac cttcgtgccc 540

cagaatcaga ccatcgagag ccccgacaac gccctgcagt tccggctgta cggcaaggac 600

tacaatgtgt acacccacag ctttctgtgc tacggaaagg accaggccct gtggcagaag 660

ctggccaagg acatccaggt ggccagcaac gagatcctgc gggacccttg cttccacccc 720

ggctacaaga aagtcgtgaa cgtgtccgac ctgtacaaga ccccctgcac caagagattc 780

gagatgaccc tgcccttcca gcagttcgag atccagggca tcggcaacta ccagcagtgc 840

caccagagca tcctggaact gttcaacacc agctactgcc cctacagcca gtgcgccttc 900

aacggcatct tcctgccacc tctgcagggg gacttcggcg ctttcagcgc cttctacttc 960

gtgatgaagt tcctgaacct gaccagcgag aaggtgtccc aggaaaaagt gacagagatg 1020

atgaagaagt tctgcgccca gccctgggag gaaatcaaga cctcctacgc tggcgtgaaa 1080

gagaagtacc tgagcgagta ctgcttcagc ggtacctaca tcctgagcct gctgctgcag 1140

ggctaccact tcaccgccga tagctgggag cacatccact tcatcggcaa gattcagggc 1200

agcgacgccg gctggacact gggctacatg ctgaatctga ccaacatg 1248

<210> 105
<211> 404
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 105
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
50 55 60

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
65 70 75 80

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
85 90 95

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
100 105 110

```
Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala
145                 150                 155                 160

Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro
                165                 170                 175

Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr
            180                 185                 190

Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys
        195                 200                 205

Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro
    210                 215                 220

Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr
225                 230                 235                 240

Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln
                245                 250                 255

Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile
            260                 265                 270

Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe
        275                 280                 285

Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser
    290                 295                 300

Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val
305                 310                 315                 320

Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro
                325                 330                 335
```

Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu
340 345 350

Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln
355 360 365

Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly
370 375 380

Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn
385 390 395 400

Leu Thr Asn Met

<210> 106
<211> 1212
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 106
aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac 60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agagtgcaga 120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg 180

accgactgca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc 240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc 300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg 360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg 420

ctgggcaagt tcagccagaa aaatcaggaa accttcggag ccctggacct gggcggagcc 480

tctacccaag tgaccttcgt gccccagaat cagaccatcg agagccccga caacgccctg 540

cagttccggc tgtacggcaa ggactacaat gtgtacaccc acagctttct gtgctacgga 600

aaggaccagg ccctgtggca gaagctggcc aaggacatcc aggtggccag caacgagatc 660

ctgcgggacc cttgcttcca ccccggctac aagaaagtcg tgaacgtgtc cgacctgtac 720

aagaccccct gcaccaagag attcgagatg accctgccct tccagcagtt cgagatccag 780

ggcatcggca actaccagca gtgccaccag agcatcctgg aactgttcaa caccagctac 840

tgcccctaca gccagtgcgc cttcaacggc atcttcctgc cacctctgca gggggacttc 900

ggcgctttca gcgccttcta cttcgtgatg aagttcctga acctgaccag cgagaaggtg 960

tcccaggaaa aagtgacaga gatgatgaag aagttctgcg cccagccctg ggaggaaatc 1020

aagacctcct acgctggcgt gaaagagaag tacctgagcg agtactgctt cagcggtacc 1080

tacatcctga gcctgctgct gcagggctac cacttcaccg ccgatagctg ggagcacatc 1140

cacttcatcg gcaagattca gggcagcgac gccggctgga cactgggcta catgctgaat 1200

ctgaccaaca tg 1212

<210> 107
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 107
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Ala Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Ala Met
50 55 60

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
65 70 75 80

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
85 90 95

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser

```
            100                 105                 110

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn
145                 150                 155                 160

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val
                165                 170                 175

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu
            180                 185                 190

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe
        195                 200                 205

Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp
    210                 215                 220

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro
225                 230                 235                 240

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

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln
            260                 265                 270

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe
        275                 280                 285

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe
    290                 295                 300

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe
305                 310                 315                 320

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
```

```
                325                 330                 335

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile
            340                 345                 350

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys
        355                 360                 365

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe
    370                 375                 380

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
385                 390                 395                 400

Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met
                405                 410                 415
```

<210> 108
<211> 1248
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 108

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aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac       60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agaggccaga      120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg      180

accgacgcca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc      240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc      300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg      360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg      420

ctgggcaagt tcagccagaa aacccggtgg ttcagcatcg tgccctacga gacaaacaat      480

caggaaacct tcggagccct ggacctgggc ggagcctcta cccaagtgac cttcgtgccc      540

cagaatcaga ccatcgagag ccccgacaac gccctgcagt tccggctgta cggcaaggac      600

tacaatgtgt acacccacag ctttctgtgc tacggaaagg accaggccct gtggcagaag      660
```

ctggccaagg acatccaggt ggccagcaac gagatcctgc gggacccttg cttccacccc 720

ggctacaaga aagtcgtgaa cgtgtccgac ctgtacaaga ccccctgcac caagagattc 780

gagatgaccc tgcccttcca gcagttcgag atccagggca tcggcaacta ccagcagtgc 840

caccagagca tcctggaact gttcaacacc agctactgcc cctacagcca gtgcgccttc 900

aacggcatct tcctgccacc tctgcagggg gacttcggcg ctttcagcgc cttctacttc 960

gtgatgaagt tcctgaacct gaccagcgag aaggtgtccc aggaaaaagt gacagagatg 1020

atgaagaagt tctgcgccca gccctgggag gaaatcaaga cctcctacgc tggcgtgaaa 1080

gagaagtacc tgagcgagta ctgcttcagc ggtacctaca tcctgagcct gctgctgcag 1140

ggctaccact tcaccgccga tagctgggag cacatccact tcatcggcaa gattcagggc 1200

agcgacgccg gctggacact gggctacatg ctgaatctga ccaacatg 1248

<210> 109
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 109
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
50 55 60

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
65 70 75 80

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
85 90 95

```
Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
            100                 105                 110

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn
145                 150                 155                 160

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val
                165                 170                 175

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu
            180                 185                 190

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe
        195                 200                 205

Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp
    210                 215                 220

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Ala Phe His Pro
225                 230                 235                 240

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

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln
            260                 265                 270

Gly Ile Gly Asn Tyr Gln Gln Ala His Gln Ser Ile Leu Glu Leu Phe
        275                 280                 285

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe
    290                 295                 300

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe
305                 310                 315                 320
```

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
325 330 335

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile
340 345 350

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys
355 360 365

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe
370 375 380

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
385 390 395 400

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

<210> 110
<211> 1248
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 110
aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac 60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agagtgcaga 120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg 180

accgactgca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc 240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc 300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg 360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg 420

ctgggcaagt tcagccagaa aacccggtgg ttcagcatcg tgccctacga gacaaacaat 480

caggaaacct tcggagccct ggacctgggc ggagcctcta cccaagtgac cttcgtgccc 540

cagaatcaga ccatcgagag ccccgacaac gccctgcagt tccggctgta cggcaaggac 600

tacaatgtgt acacccacag ctttctgtgc tacggaaagg accaggccct gtggcagaag 660

ctggccaagg acatccaggt ggccagcaac gagatcctgc gggaccctgc cttccacccc 720

ggctacaaga aagtcgtgaa cgtgtccgac ctgtacaaga ccccctgcac caagagattc 780

gagatgaccc tgcccttcca gcagttcgag atccagggca tcggcaacta ccagcaggcc 840

caccagagca tcctggaact gttcaacacc agctactgcc cctacagcca gtgcgccttc 900

aacggcatct tcctgccacc tctgcagggg gacttcggcg ctttcagcgc cttctacttc 960

gtgatgaagt tcctgaacct gaccagcgag aaggtgtccc aggaaaaagt gacagagatg 1020

atgaagaagt tctgcgccca gccctgggag gaaatcaaga cctcctacgc tggcgtgaaa 1080

gagaagtacc tgagcgagta ctgcttcagc ggtacctaca tcctgagcct gctgctgcag 1140

ggctaccact tcaccgccga tagctgggag cacatccact tcatcggcaa gattcagggc 1200

agcgacgccg gctggacact gggctacatg ctgaatctga ccaacatg 1248

<210> 111
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 111
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
50 55 60

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
65 70 75 80

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
85 90 95

```
Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
            100                 105                 110

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn
145                 150                 155                 160

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val
                165                 170                 175

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu
            180                 185                 190

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe
        195                 200                 205

Leu Ala Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp
    210                 215                 220

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro
225                 230                 235                 240

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

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln
            260                 265                 270

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe
        275                 280                 285

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe
    290                 295                 300

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe
305                 310                 315                 320
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```
Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
                325                 330                 335

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile
            340                 345                 350

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys
        355                 360                 365

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe
    370                 375                 380

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
385                 390                 395                 400

Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met
                405                 410                 415
```

<210> 112
<211> 1248
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 112
aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac 60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agagtgcaga 120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg 180

accgactgca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc 240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc 300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg 360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg 420

ctgggcaagt tcagccagaa aacccggtgg ttcagcatcg tgccctacga gacaaacaat 480

caggaaacct tcggagccct ggacctgggc ggagcctcta cccaagtgac cttcgtgccc 540

cagaatcaga ccatcgagag ccccgacaac gccctgcagt tccggctgta cggcaaggac 600

tacaatgtgt acacccacag ctttctggcc tacggaaagg accaggccct gtggcagaag 660

ctggccaagg acatccaggt ggccagcaac gagatcctgc gggacccttg cttccacccc 720

ggctacaaga aagtcgtgaa cgtgtccgac ctgtacaaga cccccgccac caagagattc 780

gagatgaccc tgcccttcca gcagttcgag atccagggca tcggcaacta ccagcagtgc 840

caccagagca tcctggaact gttcaacacc agctactgcc cctacagcca gtgcgccttc 900

aacggcatct tcctgccacc tctgcagggg gacttcggcg ctttcagcgc cttctacttc 960

gtgatgaagt tcctgaacct gaccagcgag aaggtgtccc aggaaaaagt gacagagatg 1020

atgaagaagt tctgcgccca gccctgggag gaaatcaaga cctcctacgc tggcgtgaaa 1080

gagaagtacc tgagcgagta ctgcttcagc ggtacctaca tcctgagcct gctgctgcag 1140

ggctaccact tcaccgccga tagctgggag cacatccact tcatcggcaa gattcagggc 1200

agcgacgccg gctggacact gggctacatg ctgaatctga ccaacatg 1248

<210> 113
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 113
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
50 55 60

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
65 70 75 80

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
85 90 95

```
Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
            100                 105                 110

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn
145                 150                 155                 160

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val
                165                 170                 175

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu
            180                 185                 190

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe
        195                 200                 205

Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp
    210                 215                 220

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro
225                 230                 235                 240

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

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln
            260                 265                 270

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe
        275                 280                 285

Asn Thr Ser Tyr Ala Pro Tyr Ser Gln Ala Ala Phe Asn Gly Ile Phe
    290                 295                 300

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe
305                 310                 315                 320
```

```
Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
                325                 330                 335

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile
            340                 345                 350

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys
        355                 360                 365

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe
    370                 375                 380

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
385                 390                 395                 400

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


<210> 114
<211> 1248
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 114
aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac       60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agagtgcaga      120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg      180

accgactgca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc      240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc      300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg      360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg      420

ctgggcaagt tcagccagaa aacccggtgg ttcagcatcg tgccctacga gacaaacaat      480

caggaaacct tcggagccct ggacctgggc ggagcctcta cccaagtgac cttcgtgccc      540

cagaatcaga ccatcgagag ccccgacaac gccctgcagt tccggctgta cggcaaggac      600
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tacaatgtgt acacccacag ctttctgtgc tacggaaagg accaggccct gtggcagaag 660

ctggccaagg acatccaggt ggccagcaac gagatcctgc gggacccttg cttccacccc 720

ggctacaaga aagtcgtgaa cgtgtccgac ctgtacaaga ccccctgcac caagagattc 780

gagatgaccc tgcccttcca gcagttcgag atccagggca tcggcaacta ccagcagtgc 840

caccagagca tcctggaact gttcaacacc agctacgccc cctacagcca ggccgccttc 900

aacggcatct tcctgccacc tctgcagggg gacttcggcg ctttcagcgc cttctacttc 960

gtgatgaagt tcctgaacct gaccagcgag aaggtgtccc aggaaaaagt gacagagatg 1020

atgaagaagt tctgcgccca gccctgggag gaaatcaaga cctcctacgc tggcgtgaaa 1080

gagaagtacc tgagcgagta ctgcttcagc ggtacctaca tcctgagcct gctgctgcag 1140

ggctaccact tcaccgccga tagctgggag cacatccact tcatcggcaa gattcagggc 1200

agcgacgccg gctggacact gggctacatg ctgaatctga ccaacatg 1248

<210> 115
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 115
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
50 55 60

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
65 70 75 80

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser

```
                85                  90                  95

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
            100                 105                 110

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn
145                 150                 155                 160

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val
                165                 170                 175

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu
            180                 185                 190

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe
        195                 200                 205

Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp
    210                 215                 220

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro
225                 230                 235                 240

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

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln
            260                 265                 270

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe
        275                 280                 285

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe
    290                 295                 300

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe
```

305 310 315 320

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
325 330 335

Val Thr Glu Met Met Lys Lys Phe Ala Ala Gln Pro Trp Glu Glu Ile
340 345 350

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Ala
355 360 365

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe
370 375 380

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
385 390 395 400

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

<210> 116
<211> 1248
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 116
aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac 60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agagtgcaga 120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg 180

accgactgca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc 240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc 300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg 360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg 420

ctgggcaagt tcagccagaa aacccggtgg ttcagcatcg tgccctacga gacaaacaat 480

caggaaacct tcggagccct ggacctgggc ggagcctcta cccaagtgac cttcgtgccc 540

cagaatcaga ccatcgagag ccccgacaac gccctgcagt tccggctgta cggcaaggac 600

tacaatgtgt acacccacag ctttctgtgc tacggaaagg accaggccct gtggcagaag 660

ctggccaagg acatccaggt ggccagcaac gagatcctgc gggacccttg cttccacccc 720

ggctacaaga aagtcgtgaa cgtgtccgac ctgtacaaga ccccctgcac caagagattc 780

gagatgaccc tgcccttcca gcagttcgag atccagggca tcggcaacta ccagcagtgc 840

caccagagca tcctggaact gttcaacacc agctactgcc cctacagcca gtgcgccttc 900

aacggcatct tcctgccacc tctgcagggg gacttcggcg ctttcagcgc cttctacttc 960

gtgatgaagt tcctgaacct gaccagcgag aaggtgtccc aggaaaaagt gacagagatg 1020

atgaagaagt tcgccgccca gccctgggag gaaatcaaga cctcctacgc tggcgtgaaa 1080

gagaagtacc tgagcgagta cgccttcagc ggtacctaca tcctgagcct gctgctgcag 1140

ggctaccact tcaccgccga tagctgggag cacatccact tcatcggcaa gattcagggc 1200

agcgacgccg gctggacact gggctacatg ctgaatctga ccaacatg 1248

<210> 117
<211> 404
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 117
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Ala Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Ala Met
50 55 60

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
65 70 75 80

```
Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
                85                  90                  95

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
            100                 105                 110

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala
145                 150                 155                 160

Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro
                165                 170                 175

Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr
            180                 185                 190

Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys
        195                 200                 205

Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro
    210                 215                 220

Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr
225                 230                 235                 240

Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln
                245                 250                 255

Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile
            260                 265                 270

Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe
        275                 280                 285

Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser
    290                 295                 300
```

```
Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val
305                 310                 315                 320


Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro
                325                 330                 335


Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu
            340                 345                 350


Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln
        355                 360                 365


Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly
    370                 375                 380


Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn
385                 390                 395                 400


Leu Thr Asn Met



<210> 118
<211> 1212
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 118
aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac       60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agaggccaga      120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg      180

accgacgcca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc      240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc      300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg      360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg      420

ctgggcaagt tcagccagaa aaatcaggaa accttcggag ccctggacct gggcggagcc      480

tctacccaag tgaccttcgt gccccagaat cagaccatcg agagccccga caacgccctg      540
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cagttccggc tgtacggcaa ggactacaat gtgtacaccc acagctttct gtgctacgga 600

aaggaccagg ccctgtggca gaagctggcc aaggacatcc aggtggccag caacgagatc 660

ctgcgggacc cttgcttcca ccccggctac aagaaagtcg tgaacgtgtc cgacctgtac 720

aagaccccct gcaccaagag attcgagatg accctgccct tccagcagtt cgagatccag 780

ggcatcggca actaccagca gtgccaccag agcatcctgg aactgttcaa caccagctac 840

tgcccctaca gccagtgcgc cttcaacggc atcttcctgc cacctctgca gggggacttc 900

ggcgctttca gcgccttcta cttcgtgatg aagttcctga acctgaccag cgagaaggtg 960

tcccaggaaa aagtgacaga gatgatgaag aagttctgcg cccagccctg ggaggaaatc 1020

aagacctcct acgctggcgt gaaagagaag tacctgagcg agtactgctt cagcggtacc 1080

tacatcctga gcctgctgct gcagggctac cacttcaccg ccgatagctg ggagcacatc 1140

cacttcatcg gcaagattca gggcagcgac gccggctgga cactgggcta catgctgaat 1200

ctgaccaaca tg 1212

<210> 119
<211> 404
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 119
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
50 55 60

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
65 70 75 80

```
Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
                85                  90                  95

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
            100                 105                 110

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala
145                 150                 155                 160

Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro
                165                 170                 175

Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr
            180                 185                 190

Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys
        195                 200                 205

Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro
    210                 215                 220

Ala Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr
225                 230                 235                 240

Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln
                245                 250                 255

Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Ala His Gln Ser Ile
            260                 265                 270

Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe
        275                 280                 285

Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser
    290                 295                 300
```

Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val
305 310 315 320

Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro
325 330 335

Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu
340 345 350

Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln
355 360 365

Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly
370 375 380

Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn
385 390 395 400

Leu Thr Asn Met

<210> 120
<211> 1212
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 120
aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac 60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agagtgcaga 120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg 180

accgactgca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc 240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc 300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg 360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg 420

ctgggcaagt tcagccagaa aaatcaggaa accttcggag ccctggacct gggcggagcc 480

tctacccaag tgaccttcgt gccccagaat cagaccatcg agagccccga caacgccctg 540

cagttccggc tgtacggcaa ggactacaat gtgtacaccc acagctttct gtgctacgga 600

aaggaccagg ccctgtggca gaagctggcc aaggacatcc aggtggccag caacgagatc 660

ctgcgggacc ctgccttcca ccccggctac aagaaagtcg tgaacgtgtc cgacctgtac 720

aagaccccct gcaccaagag attcgagatg accctgccct tccagcagtt cgagatccag 780

ggcatcggca actaccagca ggcccaccag agcatcctgg aactgttcaa caccagctac 840

tgcccctaca gccagtgcgc cttcaacggc atcttcctgc cacctctgca gggggacttc 900

ggcgctttca gcgccttcta cttcgtgatg aagttcctga acctgaccag cgagaaggtg 960

tcccaggaaa aagtgacaga gatgatgaag aagttctgcg cccagccctg ggaggaaatc 1020

aagacctcct acgctggcgt gaaagagaag tacctgagcg agtactgctt cagcggtacc 1080

tacatcctga gcctgctgct gcagggctac cacttcaccg ccgatagctg ggagcacatc 1140

cacttcatcg gcaagattca gggcagcgac gccggctgga cactgggcta catgctgaat 1200

ctgaccaaca tg 1212

<210> 121
<211> 404
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 121
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
50 55 60

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
65 70 75 80

```
Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
                85                  90                  95

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
            100                 105                 110

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala
145                 150                 155                 160

Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro
                165                 170                 175

Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr
            180                 185                 190

Thr His Ser Phe Leu Ala Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys
        195                 200                 205

Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro
    210                 215                 220

Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr
225                 230                 235                 240

Lys Thr Pro Ala Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln
                245                 250                 255

Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile
            260                 265                 270

Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe
        275                 280                 285

Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser
    290                 295                 300
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Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val
305                 310                 315                 320


Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro
                325                 330                 335


Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu
            340                 345                 350


Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln
        355                 360                 365


Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly
    370                 375                 380


Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn
385                 390                 395                 400


Leu Thr Asn Met



<210> 122
<211> 1212
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 122
aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac       60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agagtgcaga      120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg      180

accgactgca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc      240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc      300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg      360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg      420

ctgggcaagt tcagccagaa aaatcaggaa accttcggag ccctggacct gggcggagcc      480
```

tctacccaag tgaccttcgt gccccagaat cagaccatcg agagccccga caacgccctg 540

cagttccggc tgtacggcaa ggactacaat gtgtacaccc acagctttct ggcctacgga 600

aaggaccagg ccctgtggca gaagctggcc aaggacatcc aggtggccag caacgagatc 660

ctgcgggacc cttgcttcca ccccggctac aagaaagtcg tgaacgtgtc cgacctgtac 720

aagacccccg ccaccaagag attcgagatg accctgccct tccagcagtt cgagatccag 780

ggcatcggca actaccagca gtgccaccag agcatcctgg aactgttcaa caccagctac 840

tgcccctaca gccagtgcgc cttcaacggc atcttcctgc cacctctgca gggggacttc 900

ggcgctttca gcgccttcta cttcgtgatg aagttcctga acctgaccag cgagaaggtg 960

tcccaggaaa aagtgacaga gatgatgaag aagttctgcg cccagccctg ggaggaaatc 1020

aagacctcct acgctggcgt gaaagagaag tacctgagcg agtactgctt cagcggtacc 1080

tacatcctga gcctgctgct gcagggctac cacttcaccg ccgatagctg ggagcacatc 1140

cacttcatcg gcaagattca gggcagcgac gccggctgga cactgggcta catgctgaat 1200

ctgaccaaca tg 1212

<210> 123
<211> 404
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 123
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
50 55 60

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro

```
65                  70                  75                  80

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
                85                  90                  95

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
            100                 105                 110

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala
145                 150                 155                 160

Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro
                165                 170                 175

Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr
            180                 185                 190

Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys
        195                 200                 205

Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro
    210                 215                 220

Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr
225                 230                 235                 240

Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln
                245                 250                 255

Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile
            260                 265                 270

Leu Glu Leu Phe Asn Thr Ser Tyr Ala Pro Tyr Ser Gln Ala Ala Phe
        275                 280                 285

Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser
```

```
    290                 295                 300

Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val
305                 310                 315                 320

Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro
                325                 330                 335

Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu
            340                 345                 350

Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln
        355                 360                 365

Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly
    370                 375                 380

Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn
385                 390                 395                 400

Leu Thr Asn Met
```

<210> 124
<211> 1212
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 124
aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac 60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agagtgcaga 120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg 180

accgactgca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc 240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc 300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg 360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg 420

ctgggcaagt tcagccagaa aaatcaggaa accttcggag ccctggacct gggcggagcc 480

tctacccaag tgaccttcgt gccccagaat cagaccatcg agagccccga caacgccctg 540

cagttccggc tgtacggcaa ggactacaat gtgtacaccc acagctttct gtgctacgga 600

aaggaccagg ccctgtggca gaagctggcc aaggacatcc aggtggccag caacgagatc 660

ctgcgggacc cttgcttcca ccccggctac aagaaagtcg tgaacgtgtc cgacctgtac 720

aagacccccct gcaccaagag attcgagatg accctgccct tccagcagtt cgagatccag 780

ggcatcggca actaccagca gtgccaccag agcatcctgg aactgttcaa caccagctac 840

gccccctaca gccaggccgc cttcaacggc atcttcctgc cacctctgca gggggacttc 900

ggcgctttca gcgccttcta cttcgtgatg aagttcctga acctgaccag cgagaaggtg 960

tcccaggaaa aagtgacaga gatgatgaag aagttctgcg cccagccctg ggaggaaatc 1020

aagacctcct acgctggcgt gaaagagaag tacctgagcg agtactgctt cagcggtacc 1080

tacatcctga gcctgctgct gcagggctac cacttcaccg ccgatagctg ggagcacatc 1140

cacttcatcg gcaagattca gggcagcgac gccggctgga cactgggcta catgctgaat 1200

ctgaccaaca tg 1212

<210> 125
<211> 404
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 125
Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
1 5 10 15

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
20 25 30

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
35 40 45

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
50 55 60

```
Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
65                  70                  75                  80

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
                85                  90                  95

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
            100                 105                 110

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
        115                 120                 125

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
    130                 135                 140

Ser Gln Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala
145                 150                 155                 160

Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro
                165                 170                 175

Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr
            180                 185                 190

Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys
        195                 200                 205

Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro
    210                 215                 220

Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr
225                 230                 235                 240

Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln
                245                 250                 255

Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile
            260                 265                 270

Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe
        275                 280                 285
```

Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser
290 295 300

Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val
305 310 315 320

Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Ala Ala Gln Pro
325 330 335

Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu
340 345 350

Ser Glu Tyr Ala Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln
355 360 365

Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly
370 375 380

Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn
385 390 395 400

Leu Thr Asn Met

<210> 126
<211> 1212
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 126
aacgtgaagt acggcatcgt gctggatgcc ggcagcagcc acaccagcct gtacatctac 60

aagtggcctg ccgagaaaga aaacgatacc ggtgtcgtgc accaggtgga agagtgcaga 120

gtgaagggcc ctggcatcag caagttcgtg cagaaagtga acgagatcgg catctacctg 180

accgactgca tggaacgggc cagagaagtg atccccagaa gccagcacca ggaaaccccc 240

gtgtacctgg gagccacagc cggcatgaga ctgctgcgga tggaaagcga ggaactggcc 300

gacagagtgc tggacgtggt ggaaagaagc ctgagcaact acccattcga ttttcaaggg 360

gccagaatca tcaccggcca ggaagagggc gcttacggct ggatcaccat caactacctg 420

ctgggcaagt tcagccagaa aaatcaggaa accttcggag ccctggacct gggcggagcc 480

tctacccaag tgaccttcgt gccccagaat cagaccatcg agagccccga caacgccctg 540

cagttccggc tgtacggcaa ggactacaat gtgtacaccc acagctttct gtgctacgga 600

aaggaccagg ccctgtggca gaagctggcc aaggacatcc aggtggccag caacgagatc 660

ctgcgggacc cttgcttcca ccccggctac aagaaagtcg tgaacgtgtc cgacctgtac 720

aagacccccct gcaccaagag attcgagatg accctgccct tccagcagtt cgagatccag 780

ggcatcggca actaccagca gtgccaccag agcatcctgg aactgttcaa caccagctac 840

tgcccctaca gccagtgcgc cttcaacggc atcttcctgc cacctctgca gggggacttc 900

ggcgctttca gcgccttcta cttcgtgatg aagttcctga acctgaccag cgagaaggtg 960

tcccaggaaa aagtgacaga gatgatgaag aagttcgccg cccagccctg ggaggaaatc 1020

aagacctcct acgctggcgt gaaagagaag tacctgagcg agtacgcctt cagcggtacc 1080

tacatcctga gcctgctgct gcagggctac cacttcaccg ccgatagctg ggagcacatc 1140

cacttcatcg gcaagattca gggcagcgac gccggctgga cactgggcta catgctgaat 1200

ctgaccaaca tg 1212

<210> 127
<211> 431
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 127
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

```
Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser
145                 150                 155                 160

Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp
                165                 170                 175

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

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

Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala
    210                 215                 220

Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile
225                 230                 235                 240

Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val
                245                 250                 255

Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu
            260                 265                 270

Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys
        275                 280                 285
```

```
His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Phe Asn Gly Ile Phe
    290                 295                 300

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe
305                 310                 315                 320

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
                325                 330                 335

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile
            340                 345                 350

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys
        355                 360                 365

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe
    370                 375                 380

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
385                 390                 395                 400

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

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425                 430


<210> 128
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 128
acacagaaca aagccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc       60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga taccggtgtc      120

gtgcaccagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa      180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccagaga agtgatcccc      240
```

agaagccagc accaggaaac ccccgtgtac ctgggagcca cagccggcat gagactgctg 300

cggatggaaa gcgaggaact ggccgacaga gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggggccaga atcatcaccg gccaggaaga gggcgcttac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaaaacccg gtggttcagc 480

atcgtgccct acgagacaaa caatcaggaa accttcggag ccctggacct gggcggagcc 540

tctacccaag tgaccttcgt gccccagaat cagaccatcg agagccccga caacgccctg 600

cagttccggc tgtacggcaa ggactacaat gtgtacaccc acagctttct gtgctacgga 660

aaggaccagg ccctgtggca gaagctggcc aaggacatcc aggtggccag caacgagatc 720

ctgcgggacc cttgcttcca ccccggctac aagaaagtcg tgaacgtgtc cgacctgtac 780

aagacccccct gcaccaagag attcgagatg accctgccct tccagcagtt cgagatccag 840

ggcatcggca actaccagca gtgccaccag agcatcctgg aactgttcaa caccagcttc 900

aacggcatct tcctgccacc tctgcagggg gacttcggcg ctttcagcgc cttctacttc 960

gtgatgaagt tcctgaacct gaccagcgag aaggtgtccc aggaaaaagt gacagagatg 1020

atgaagaagt tctgcgccca gccctgggag gaaatcaaga cctcctacgc tggcgtgaaa 1080

gagaagtacc tgagcgagta ctgcttcagc ggtacctaca tcctgagcct gctgctgcag 1140

ggctaccact tcaccgccga tagctgggag cacatccact tcatcggcaa gattcagggc 1200

agcgacgccg gctggacact gggctacatg ctgaatctga ccaacatgat ccccgccgag 1260

cagcccctga gcacacctct gtctcacagc acc 1293

<210> 129
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 129
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

```
Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser
145                 150                 155                 160

Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp
                165                 170                 175

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

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

Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala
    210                 215                 220

Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile
225                 230                 235                 240

Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val
                245                 250                 255
```

```
Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu
            260                 265                 270

Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys
        275                 280                 285

His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Ala Pro Tyr Ser
    290                 295                 300

Gln Ala Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe
305                 310                 315                 320

Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr
                325                 330                 335

Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe
            340                 345                 350

Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys
        355                 360                 365

Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser
    370                 375                 380

Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile
385                 390                 395                 400

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly
                405                 410                 415

Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser
            420                 425                 430

Thr Pro Leu Ser His Ser Thr
        435


<210> 130
<211> 1317
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
```

polynucleotide"

<400> 130
acacagaaca aagccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga taccggtgtc 120

gtgcaccagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccagaga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtac ctgggagcca cagccggcat gagactgctg 300

cggatggaaa gcgaggaact ggccgacaga gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggggccaga atcatcaccg gccaggaaga gggcgcttac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaaaacccg gtggttcagc 480

atcgtgccct acgagacaaa caatcaggaa accttcggag ccctggacct gggcggagcc 540

tctacccaag tgaccttcgt gccccagaat cagaccatcg agagccccga caacgccctg 600

cagttccggc tgtacggcaa ggactacaat gtgtacaccc acagctttct gtgctacgga 660

aaggaccagg ccctgtggca gaagctggcc aaggacatcc aggtggccag caacgagatc 720

ctgcgggacc cttgcttcca ccccggctac aagaaagtcg tgaacgtgtc cgacctgtac 780

aagacccccct gcaccaagag attcgagatg accctgccct tccagcagtt cgagatccag 840

ggcatcggca actaccagca gtgccaccag agcatcctgg aactgttcaa caccagctac 900

gccccctaca gccaggccgc cttcaacggc atcttcctgc cacctctgca gggggacttc 960

ggcgctttca gcgccttcta cttcgtgatg aagttcctga acctgaccag cgagaaggtg 1020

tcccaggaaa aagtgacaga gatgatgaag aagttctgcg cccagccctg ggaggaaatc 1080

aagacctcct acgctggcgt gaaagagaag tacctgagcg agtactgctt cagcggtacc 1140

tacatcctga gcctgctgct gcagggctac cacttcaccg ccgatagctg ggagcacatc 1200

cacttcatcg gcaagattca gggcagcgac gccggctgga cactgggcta catgctgaat 1260

ctgaccaaca tgatccccgc cgagcagccc ctgagcacac ctctgtctca cagcacc 1317

<210> 131
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 131
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Gly
1 5 10 15

<210> 132
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 132
gcccccacca gcagcagcac caagaagacc cagctgacca gcagcggc 48

<210> 133
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 133
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser
1 5 10 15

<210> 134
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 134
gcccctacca gcagcagcac caagaaaacc cagctgacca gcagc 45

<210> 135
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 135
Ala Pro Thr Ser Ser Ser
1 5

<210> 136
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 136
gcccctacca gcagcagc 18

<210> 137
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 137
Ala Pro Thr
1

<210> 138
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 138
gcccctacc 9

<210> 139
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 139
Ala Pro Thr Ser Ser Ser Thr Lys Lys
1 5

<210> 140
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 140
gcccctacca gcagcagcac caagaaa 27

<210> 141
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 141
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
1 5 10

<210> 142
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 142
gcccctacca gcagcagcac caagaaaacc cagctg 36

<210> 143
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 143
Ser Ser Ser Thr Lys Lys Thr Gln Leu
1 5

<210> 144
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 144
agcagcagca ccaagaaaac ccagctg 27

<210> 145
<211> 426
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 145
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
50 55 60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80

```
Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Asp Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe
145                 150                 155                 160

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

Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu
            180                 185                 190

Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly
        195                 200                 205

Arg Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala
    210                 215                 220

Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys
225                 230                 235                 240

Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe
                245                 250                 255

Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn
            260                 265                 270

Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr
        275                 280                 285

Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu
    290                 295                 300
```

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

Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met
325 330 335

Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr
340 345 350

Ala Gly Gln Glu Arg Trp Leu Arg Asp Tyr Cys Phe Ser Gly Thr Tyr
355 360 365

Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp
370 375 380

Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp
385 390 395 400

Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln
405 410 415

Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425

<210> 146
<211> 1278
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 146
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccagaga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggacga gggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaatca ggaaaccttc 480

ggcgccctgg acctgggcgg agcttctacc caagtgacct tcgtgcccca gaatcagacc 540

atcgagagcc ccgacaacgc cctgcagttc cggctgtacg gcaaggacta caatgtgtac 600

acccacagct ttctgtgcta cggccgggac caggctctgt ggcagaagct ggccaaggac 660

atccaggtgg ccagcaacga gatcctgcgg gacccttgct tccaccccgg ctacaagaaa 720

gtcgtgaacg tgtccgacct gtacaagacc ccctgcacca agagattcga gatgaccctg 780

cccttccagc agttcgagat ccagggcatc ggcaactacc agcagtgcca ccagagcatc 840

ctggaactgt tcaacaccag ctactgcccc tacagccagt gcgccttcaa cggcatcttc 900

ctgccacctc tgcaggggga tttcggcgcc ttcagcaact tctactacgt gatgaagttc 960

ctgaacctga ccagcgagaa ggtgtcccag gaaaaagtga cagagatgat gaagaagttc 1020

tgcgcccagc cctgggagga aatcaagacc tcttacgccg gacaggaacg gtggctgcgg 1080

gactactgtt tcagcggcac ctacatcctg tccctgctgc tgcagggcta ccacttcacc 1140

gccgatagct gggagcacat ccacttcatc ggcaagattc agggcagcga cgccggctgg 1200

acactgggct acatgctgaa tctgaccaac atgatccccg ccgagcagcc cctgagcaca 1260

cctctgtctc acagcacc 1278

<210> 147
<211> 537
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 147
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30

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

```
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65                  70                  75                  80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85                  90                  95

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

Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala
        115                 120                 125

Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys
    130                 135                 140

Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val Lys
145                 150                 155                 160

Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly Ile
                165                 170                 175

Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg Ser
            180                 185                 190

Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met Arg
        195                 200                 205

Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp Val
    210                 215                 220

Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg
225                 230                 235                 240

Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn
                245                 250                 255

Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe Gly Ala
            260                 265                 270
```

```
Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn
        275                 280                 285

Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly
    290                 295                 300

Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp
305                 310                 315                 320

Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn
                325                 330                 335

Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val
            340                 345                 350

Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met
        355                 360                 365

Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln
    370                 375                 380

Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro
385                 390                 395                 400

Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly
                405                 410                 415

Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn
            420                 425                 430

Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys
        435                 440                 445

Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly
    450                 455                 460

Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile
465                 470                 475                 480

Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu
                485                 490                 495
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His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr
            500                 505                 510


Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro
        515                 520                 525


Leu Ser Thr Pro Leu Ser His Ser Thr
    530                 535


<210> 148
<211> 1611
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 148
acggtggccg ctcccagcgt gttcatcttc ccccccagcg acgagcagct gaagagcggc       60

accgccagcg tggtgtgcct gctgaacaac ttctaccccc gggaggccaa ggtgcagtgg      120

aaggtggaca acgccctgca gagcggcaac agccaggaaa gcgtcaccga gcaggacagc      180

aaggactcca cctacagcct gagcagcacc ctgaccctga gcaaggccga ctacgagaag      240

cacaaggtgt acgcctgcga ggtgacccac cagggcctgt ccagccccgt gaccaagagc      300

ttcaaccggg gcgagggagg cggaggatct acccagaaca aggccctgcc cgagaacgtg      360

aagtacggca tcgtgctgga tgccggcagc agccacacca gcctgtacat ctacaagtgg      420

cctgccgaga aagaaaacga caccggcgtg gtgcatcagg tggaagagtg cagagtgaag      480

ggccctggca tcagcaagtt cgtgcagaaa gtgaacgaga tcggcatcta cctgaccgac      540

tgcatggaac gggccaggga agtgatcccc agaagccagc accaggaaac ccccgtgtat      600

ctgggagcca ccgccggcat gagactgctg agaatggaaa gcgaggaact ggccgaccgg      660

gtgctggacg tggtggaaag aagcctgagc aactacccat tcgattttca aggcgccaga      720

atcatcaccg gccaggaaga aggcgcctac ggctggatca ccatcaacta cctgctgggc      780

aagttcagcc agaagaatca ggaaaccttc ggcgccctgg acctgggcgg agcttctacc      840

caagtgacct tcgtgcccca gaatcagacc atcgagagcc ccgacaacgc cctgcagttc      900

cggctgtacg gcaaggacta caatgtgtac acccacagct ttctgtgcta cggaaaggac      960
```

caggctctgt ggcagaagct ggccaaggac atccaggtgg ccagcaacga gatcctgcgg 1020

gacccttgct tccaccccgg ctacaagaaa gtcgtgaacg tgtccgacct gtacaagacc 1080

ccctgcacca agagattcga gatgaccctg cccttccagc agttcgagat ccagggcatc 1140

ggcaattacc agcagtgcca ccagagcatc ctggaactgt tcaacaccag ctactgcccc 1200

tacagccagt gcgccttcaa cggcatcttc ctgccacctc tgcaggggga tttcggcgcc 1260

ttcagcgcct tctacttcgt gatgaagttc ctgaacctga ccagcgagaa ggtgtcccag 1320

gaaaaagtga cagagatgat gaagaagttc tgcgcccagc cctgggagga aatcaagacc 1380

tcctacgctg gcgtgaaaga gaagtacctg agcgagtact gcttcagcgg cacctacatc 1440

ctgagcctgc tgctgcaggg ctaccacttc accgccgata gctgggagca catccacttc 1500

atcggcaaga ttcagggcag cgacgccggc tggacactgg gctacatgct gaatctgacc 1560

aacatgatcc ccgccgagca gcccctgagc acacctctga gccacagcac c 1611

<210> 149
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 149
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15

Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Gly Gly Gly Gly
65 70 75 80

Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val
85 90 95

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Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro
            100                 105                 110

Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys
        115                 120                 125

Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu
    130                 135                 140

Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile
145                 150                 155                 160

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

Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val
            180                 185                 190

Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln
        195                 200                 205

Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile
    210                 215                 220

Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr
225                 230                 235                 240

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
                245                 250                 255

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
            260                 265                 270

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
        275                 280                 285

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
    290                 295                 300

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
305                 310                 315                 320
```

```
Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
                325                 330                 335

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
            340                 345                 350

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
        355                 360                 365

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
    370                 375                 380

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
385                 390                 395                 400

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
                405                 410                 415

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
            420                 425                 430

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
        435                 440                 445

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

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
465                 470                 475                 480

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
                485                 490                 495

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            500                 505
```

<210> 150
<211> 1524
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 150
atgcaaatct tcgtgaagac cctgactggt aagaccatca ccctcgaggt ggagcccagt 60

gacaccatcg agaatgtcaa ggcaaagatc caagataagg aaggcatccc tcctgatcag 120

cagaggttga tctttgctgg gaaacagctg gaagatggac gcaccctgtc tgactacaac 180

atccagaaag agtccactct gcacttggtc ctgcgcttga gggggggtgg aggcggagga 240

tctacccaga acaaggccct gcccgagaac gtgaagtacg gcatcgtgct ggatgccggc 300

agcagccaca ccagcctgta catctacaag tggcctgccg agaaagaaaa cgacaccggc 360

gtggtgcatc aggtggaaga gtgcagagtg aagggccctg gcatcagcaa gttcgtgcag 420

aaagtgaacg agatcggcat ctacctgacc gactgcatgg aacgggccag ggaagtgatc 480

cccagaagcc agcaccagga aacccccgtg tatctgggag ccaccgccgg catgagactg 540

ctgagaatgg aaagcgagga actggccgac cgggtgctgg acgtggtgga aagaagcctg 600

agcaactacc cattcgattt tcaaggcgcc agaatcatca ccggccagga agaaggcgcc 660

tacggctgga tcaccatcaa ctacctgctg ggcaagttca gccagaagaa tcaggaaacc 720

ttcggcgccc tggacctggg cggagcttct acccaagtga ccttcgtgcc ccagaatcag 780

accatcgaga gccccgacaa cgccctgcag ttccggctgt acggcaagga ctacaatgtg 840

tacacccaca gctttctgtg ctacggaaag gaccaggctc tgtggcagaa gctggccaag 900

gacatccagg tggccagcaa cgagatcctg cgggaccctt gcttccaccc cggctacaag 960

aaagtcgtga acgtgtccga cctgtacaag acccccctgca ccaagagatt cgagatgacc 1020

ctgcccttcc agcagttcga gatccagggc atcggcaatt accagcagtg ccaccagagc 1080

atcctggaac tgttcaacac cagctactgc ccctacagcc agtgcgcctt caacggcatc 1140

ttcctgccac ctctgcaggg ggatttcggc gccttcagcg ccttctactt cgtgatgaag 1200

ttcctgaacc tgaccagcga gaaggtgtcc caggaaaaag tgacagagat gatgaagaag 1260

ttctgcgccc agccctggga ggaaatcaag acctcctacg ctggcgtgaa agagaagtac 1320

ctgagcgagt actgcttcag cggcacctac atcctgagcc tgctgctgca gggctaccac 1380

ttcaccgccg atagctggga gcacatccac ttcatcggca agattcaggg cagcgacgcc 1440

ggctggacac tgggctacat gctgaatctg accaacatga tccccgccga gcagcccctg 1500

agcacacctc tgagccacag cacc 1524

<210> 151
<211> 618
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 151
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

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

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

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Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Gly Gly Gly Gly Ser Thr
            180                 185                 190

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

Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
    210                 215                 220

Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
225                 230                 235                 240

Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
                245                 250                 255

Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg
            260                 265                 270

Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
        275                 280                 285

Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp
    290                 295                 300

Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
305                 310                 315                 320

Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile
                325                 330                 335

Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe Gly
            340                 345                 350

Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln
        355                 360                 365

Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr
    370                 375                 380

Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys
385                 390                 395                 400
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Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser
                405                 410                 415

Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val
            420                 425                 430

Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu
        435                 440                 445

Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr
    450                 455                 460

Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys
465                 470                 475                 480

Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln
                485                 490                 495

Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu
            500                 505                 510

Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met
        515                 520                 525

Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala
    530                 535                 540

Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr
545                 550                 555                 560

Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp
                565                 570                 575

Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp
            580                 585                 590

Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln
        595                 600                 605

Pro Leu Ser Thr Pro Leu Ser His Ser Thr
    610                 615
```

<210> 152
<211> 1854
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 152
gacgcccaca agagcgaggt ggcccaccgg ttcaaggacc tgggcgagga aaacttcaag 60

gccctggtgc tgatcgcctt cgcccagtac ctgcagcaga gccccttcga agatcacgta 120

aagttagtca acgaggttac ggaattcgca aagacatgcg ttgctgacga atccgctgag 180

aattgtgaca agagtttgca cactttattc ggagataagt tgtgtactgt agctactttg 240

agagagactt acggtgaaat ggctgactgc tgtgcaaaac aggaaccaga acgtaacgaa 300

tgtttccttc agcataagga tgataaccct aaccttccaa ggcttgttag gccagaagtc 360

gacgtgatgt gcaccgcctt ccatgataat gaagagactt ttcttaaaaa gtacctatac 420

gagattgcaa ggcgtcatcc atatttttac gccccagagc tgttgttttt cgcaaagaga 480

tacaaagctg catttactga gtgttgccaa gctgccgaca aggccgcttg tttgctacca 540

aagttggacg aattgagagg aggcggagga tctacccaga acaaggccct gcccgagaac 600

gtgaagtacg gcatcgtgct ggatgccggc agcagccaca ccagcctgta catctacaag 660

tggcctgccg agaaagaaaa cgacaccggc gtggtgcatc aggtggaaga gtgcagagtg 720

aagggccctg gcatcagcaa gttcgtgcag aaagtgaacg agatcggcat ctacctgacc 780

gactgcatgg aacgggccag ggaagtgatc cccagaagcc agcaccagga aacccccgtg 840

tatctgggag ccaccgccgg catgagactg ctgagaatgg aaagcgagga actggccgac 900

cgggtgctgg acgtggtgga aagaagcctg agcaactacc cattcgattt tcaaggcgcc 960

agaatcatca ccggccagga agaaggcgcc tacggctgga tcaccatcaa ctacctgctg 1020

ggcaagttca gccagaagaa tcaggaaacc ttcggcgccc tggacctggg cggagcttct 1080

acccaagtga ccttcgtgcc ccagaatcag accatcgaga gccccgacaa cgccctgcag 1140

ttccggctgt acggcaagga ctacaatgtg tacacccaca gctttctgtg ctacggaaag 1200

gaccaggctc tgtggcagaa gctggccaag gacatccagg tggccagcaa cgagatcctg 1260

cgggaccctt gcttccaccc cggctacaag aaagtcgtga acgtgtccga cctgtacaag 1320

acccccctgca ccaagagatt cgagatgacc ctgcccttcc agcagttcga gatccagggc 1380

atcggcaatt accagcagtg ccaccagagc atcctggaac tgttcaacac cagctactgc 1440

ccctacagcc agtgcgcctt caacggcatc ttcctgccac ctctgcaggg ggatttcggc 1500

gccttcagcg ccttctactt cgtgatgaag ttcctgaacc tgaccagcga gaaggtgtcc 1560

caggaaaaag tgacagagat gatgaagaag ttctgcgccc agccctggga ggaaatcaag 1620

acctcctacg ctggcgtgaa agagaagtac ctgagcgagt actgcttcag cggcacctac 1680

atcctgagcc tgctgctgca gggctaccac ttcaccgccg atagctggga gcacatccac 1740

ttcatcggca agattcaggg cagcgacgcc ggctggacac tgggctacat gctgaatctg 1800

accaacatga tccccgccga gcagcccctg agcacacctc tgagccacag cacc 1854

<210> 153
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 153
Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
1 5 10 15

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
20 25 30

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
35 40 45

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
50 55 60

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
65 70 75 80

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
85 90 95

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
100 105 110

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

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
    130                 135                 140

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
145                 150                 155                 160

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
                165                 170                 175

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
            180                 185                 190

Pro Gly Gly Gly Gly Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val
        195                 200                 205

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
    210                 215                 220

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
225                 230                 235                 240

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
                245                 250                 255

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
            260                 265                 270

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
        275                 280                 285

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
    290                 295                 300

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
305                 310                 315                 320

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
                325                 330                 335
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Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
            340                 345                 350

Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr
        355                 360                 365

Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn
    370                 375                 380

Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His
385                 390                 395                 400

Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala
                405                 410                 415

Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe
            420                 425                 430

His Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr
        435                 440                 445

Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu
    450                 455                 460

Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu
465                 470                 475                 480

Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly
                485                 490                 495

Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe
            500                 505                 510

Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln
        515                 520                 525

Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu
    530                 535                 540

Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu
545                 550                 555                 560
```

Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr
565 570 575

His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile
580 585 590

Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr
595 600 605

Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser
610 615 620

Thr
625

<210> 154
<211> 1875
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 154
gacgagggta aggcatcatc tgccaagcag agattaaaat gtgcatcttt gcaaaaattt 60

ggagagagag cttttaaggc atgggctgtt gcccgactaa gccaaagatt cccaaaagcc 120

gaatttgctg aagtatccaa gctggtgact gatttgacta aagtacatac agaatgttgc 180

catggcgacc ttttagaatg tgctgatgac agagcagatt tggctaagta tatctgcgaa 240

aatcaagatt caatcagctc taagctgaag gaatgttgcg agaaaccact gttagaaaaa 300

tcgcattgta ttgctgaagt tgaaaatgat gagatgcctg ctgacttgcc ttctcttgcc 360

gctgattttg ttgagtcgaa ggatgtctgt aagaattatg ctgaagctaa agacgttttc 420

ctgggtatgt tcttatatga gtacgcaaga cgtcacccag attactctgt ggttctgcta 480

ctgagattgg ctaaaacata cgagacaacg ctggagaagt gctgtgctgc cgctgaccct 540

catgagtgct atgcaaaggt ttttgatgaa ttcaaaccag gaggcggagg atctacccag 600

aacaaggccc tgcccgagaa cgtgaagtac ggcatcgtgc tggatgccgg cagcagccac 660

accagcctgt acatctacaa gtggcctgcc gagaaagaaa acgacaccgg cgtggtgcat 720

caggtggaag agtgcagagt gaagggccct ggcatcagca agttcgtgca gaaagtgaac 780

gagatcggca tctacctgac cgactgcatg gaacgggcca gggaagtgat ccccagaagc 840

cagcaccagg aaacccccgt gtatctggga gccaccgccg gcatgagact gctgagaatg 900

gaaagcgagg aactggccga ccgggtgctg gacgtggtgg aaagaagcct gagcaactac 960

ccattcgatt ttcaaggcgc cagaatcatc accggccagg aagaaggcgc ctacggctgg 1020

atcaccatca actacctgct gggcaagttc agccagaaga atcaggaaac cttcggcgcc 1080

ctggacctgg gcggagcttc tacccaagtg accttcgtgc cccagaatca gaccatcgag 1140

agccccgaca acgccctgca gttccggctg tacggcaagg actacaatgt gtacacccac 1200

agctttctgt gctacggaaa ggaccaggct ctgtggcaga agctggccaa ggacatccag 1260

gtggccagca acgagatcct gcgggaccct tgcttccacc ccggctacaa gaaagtcgtg 1320

aacgtgtccg acctgtacaa gacccctgc accaagagat tcgagatgac cctgcccttc 1380

cagcagttcg agatccaggg catcggcaat taccagcagt gccaccagag catcctggaa 1440

ctgttcaaca ccagctactg cccctacagc cagtgcgcct tcaacggcat cttcctgcca 1500

cctctgcagg gggatttcgg cgccttcagc gccttctact tcgtgatgaa gttcctgaac 1560

ctgaccagcg agaaggtgtc ccaggaaaaa gtgacagaga tgatgaagaa gttctgcgcc 1620

cagccctggg aggaaatcaa gacctcctac gctggcgtga aagagaagta cctgagcgag 1680

tactgcttca gcggcaccta catcctgagc ctgctgctgc agggctacca cttcaccgcc 1740

gatagctggg agcacatcca cttcatcggc aagattcagg gcagcgacgc cggctggaca 1800

ctgggctaca tgctgaatct gaccaacatg atccccgccg agcagcccct gagcacacct 1860

ctgagccaca gcacc 1875

<210> 155
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 155
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

```
Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
            20                  25                  30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
        35                  40                  45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50                  55                  60

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65                  70                  75                  80

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
                85                  90                  95

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

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
        115                 120                 125

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
    130                 135                 140

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser
145                 150                 155                 160

Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp
                165                 170                 175

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

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

Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala
    210                 215                 220

Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile
225                 230                 235                 240
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Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val
                245                 250                 255

Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu
            260                 265                 270

Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys
        275                 280                 285

His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser
    290                 295                 300

Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe
305                 310                 315                 320

Gly Ala Phe Ser Ala Phe Tyr Ser Val Met Lys Phe Leu Asn Leu Thr
                325                 330                 335

Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe
            340                 345                 350

Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys
        355                 360                 365

Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser
    370                 375                 380

Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile
385                 390                 395                 400

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly
                405                 410                 415

Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser
            420                 425                 430

Thr Pro Leu Ser His Ser Thr
        435
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<210> 156
<211> 1317
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 156
acccagaaca aggccctgcc cgagaacgtg aagtacggca tcgtgctgga tgccggcagc 60

agccacacca gcctgtacat ctacaagtgg cctgccgaga aagaaaacga caccggcgtg 120

gtgcatcagg tggaagagtg cagagtgaag ggccctggca tcagcaagtt cgtgcagaaa 180

gtgaacgaga tcggcatcta cctgaccgac tgcatggaac gggccaggga agtgatcccc 240

agaagccagc accaggaaac ccccgtgtat ctgggagcca ccgccggcat gagactgctg 300

agaatggaaa gcgaggaact ggccgaccgg gtgctggacg tggtggaaag aagcctgagc 360

aactacccat tcgattttca aggcgccaga atcatcaccg gccaggaaga aggcgcctac 420

ggctggatca ccatcaacta cctgctgggc aagttcagcc agaagaccag atggttcagc 480

atcgtgccct acgagacaaa caatcaggaa accttcggcg ccctggacct gggcggagct 540

tctacccaag tgaccttcgt gccccagaat cagaccatcg agagccccga caacgccctg 600

cagttccggc tgtacggcaa ggactacaat gtgtacaccc acagctttct gtgctacgga 660

aaggaccagg ctctgtggca gaagctggcc aaggacatcc aggtggccag caacgagatc 720

ctgcgggacc cttgcttcca ccccggctac aagaaagtcg tgaacgtgtc cgacctgtac 780

aagacccccct gcaccaagag attcgagatg accctgccct tccagcagtt cgagatccag 840

ggcatcggca attaccagca gtgccaccag agcatcctgg aactgttcaa caccagctac 900

tgcccctaca gccagtgcgc cttcaacggc atcttcctgc cacctctgca gggggatttc 960

ggcgccttca gcgccttcta ctccgtgatg aagttcctga acctgaccag cgagaaggtg 1020

tcccaggaaa aagtgacaga gatgatgaag aagttctgcg cccagccctg ggaggaaatc 1080

aagacctcct acgctggcgt gaaagagaag tacctgagcg agtactgctt cagcggcacc 1140

tacatcctga gcctgctgct gcagggctac cacttcaccg ccgatagctg ggagcacatc 1200

cacttcatcg gcaagattca gggcagcgac gccggctgga cactgggcta catgctgaat 1260

ctgaccaaca tgatccccgc cgagcagccc ctgagcacac ctctgagcca cagcacc 1317

<210> 157
<211> 90
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 157
tcgcgatcct ggaaggcgtg cactgcgccc ctaccagcag cagcaccaag aaaacccagc 60

tgaccagcag cacccagaac aaggccctgc 90

<210> 158
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 158
tagaaggcac agtcgagg 18

<210> 159
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 159
ctggtcgcga tcctggaagg cgtgcactgc gcccctacca gcagcagcac ccagaacaag 60

gccctg 66

<210> 160
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 160
ctggtcgcga tcctggaagg cgtgcactgc gcccctacca gcagcagcac ccagaacaag 60

gccctg 66

<210> 161
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 161
ctggtcgcga tcctggaagg cgtgcactgc gcccctacca cccagaacaa ggccctg 57

<210> 162
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 162
ctggtcgcga tcctggaagg cgtgcactgc gcccctacca gcagcagcac caagaaaacc 60

cagaacaagg ccctg 75

<210> 163
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 163
ctggtcgcga tcctggaagg cgtgcactgc gcccctacca gcagcagcac caagaaaacc 60

cagctgaccc agaacaaggc cctg 84

<210> 164
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 164
ctggtcgcga tcctggaagg cgtgcactgc agcagcagca ccaagaaaac ccagctgacc 60

cagaacaagg ccctg 75

<210> 165
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 165
catacgattt aggtga 16

<210> 166
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 166
tagaaggcac agtcgagg 18

<210> 167
<211> 76
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 167
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15

Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
        35   40   45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
    50   55   60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly
65   70   75

<210> 168
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 168
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1   5   10   15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30

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

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95

Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 169
<211> 186
<212> PRT
<213> Homo sapiens

<400> 169
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1   5   10   15

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

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35   40   45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50   55   60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65   70   75   80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85   90   95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100   105   110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115   120   125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130   135   140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145   150   155   160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165   170   175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
            180   185

<210> 170
<211> 193
<212> PRT
<213> Homo sapiens

<400> 170
Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser

1 5 10 15

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
20 25 30

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
35 40 45

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
50 55 60

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
65 70 75 80

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
85 90 95

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
100 105 110

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

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
130 135 140

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
145 150 155 160

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
165 170 175

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
180 185 190

Pro

<210> 171
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 171
ctgccgagaa agaacaggac accggcgtgg 30

<210> 172
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 172
ccacgccggt gtcctgttct ttctcggcag 30

<210> 173
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 173
cgtgccccag aatcaggcca tcgagagcc 29

<210> 174
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 174
ggctctcgat ggcctgattc tggggcacg 29

<210> 175
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 175
ggctacaaga aagtcgtgca ggtgtccgac ctgtacaaga c 41

<210> 176
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 176
gtcttgtaca ggtcggacac ctgcacgact ttcttgtagc c 41

<210> 177
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 177
gcatcctgga actgttccag accagctact gcccc 35

<210> 178
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 178
ggggcagtag ctggtctgga acagttccag gatgc 35

<210> 179
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 179
ccgtgatgaa gttcctgcag ctgaccagcg agaag 35

<210> 180
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 180
cttctcgctg gtcagctgca ggaacttcat cacgg 35

<210> 181
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 181
cactgggcta catgctgcag ctgaccaaca tgatcc 36

<210> 182
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 182
ggatcatgtt ggtcagctgc agcatgtagc ccagtg 36

<210> 183
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 183
ctacatcctg agcctgctgc agcagggcta ccacttcac 39

<210> 184
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 184
gtgaagtggt agccctgctg cagcaggctc aggatgtag 39

<210> 185
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 185
gagaagtacc tgagcgagtt ttgcttcagc ggcacctaca tcc 43

<210> 186
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 186
ggatgtaggt gccgctgaag caaaactcgc tcaggtactt ctc 43

<210> 187
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 187
gttcgagatc cagggcaccg gcaattacca gcagtg 36

<210> 188
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 188
cactgctggt aattgccggt gccctggatc tcgaac 36

<210> 189
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 189
cgccgatagc tgggagcaca tccacttcat cggcaag 37

<210> 190
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 190
cttgccgatg aagtggatgt gctcccagct atcggcg 37

<210> 191
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 191
gagatcggca tctacctgac cgactgcatg gaacgggcca tggaagtgat ccccagaagc 60

cagcaccagg aaacccccgt gtatctggga gccaccgccg gcatgagact gctgagaatg 120

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 192
gagatcggca tctacctgac cgact 25

<210> 193
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 193
cattctcagc agtctcat 18

<210> 194
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 194
cttcagcgcc ttctactccg tgatgaagtt cctgaacctg accagcgaga aggtgtccca 60

ggaaaaagtg acagagatga tgaagaagtt ctgcgcccag ccctgggagg aaatcaagac 120

<210> 195

<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 195
cttcagcgcc ttctactcc 19

<210> 196
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 196
ggtcttgatt tcctcccag 19

<210> 197
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 197
ctgggaggaa atcaagacct cctacgctgg cgtgaaagag aagtacctga gcgagttctg 60

cttcagcggc acctacatcc tgagcctgct gctgcagggc taccacttca ccgccgata 119

<210> 198
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 198
ctgggaggaa atcaagacct cctacgctgg cgtgaaagag aagtacctga gcgagtactg 60

cttcagcggc acctacatcc tgagcctgct gcagcagggc taccacttca ccgccgata 119

<210> 199
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 199
ctgggaggaa atcaagacct cctacgctgg cgtgaaagag aagtacctga gcgagttctg 60

cttcagcggc acctacatcc tgagcctgct gcagcagggc taccacttca ccgccgata 119

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 200
ctgggaggaa atcaagacc 19

<210> 201
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 201
tatcggcggt gaagtggta 19

<210> 202
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 202
ctgggaggaa atcaagacct cctacgctgg cgtgaaagag aagtacctga gcgagtactg 60

cttcagcggc acctacatcc tgagcctgct gctgcagggc taccacttca ccgccgata 119

<210> 203
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 203
caccggccag gaagccggcg cctacg 26

<210> 204
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 204
cgtaggcgcc ggcttcctgg ccggtg 26

<210> 205
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 205
ggacctgggc ggagctgcta cccaagtgac cttc 34

<210> 206
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 206
gaaggtcact tgggtagcag ctccgcccag gtcc 34

<210> 207
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 207
ctggatcacc atcaactacc tgctgggcaa gttcagccag aagaccagat ggttcagcat 60

cgtgccctac gagacaaaca 80

<210> 208
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 208
tcacttgggt agaagctccg cccaggtcca gggcgccgaa ggtttcctga ttgtttgtct 60

cgtagggca 69

<210> 209
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 209
Ala Pro Thr Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
1 5 10 15

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
20 25 30

```
Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
        35                  40                  45

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
    50                  55                  60

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu
65                  70                  75                  80

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
                85                  90                  95

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

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
        115                 120                 125

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
    130                 135                 140

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln
145                 150                 155                 160

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
                165                 170                 175

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
            180                 185                 190

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
        195                 200                 205

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
    210                 215                 220

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
225                 230                 235                 240

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
                245                 250                 255
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Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
            260                 265                 270

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
        275                 280                 285

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
    290                 295                 300

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

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
                325                 330                 335

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
            340                 345                 350

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
        355                 360                 365

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
    370                 375                 380

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
385                 390                 395                 400

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
                405                 410                 415

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425                 430


<210> 210
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"
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<400> 210
gcccctacca cccagaacaa ggccctgccc gagaacgtga agtacggcat cgtgctggat 60

gccggcagca gccacaccag cctgtacatc tacaagtggc ctgccgagaa agaaaacgac 120

accggcgtgg tgcatcaggt ggaagagtgc agagtgaagg gccctggcat cagcaagttc 180

gtgcagaaag tgaacgagat cggcatctac ctgaccgact gcatggaacg ggccatggaa 240

gtgatcccca gaagccagca ccaggaaacc cccgtgtatc tgggagccac cgccggcatg 300

agactgctga gaatggaaag cgaggaactg gccgaccggg tgctggacgt ggtggaaaga 360

agcctgagca actacccatt cgattttcaa ggcgccagaa tcatcaccgg ccaggaagaa 420

ggcgcctacg gctggatcac catcaactac ctgctgggca agttcagcca gaagaatcag 480

gaaaccttcg gcgccctgga cctgggcgga gcttctaccc aagtgacctt cgtgccccag 540

aatcagacca tcgagagccc cgacaacgcc ctgcagttcc ggctgtacgg caaggactac 600

aatgtgtaca cccacagctt tctgtgctac ggaaaggacc aggctctgtg gcagaagctg 660

gccaaggaca tccaggtggc cagcaacgag atcctgcggg acccttgctt ccaccccggc 720

tacaagaaag tcgtgaacgt gtccgacctg tacaagaccc cctgcaccaa gagattcgag 780

atgaccctgc ccttccagca gttcgagatc cagggcatcg gcaattacca gcagtgccac 840

cagagcatcc tggaactgtt caacaccagc tactgcccct acagccagtg cgccttcaac 900

ggcatcttcc tgccacctct gcaggggggat ttcggcgcct tcagcgcctt ctacttcgtg 960

atgaagttcc tgaacctgac cagcgagaag gtgtcccagg aaaaagtgac agagatgatg 1020

aagaagttct gcgcccagcc ctgggaggaa atcaagacct cctacgctgg cgtgaaagag 1080

aagtacctga gcgagtactg cttcagcggc acctacatcc tgagcctgct gctgcagggc 1140

taccacttca ccgccgatag ctgggagcac atccacttca tcggcaagat tcagggcagc 1200

gacgccggct ggacactggg ctacatgctg aatctgacca acatgatccc cgccgagcag 1260

cccctgagca cacctctgag ccacagcacc 1290

<210> 211
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 211
Ala Pro Thr Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
1   5   10   15

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
            20   25   30

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
        35   40   45

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
    50   55   60

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu
65   70   75   80

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
                85   90   95

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

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
        115   120   125

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
    130   135   140

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln
145   150   155   160

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
                165   170   175

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
            180   185   190

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
        195   200   205

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
    210   215   220

```
Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
225                 230                 235                 240

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
                245                 250                 255

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

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
        275                 280                 285

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
    290                 295                 300

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

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
                325                 330                 335

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
            340                 345                 350

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Phe Cys Phe
        355                 360                 365

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
    370                 375                 380

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
385                 390                 395                 400

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
                405                 410                 415

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425                 430
```

<210> 212
<211> 1290
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 212
gcccctacca cccagaacaa ggccctgccc gagaacgtga agtacggcat cgtgctggat 60

gccggcagca gccacaccag cctgtacatc tacaagtggc ctgccgagaa agaaaacgac 120

accggcgtgg tgcatcaggt ggaagagtgc agagtgaagg gccctggcat cagcaagttc 180

gtgcagaaag tgaacgagat cggcatctac ctgaccgact gcatggaacg ggccatggaa 240

gtgatcccca gaagccagca ccaggaaacc cccgtgtatc tgggagccac cgccggcatg 300

agactgctga gaatggaaag cgaggaactg gccgaccggg tgctggacgt ggtggaaaga 360

agcctgagca actacccatt cgattttcaa ggcgccagaa tcatcaccgg ccaggaagaa 420

ggcgcctacg gctggatcac catcaactac ctgctgggca agttcagcca gaagaatcag 480

gaaaccttcg gcgccctgga cctgggcgga gcttctaccc aagtgacctt cgtgccccag 540

aatcagacca tcgagagccc cgacaacgcc ctgcagttcc ggctgtacgg caaggactac 600

aatgtgtaca cccacagctt tctgtgctac ggaaaggacc aggctctgtg gcagaagctg 660

gccaaggaca tccaggtggc cagcaacgag atcctgcggg acccttgctt ccaccccggc 720

tacaagaaag tcgtgaacgt gtccgacctg tacaagaccc cctgcaccaa gagattcgag 780

atgaccctgc ccttccagca gttcgagatc cagggcatcg gcaattacca gcagtgccac 840

cagagcatcc tggaactgtt caacaccagc tactgcccct acagccagtg cgccttcaac 900

ggcatcttcc tgccacctct gcaggggggat ttcggcgcct tcagcgcctt ctacttcgtg 960

atgaagttcc tgaacctgac cagcgagaag gtgtcccagg aaaaagtgac agagatgatg 1020

aagaagttct gcgcccagcc ctgggaggaa atcaagacct cctacgctgg cgtgaaagag 1080

aagtacctga gcgagttttg cttcagcggc acctacatcc tgagcctgct gctgcagggc 1140

taccacttca ccgccgatag ctgggagcac atccacttca tcggcaagat tcagggcagc 1200

gacgccggct ggacactggg ctacatgctg aatctgacca acatgatccc cgccgagcag 1260

cccctgagca cacctctgag ccacagcacc 1290

<210> 213
<211> 433
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 213
Ala Pro Thr Ser Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val
1 5 10 15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
20 25 30

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
35 40 45

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
50 55 60

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
65 70 75 80

Ala Met Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
85 90 95

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
100 105 110

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
115 120 125

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
130 135 140

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
145 150 155 160

Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr
165 170 175

Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn
180 185 190

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Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His
        195                 200                 205

Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala
    210                 215                 220

Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe
225                 230                 235                 240

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

Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu
            260                 265                 270

Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu
        275                 280                 285

Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly
    290                 295                 300

Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe
305                 310                 315                 320

Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln
                325                 330                 335

Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu
            340                 345                 350

Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu
        355                 360                 365

Phe Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr
    370                 375                 380

His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile
385                 390                 395                 400

Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr
                405                 410                 415
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Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser
420 425 430

Thr

<210> 214
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 214
gcccctacca gcagcagcac ccagaacaag gccctgcccg agaacgtgaa gtacggcatc 60

gtgctggatg ccggcagcag ccacaccagc ctgtacatct acaagtggcc tgccgagaaa 120

gaaaacgaca ccggcgtggt gcatcaggtg gaagagtgca gagtgaaggg ccctggcatc 180

agcaagttcg tgcagaaagt gaacgagatc ggcatctacc tgaccgactg catggaacgg 240

gccatggaag tgatccccag aagccagcac caggaaaccc ccgtgtatct gggagccacc 300

gccggcatga gactgctgag aatggaaagc gaggaactgg ccgaccgggt gctggacgtg 360

gtggaaagaa gcctgagcaa ctacccattc gattttcaag gcgccagaat catcaccggc 420

caggaagaag gcgcctacgg ctggatcacc atcaactacc tgctgggcaa gttcagccag 480

aagaatcagg aaaccttcgg cgccctggac ctgggcggag cttctaccca agtgaccttc 540

gtgccccaga atcagaccat cgagagcccc gacaacgccc tgcagttccg gctgtacggc 600

aaggactaca atgtgtacac ccacagcttt ctgtgctacg gaaaggacca ggctctgtgg 660

cagaagctgg ccaaggacat ccaggtggcc agcaacgaga tcctgcggga cccttgcttc 720

caccccggct acaagaaagt cgtgaacgtg tccgacctgt acaagacccc ctgcaccaag 780

agattcgaga tgaccctgcc cttccagcag ttcgagatcc agggcatcgg caattaccag 840

cagtgccacc agagcatcct ggaactgttc aacaccagct actgccccta cagccagtgc 900

gccttcaacg gcatcttcct gccacctctg caggggggatt tcggcgcctt cagcgccttc 960

tacttcgtga tgaagttcct gaacctgacc agcgagaagg tgtcccagga aaaagtgaca 1020

gagatgatga agaagttctg cgcccagccc tgggaggaaa tcaagacctc ctacgctggc 1080

gtgaaagaga agtacctgag cgagttctgc ttcagcggca cctacatcct gagcctgctg 1140

ctgcagggct accacttcac cgccgatagc tgggagcaca tccacttcat cggcaagatt 1200

cagggcagcg acgccggctg gacactgggc tacatgctga atctgaccaa catgatcccc 1260

gccgagcagc ccctgagcac acctctgagc cacagcacc 1299

<210> 215
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 215
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr
1 5 10 15

Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20 25 30

Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
35 40 45

Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
50 55 60

Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
65 70 75 80

Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu Val Ile Pro Arg
85 90 95

Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
100 105 110

Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp
115 120 125

Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
130 135 140

Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile

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145                 150                 155                 160

Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe Gly
                165                 170                 175

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

Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr
        195                 200                 205

Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys
    210                 215                 220

Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser
225                 230                 235                 240

Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val
                245                 250                 255

Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu
            260                 265                 270

Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr
        275                 280                 285

Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys
    290                 295                 300

Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln
305                 310                 315                 320

Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu
                325                 330                 335

Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met
            340                 345                 350

Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala
        355                 360                 365

Gly Val Asn Glu Lys Tyr Leu Ser Glu Phe Cys Phe Ser Gly Thr Tyr
```

370 375 380

Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp
385 390 395 400

Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp
405 410 415

Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln
420 425 430

Pro Leu Ser Thr Pro Leu Ser His Ser Thr
435 440

<210> 216
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 216
gcccctacca gcagcagcac caagaaaacc cagctgacca gcagcaccca gaacaaggcc 60

ctgcccgaga acgtgaagta cggcatcgtg ctggatgccg gcagcagcca caccagcctg 120

tacatctaca agtggcctgc cgagaaagaa aacgacaccg gcgtggtgca tcaggtggaa 180

gagtgcagag tgaagggccc tggcatcagc aagttcgtgc agaaagtgaa cgagatcggc 240

atctacctga ccgactgcat ggaacgggcc atggaagtga tccccagaag ccagcaccag 300

gaaaccccg tgtatctggg agccaccgcc ggcatgagac tgctgagaat ggaaagcgag 360

gaactggccg accgggtgct ggacgtggtg gaaagaagcc tgagcaacta cccattcgat 420

tttcaaggcg ccagaatcat caccggccag gaagaaggcg cctacggctg gatcaccatc 480

aactacctgc tgggcaagtt cagccagaag aatcaggaaa ccttcggcgc cctggacctg 540

ggcggagctt ctacccaagt gaccttcgtg ccccagaatc agaccatcga gagccccgac 600

aacgccctgc agttccggct gtacggcaag gactacaatg tgtacaccca cagctttctg 660

tgctacggaa aggaccaggc tctgtggcag aagctggcca aggacatcca ggtggccagc 720

aacgagatcc tgcgggaccc ttgcttccac cccggctaca agaaagtcgt gaacgtgtcc 780

gacctgtaca agacccccctg caccaagaga ttcgagatga ccctgccctt ccagcagttc 840

gagatccagg gcatcggcaa ttaccagcag tgccaccaga gcatcctgga actgttcaac 900

accagctact gcccctacag ccagtgcgcc ttcaacggca tcttcctgcc acctctgcag 960

ggggatttcg gcgccttcag cgccttctac ttcgtgatga agttcctgaa cctgaccagc 1020

gagaaggtgt cccaggaaaa agtgacagag atgatgaaga agttctgcgc ccaaccctgg 1080

gaggaaatca agacctccta cgctggcgtg aacgagaagt acctgagcga gttttgcttc 1140

agcggcacct acatcctgag cctgctgctg cagggctacc acttcaccgc cgatagctgg 1200

gagcacatcc acttcatcgg caagattcag ggcagcgacg ccggctggac actgggctac 1260

atgctgaatc tgaccaacat gatccccgcc gagcagcccc tgagcacacc tctgagccac 1320

agcacc 1326

<210> 217
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 217
Ala Pro Thr Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
1 5 10 15

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
20 25 30

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
35 40 45

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
50 55 60

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu
65 70 75 80

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
85 90 95

```
Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp
            100                 105                 110

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
        115                 120                 125

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
    130                 135                 140

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln
145                 150                 155                 160

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
                165                 170                 175

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
            180                 185                 190

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
        195                 200                 205

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
    210                 215                 220

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
225                 230                 235                 240

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
                245                 250                 255

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

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
        275                 280                 285

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
    290                 295                 300

Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
305                 310                 315                 320
```

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
325 330 335

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
340 345 350

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Phe Cys Phe
355 360 365

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr
370 375 380

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
385 390 395 400

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
405 410 415

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425 430

<210> 218
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 218
gcccctacca cccagaacaa ggccctgccc gagaacgtga agtacggcat cgtgctggat 60

gccggcagca gccacaccag cctgtacatc tacaagtggc ctgccgagaa agaaaacgac 120

accggcgtgg tgcatcaggt ggaagagtgc agagtgaagg gccctggcat cagcaagttc 180

gtgcagaaag tgaacgagat cggcatctac ctgaccgact gcatggaacg ggccatggaa 240

gtgatcccca gaagccagca ccaggaaacc cccgtgtatc tgggagccac cgccggcatg 300

agactgctga gaatggaaag cgaggaactg gccgaccggg tgctggacgt ggtggaaaga 360

agcctgagca actacccatt cgattttcaa ggcgccagaa tcatcaccgg ccaggaagaa 420

ggcgcctacg gctggatcac catcaactac ctgctgggca agttcagcca gaagaatcag 480

gaaaccttcg gcgccctgga cctgggcgga gcttctaccc aagtgacctt cgtgccccag 540

aatcagacca tcgagagccc cgacaacgcc ctgcagttcc ggctgtacgg caaggactac 600

aatgtgtaca cccacagctt tctgtgctac ggaaaggacc aggctctgtg gcagaagctg 660

gccaaggaca tccaggtggc cagcaacgag atcctgcggg acccttgctt ccaccccggc 720

tacaagaaag tcgtgaacgt gtccgacctg tacaagaccc cctgcaccaa gagattcgag 780

atgaccctgc ccttccagca gttcgagatc cagggcatcg gcaattacca gcagtgccac 840

cagagcatcc tggaactgtt caacaccagc tactgcccct acagccagtg cgccttcaac 900

ggcatcttcc tgccacctct gcaggggggat ttcggcgcct tcagcgcctt ctacttcgtg 960

atgaagttcc tgaacctgac cagcgagaag gtgtcccagg aaaaagtgac agagatgatg 1020

aagaagttct gcgcccagcc ctgggaggaa atcaagacct cctacgctgg cgtgaaagag 1080

aagtacctga gcgagttctg cttcagcggc acctacatcc tgagcctgct gcagcagggc 1140

taccacttca ccgccgatag ctgggagcac atccacttca tcggcaagat tcagggcagc 1200

gacgccggct ggacactggg ctacatgctg aatctgacca acatgatccc cgccgagcag 1260

cccctgagca cacctctgag ccacagcacc 1290

<210> 219
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 219
Ala Pro Thr Ser Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val
1 5 10 15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
20 25 30

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
35 40 45

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
50 55 60

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg

65 70 75 80

Ala Met Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
85 90 95

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
100 105 110

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
115 120 125

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
130 135 140

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
145 150 155 160

Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr
165 170 175

Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn
180 185 190

Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His
195 200 205

Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala
210 215 220

Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe
225 230 235 240

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

Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu
260 265 270

Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu
275 280 285

Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly

```
    290                 295                 300

Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe
305                 310                 315                 320

Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln
                325                 330                 335

Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu
            340                 345                 350

Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu
        355                 360                 365

Phe Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr
    370                 375                 380

His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile
385                 390                 395                 400

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

Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser
            420                 425                 430

Thr
```

<210> 220
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 220
gcccctacca gcagcagcac ccagaacaag gccctgcccg agaacgtgaa gtacggcatc 60

gtgctggatg ccggcagcag ccacaccagc ctgtacatct acaagtggcc tgccgagaaa 120

gaaaacgaca ccggcgtggt gcatcaggtg gaagagtgca gagtgaaggg ccctggcatc 180

agcaagttcg tgcagaaagt gaacgagatc ggcatctacc tgaccgactg catggaacgg 240

gccatggaag tgatccccag aagccagcac caggaaaccc ccgtgtatct gggagccacc 300

gccggcatga gactgctgag aatggaaagc gaggaactgg ccgaccgggt gctggacgtg 360

gtggaaagaa gcctgagcaa ctacccattc gattttcaag gcgccagaat catcaccggc 420

caggaagaag gcgcctacgg ctggatcacc atcaactacc tgctgggcaa gttcagccag 480

aagaatcagg aaaccttcgg cgccctggac ctgggcggag cttctaccca agtgaccttc 540

gtgccccaga atcagaccat cgagagcccc gacaacgccc tgcagttccg gctgtacggc 600

aaggactaca atgtgtacac ccacagcttt ctgtgctacg gaaaggacca ggctctgtgg 660

cagaagctgg ccaaggacat ccaggtggcc agcaacgaga tcctgcggga cccttgcttc 720

caccccggct acaagaaagt cgtgaacgtg tccgacctgt acaagacccc ctgcaccaag 780

agattcgaga tgaccctgcc cttccagcag ttcgagatcc agggcatcgg caattaccag 840

cagtgccacc agagcatcct ggaactgttc aacaccagct actgccccta cagccagtgc 900

gccttcaacg gcatcttcct gccacctctg caggggggatt tcggcgcctt cagcgccttc 960

tacttcgtga tgaagttcct gaacctgacc agcgagaagg tgtcccagga aaaagtgaca 1020

gagatgatga agaagttctg cgcccagccc tgggaggaaa tcaagacctc ctacgctggc 1080

gtgaaagaga agtacctgag cgagttctgc ttcagcggca cctacatcct gagcctgctg 1140

cagcagggct accacttcac cgccgatagc tgggagcaca tccacttcat cggcaagatt 1200

cagggcagcg acgccggctg gacactgggc tacatgctga atctgaccaa catgatcccc 1260

gccgagcagc ccctgagcac acctctgagc cacagcacc 1299

<210> 221
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 221
Ala Pro Thr Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
1 5 10 15

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
20 25 30

```
Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
        35                  40                  45

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
    50                  55                  60

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu
65                  70                  75                  80

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
                85                  90                  95

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

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
        115                 120                 125

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
    130                 135                 140

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln
145                 150                 155                 160

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
                165                 170                 175

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
            180                 185                 190

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
        195                 200                 205

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
    210                 215                 220

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
225                 230                 235                 240

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
                245                 250                 255
```

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

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
        275                 280                 285

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
    290                 295                 300

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

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
                325                 330                 335

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
            340                 345                 350

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
        355                 360                 365

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
    370                 375                 380

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
385                 390                 395                 400

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
                405                 410                 415

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425                 430


<210> 222
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"
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<400> 222
gcccctacca cccagaacaa ggccctgccc gagaacgtga agtacggcat cgtgctggat 60

gccggcagca gccacaccag cctgtacatc tacaagtggc ctgccgagaa agaaaacgac 120

accggcgtgg tgcatcaggt ggaagagtgc agagtgaagg gccctggcat cagcaagttc 180

gtgcagaaag tgaacgagat cggcatctac ctgaccgact gcatggaacg ggccatggaa 240

gtgatcccca gaagccagca ccaggaaacc cccgtgtatc tgggagccac cgccggcatg 300

agactgctga gaatggaaag cgaggaactg gccgaccggg tgctggacgt ggtggaaaga 360

agcctgagca actacccatt cgattttcaa ggcgccagaa tcatcaccgg ccaggaagaa 420

ggcgcctacg gctggatcac catcaactac ctgctgggca agttcagcca gaagaatcag 480

gaaaccttcg gcgccttgga cctgggcgga gcttctaccc aagtgacctt cgtgccccag 540

aatcagacca tcgagagccc cgacaacgcc ctgcagttcc ggctgtacgg caaggactac 600

aatgtgtaca cccacagctt tctgtgctac ggaaaggacc aggctctgtg gcagaagctg 660

gccaaggaca tccaggtggc cagcaacgag atcctgcggg acccttgctt ccaccccggc 720

tacaagaaag tcgtgaacgt gtccgacctg tacaagaccc cctgcaccaa gagattcgag 780

atgaccctgc ccttccagca gttcgagatc cagggcatcg gcaattacca gcagtgccac 840

cagagcatcc tggaactgtt caacaccagc tactgcccct acagccagtg cgccttcaac 900

ggcatcttcc tgccacctct gcaggggggat ttcggcgcct tcagcgcctt ctactccgtg 960

atgaagttcc tgaacctgac cagcgagaag gtgtcccagg aaaaagtgac agagatgatg 1020

aagaagttct gcgcccagcc ctgggaggaa atcaagacct cctacgctgg cgtgaaagag 1080

aagtacctga gcgagtactg cttcagcggc acctacatcc tgagcctgct gctgcagggc 1140

taccacttca ccgccgatag ctgggagcac atccacttca tcggcaagat tcagggcagc 1200

gacgccggct ggacactggg ttacatgctg aatctgacca acatgatccc cgccgagcag 1260

cccctgagca cacctctgag ccacagcacc 1290

<210> 223
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 223
Ala Pro Thr Ser Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val
1   5   10   15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
            20   25   30

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
        35   40   45

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
    50   55   60

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
65   70   75   80

Ala Met Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
                85   90   95

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
            100   105   110

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
        115   120   125

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
    130   135   140

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
145   150   155   160

Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr
                165   170   175

Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn
            180   185   190

Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His
        195   200   205

Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala
    210   215   220

```
Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe
225                 230                 235                 240

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

Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu
            260                 265                 270

Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu
        275                 280                 285

Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly
    290                 295                 300

Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe
305                 310                 315                 320

Tyr Ser Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln
                325                 330                 335

Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu
            340                 345                 350

Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu
        355                 360                 365

Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr
    370                 375                 380

His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile
385                 390                 395                 400

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

Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser
            420                 425                 430

Thr
```

<210> 224
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 224
gcccctacca gcagcagcac ccagaacaag gccctgcccg agaacgtgaa gtacggcatc 60

gtgctggatg ccggcagcag ccacaccagc ctgtacatct acaagtggcc tgccgagaaa 120

gaaaacgaca ccggcgtggt gcatcaggtg gaagagtgca gagtgaaggg ccctggcatc 180

agcaagttcg tgcagaaagt gaacgagatc ggcatctacc tgaccgactg catggaacgg 240

gccatggaag tgatccccag aagccagcac caggaaaccc ccgtgtatct gggagccacc 300

gccggcatga gactgctgag aatggaaagc gaggaactgg ccgaccgggt gctggacgtg 360

gtggaaagaa gcctgagcaa ctacccattc gattttcaag gcgccagaat catcaccggc 420

caggaagaag gcgcctacgg ctggatcacc atcaactacc tgctgggcaa gttcagccag 480

aagaatcagg aaaccttcgg cgccttggac ctgggcggag cttctaccca agtgaccttc 540

gtgccccaga atcagaccat cgagagcccc gacaacgccc tgcagttccg gctgtacggc 600

aaggactaca atgtgtacac ccacagcttt ctgtgctacg gaaaggacca ggctctgtgg 660

cagaagctgg ccaaggacat ccaggtggcc agcaacgaga tcctgcggga cccttgcttc 720

caccccggct acaagaaagt cgtgaacgtg tccgacctgt acaagacccc ctgcaccaag 780

agattcgaga tgaccctgcc cttccagcag ttcgagatcc agggcatcgg caattaccag 840

cagtgccacc agagcatcct ggaactgttc aacaccagct actgccccta cagccagtgc 900

gccttcaacg gcatcttcct gccacctctg caggggggatt tcggcgcctt cagcgccttc 960

tactccgtga tgaagttcct gaacctgacc agcgagaagg tgtcccagga aaaagtgaca 1020

gagatgatga agaagttctg cgcccagccc tgggaggaaa tcaagacctc ctacgctggc 1080

gtgaaagaga agtacctgag cgagtactgc ttcagcggca cctacatcct gagcctgctg 1140

ctgcagggct accacttcac cgccgatagc tgggagcaca tccacttcat cggcaagatt 1200

cagggcagcg acgccggctg gacactgggt tacatgctga atctgaccaa catgatcccc 1260

gccgagcagc ccctgagcac acctctgagc cacagcacc 1299

<210> 225
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 225
Ala Pro Thr Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
1 5 10 15

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
20 25 30

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
35 40 45

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
50 55 60

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu
65 70 75 80

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
85 90 95

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

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
115 120 125

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
130 135 140

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln
145 150 155 160

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
165 170 175

```
Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
            180                 185                 190

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
        195                 200                 205

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
    210                 215                 220

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
225                 230                 235                 240

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
                245                 250                 255

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

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
        275                 280                 285

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
    290                 295                 300

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

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
                325                 330                 335

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
            340                 345                 350

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Phe Cys Phe
        355                 360                 365

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr
    370                 375                 380

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
385                 390                 395                 400
```

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
405 410 415

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425 430

<210> 226
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 226
gcccctacca cccagaacaa ggccctgccc gagaacgtga agtacggcat cgtgctggat 60

gccggcagca gccacaccag cctgtacatc tacaagtggc ctgccgagaa agaaaacgac 120

accggcgtgg tgcatcaggt ggaagagtgc agagtgaagg gccctggcat cagcaagttc 180

gtgcagaaag tgaacgagat cggcatctac ctgaccgact gcatggaacg ggccagggaa 240

gtgatcccca gaagccagca ccaggaaacc cccgtgtatc tgggagccac cgccggcatg 300

agactgctga gaatggaaag cgaggaactg gccgaccggg tgctggacgt ggtggaaaga 360

agcctgagca actacccatt cgattttcaa ggcgccagaa tcatcaccgg ccaggaagaa 420

ggcgcctacg gctggatcac catcaactac ctgctgggca agttcagcca gaagaatcag 480

gaaaccttcg gcgccctgga cctgggcgga gcttctaccc aagtgacctt cgtgccccag 540

aatcagacca tcgagagccc cgacaacgcc ctgcagttcc ggctgtacgg caaggactac 600

aatgtgtaca cccacagctt tctgtgctac ggaaaggacc aggctctgtg gcagaagctg 660

gccaaggaca tccaggtggc cagcaacgag atcctgcggg acccttgctt ccaccccggc 720

tacaagaaag tcgtgaacgt gtccgacctg tacaagaccc cctgcaccaa gagattcgag 780

atgaccctgc ccttccagca gttcgagatc cagggcatcg gcaattacca gcagtgccac 840

cagagcatcc tggaactgtt caacaccagc tactgcccct acagccagtg cgccttcaac 900

ggcatcttcc tgccacctct gcaggggggat ttcggcgcct tcagcgcctt ctacttcgtg 960

atgaagttcc tgaacctgac cagcgagaag gtgtcccagg aaaaagtgac agagatgatg 1020

aagaagttct gcgcccagcc ctgggaggaa atcaagacct cctacgctgg cgtgaaagag 1080

aagtacctga gcgagttttg cttcagcggc acctacatcc tgagcctgct gcagcagggc 1140

taccacttca ccgccgatag ctgggagcac atccacttca tcggcaagat tcagggcagc 1200

gacgccggct ggacactggg ctacatgctg aatctgacca acatgatccc cgccgagcag 1260

cccctgagca cacctctgag ccacagcacc 1290

<210> 227
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 227
Ala Pro Thr Ser Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val
1 5 10 15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
20 25 30

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
35 40 45

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
50 55 60

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
65 70 75 80

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
85 90 95

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
100 105 110

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
115 120 125

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
130 135 140

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln

```
145                 150                 155                 160

Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr
                165                 170                 175

Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn
            180                 185                 190

Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His
        195                 200                 205

Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala
    210                 215                 220

Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe
225                 230                 235                 240

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

Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu
            260                 265                 270

Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu
        275                 280                 285

Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly
    290                 295                 300

Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe
305                 310                 315                 320

Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln
                325                 330                 335

Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu
            340                 345                 350

Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu
        355                 360                 365

Phe Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr
```

```
    370                 375                 380

His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile
385                 390                 395                 400

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

Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser
            420                 425                 430

Thr
```

<210> 228
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 228
gcccctacca gcagcagcac ccagaacaag gccctgcccg agaacgtgaa gtacggcatc 60

gtgctggatg ccggcagcag ccacaccagc ctgtacatct acaagtggcc tgccgagaaa 120

gaaaacgaca ccggcgtggt gcatcaggtg gaagagtgca gagtgaaggg ccctggcatc 180

agcaagttcg tgcagaaagt gaacgagatc ggcatctacc tgaccgactg catggaacgg 240

gccagggaag tgatccccag aagccagcac caggaaaccc ccgtgtatct gggagccacc 300

gccggcatga gactgctgag aatggaaagc gaggaactgg ccgaccgggt gctggacgtg 360

gtggaaagaa gcctgagcaa ctacccattc gattttcaag gcgccagaat catcaccggc 420

caggaagaag gcgcctacgg ctggatcacc atcaactacc tgctgggcaa gttcagccag 480

aagaatcagg aaaccttcgg cgccctggac ctgggcggag cttctaccca agtgaccttc 540

gtgccccaga atcagaccat cgagagcccc gacaacgccc tgcagttccg gctgtacggc 600

aaggactaca atgtgtacac ccacagcttt ctgtgctacg gaaaggacca ggctctgtgg 660

cagaagctgg ccaaggacat ccaggtggcc agcaacgaga tcctgcggga cccttgcttc 720

caccccggct acaagaaagt cgtgaacgtg tccgacctgt acaagacccc ctgcaccaag 780

agattcgaga tgaccctgcc cttccagcag ttcgagatcc agggcatcgg caattaccag 840

cagtgccacc agagcatcct ggaactgttc aacaccagct actgccccta cagccagtgc 900

gccttcaacg gcatcttcct gccacctctg caggggggatt tcggcgcctt cagcgccttc 960

tacttcgtga tgaagttcct gaacctgacc agcgagaagg tgtcccagga aaaagtgaca 1020

gagatgatga agaagttctg cgcccagccc tgggaggaaa tcaagacctc ctacgctggc 1080

gtgaaagaga agtacctgag cgagttttgc ttcagcggca cctacatcct gagcctgctg 1140

cagcagggct accacttcac cgccgatagc tgggagcaca tccacttcat cggcaagatt 1200

cagggcagcg acgccggctg gacactgggc tacatgctga atctgaccaa catgatcccc 1260

gccgagcagc ccctgagcac acctctgagc cacagcacc 1299

<210> 229
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 229
Ala Pro Thr Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
1 5 10 15

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
20 25 30

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
35 40 45

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
50 55 60

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu
65 70 75 80

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
85 90 95

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

```
Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
        115                 120                 125

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
    130                 135                 140

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln
145                 150                 155                 160

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
                165                 170                 175

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
            180                 185                 190

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
        195                 200                 205

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
    210                 215                 220

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
225                 230                 235                 240

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
                245                 250                 255

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

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
        275                 280                 285

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
    290                 295                 300

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

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
                325                 330                 335
```

```
Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
            340                 345                 350

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
        355                 360                 365

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
    370                 375                 380

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
385                 390                 395                 400

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
                405                 410                 415

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425                 430
```

<210> 230
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 230
```
gcccctacca cccagaacaa ggccctgccc gagaacgtga agtacggcat cgtgctggac       60

gccggctcct cccacacctc cctgtacatc tacaagtggc ctgccgagaa agaaaacgac      120

accggcgtgg tgcaccaagt ggaagagtgc agagtgaagg gccccggcat ctccaagttc      180

gtgcagaaag tgaacgagat cggcatctac ctgaccgact gcatggaacg ggccagagaa      240

gtgatccctc ggtcccagca ccaggaaacc cctgtctacc tgggcgccac cgccggcatg      300

cggctgctgc ggatggaatc cgaggaactg gccgaccggg tgctggacgt ggtggaacgg      360

tccctgtcca actacccatt cgattttcaa ggcgccagaa tcatcaccgg ccaggaagag      420

ggcgcctacg gctggatcac catcaactac ctgctgggca agttctccca gaagaatcag      480

gaaaccttcg gcgccctgga cctgggcgga gccagcaccc aagtcacatt cgtgccccag      540

aaccagacca tcgagagccc cgacaacgcc ctgcagttcc ggctgtacgg caaggactac      600
```

aacgtgtaca cccacagctt tctgtgctac ggcaaggacc aggccctgtg gcagaagctg 660

gccaaggaca tccaagtggc ctccaacgag atcctgcggg acccctgctt ccaccccggc 720

tacaagaaag tggtcaacgt gtccgacctg tacaagaccc cttgcaccaa gagattcgag 780

atgaccctgc ccttccagca gttcgagatc cagggcatcg gcaactacca gcagtgccac 840

cagtccatcc tggaactgtt caacacctcc tactgccct actcccagtg cgccttcaac 900

ggcatcttcc tgcctccact gcagggcgac ttcggcgcct tctccgcctt ctactccgtg 960

atgaagttcc tgaacctgac ctccgagaaa gtgtcccagg aaaaagtgac cgagatgatg 1020

aagaagttct gcgcccagcc ctgggaggaa atcaagacct cctacgctgg cgtgaaagag 1080

aagtacctgt ccgagtactg cttctccggc acctacatcc tgtccctgct gctgcagggc 1140

taccacttca ccgccgacag ctgggagcac atccacttca tcggcaagat ccagggatcc 1200

gacgctggct ggaccctggg ctacatgctg aatctgacca acatgatccc cgccgagcag 1260

cccctgtcca cccctctgtc tcactccacc 1290

<210> 231
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 231
Ala Pro Thr Ser Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val
1 5 10 15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
20 25 30

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
35 40 45

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
50 55 60

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
65 70 75 80

```
Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
                85                  90                  95

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
            100                 105                 110

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
        115                 120                 125

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
    130                 135                 140

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
145                 150                 155                 160

Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr
                165                 170                 175

Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn
            180                 185                 190

Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His
        195                 200                 205

Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala
    210                 215                 220

Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe
225                 230                 235                 240

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

Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu
            260                 265                 270

Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu
        275                 280                 285

Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly
    290                 295                 300
```

Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe
305 310 315 320

Tyr Ser Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln
325 330 335

Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu
340 345 350

Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu
355 360 365

Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr
370 375 380

His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile
385 390 395 400

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

Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser
420 425 430

Thr

<210> 232
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 232
gcccctacca gcagcagcac ccagaacaag gccctgcccg agaacgtgaa gtacggcatc 60

gtgctggatg ccggcagcag ccacaccagc ctgtacatct acaagtggcc tgccgagaaa 120

gaaaacgaca ccggcgtggt gcatcaggtg gaagagtgca gagtgaaggg ccctggcatc 180

agcaagttcg tgcagaaagt gaacgagatc ggcatctacc tgaccgactg catggaacgg 240

gccagggaag tgatccccag aagccagcac caggaaaccc ccgtgtatct gggagccacc 300

gccggcatga gactgctgag aatggaaagc gaggaactgg ccgaccgggt gctggacgtg 360

gtggaaagaa gcctgagcaa ctacccattc gattttcaag gcgccagaat catcaccggc 420

caggaagaag gcgcctacgg ctggatcacc atcaactacc tgctgggcaa gttcagccag 480

aagaatcagg aaaccttcgg cgccttggac ctgggcggag cttctaccca agtgaccttc 540

gtgccccaga atcagaccat cgagagcccc gacaacgccc tgcagttccg gctgtacggc 600

aaggactaca atgtgtacac ccacagcttt ctgtgctacg gaaaggacca ggctctgtgg 660

cagaagctgg ccaaggacat ccaggtggcc agcaacgaga tcctgcggga cccttgcttc 720

caccccggct acaagaaagt cgtgaacgtg tccgacctgt acaagacccc ctgcaccaag 780

agattcgaga tgaccctgcc cttccagcag ttcgagatcc agggcatcgg caattaccag 840

cagtgccacc agagcatcct ggaactgttc aacaccagct actgccccta cagccagtgc 900

gccttcaacg gcatcttcct gccacctctg caggggggatt tcggcgcctt cagcgccttc 960

tactccgtga tgaagttcct gaacctgacc agcgagaagg tgtcccagga aaaagtgaca 1020

gagatgatga agaagttctg cgcccagccc tgggaggaaa tcaagacctc ctacgctggc 1080

gtgaaagaga agtacctgag cgagtactgc ttcagcggca cctacatcct gagcctgctg 1140

ctgcagggct accacttcac cgccgatagc tgggagcaca tccacttcat cggcaagatt 1200

cagggcagcg acgccggctg gacactgggt tacatgctga atctgaccaa catgatcccc 1260

gccgagcagc ccctgagcac acctctgagc cacagcacc 1299

<210> 233
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 233
Ala Pro Thr Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
1 5 10 15

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
20 25 30

```
Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
        35                  40                  45

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
    50                  55                  60

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Met Glu
65                  70                  75                  80

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
                85                  90                  95

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

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
        115                 120                 125

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
    130                 135                 140

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln
145                 150                 155                 160

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
                165                 170                 175

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
            180                 185                 190

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
        195                 200                 205

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
    210                 215                 220

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
225                 230                 235                 240

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
                245                 250                 255
```

```
Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
            260                 265                 270


Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
        275                 280                 285


Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
    290                 295                 300


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


Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
                325                 330                 335


Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
            340                 345                 350


Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
        355                 360                 365


Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr
    370                 375                 380


Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
385                 390                 395                 400


Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
                405                 410                 415


Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425                 430


<210> 234
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 234
gcccctacca cccagaacaa ggccctgccc gagaacgtga agtacggcat cgtgctggat       60
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gccggcagca gccacaccag cctgtacatc tacaagtggc ctgccgagaa agaaaacgac 120

accggcgtgg tgcatcaggt ggaagagtgc agagtgaagg gccctggcat cagcaagttc 180

gtgcagaaag tgaacgagat cggcatctac ctgaccgact gcatggaacg ggccatggaa 240

gtgatcccca gaagccagca ccaggaaacc cccgtgtatc tgggagccac cgccggcatg 300

agactgctga gaatggaaag cgaggaactg gccgaccggg tgctggacgt ggtggaaaga 360

agcctgagca actacccatt cgattttcaa ggcgccagaa tcatcaccgg ccaggaagaa 420

ggcgcctacg gctggatcac catcaactac ctgctgggca agttcagcca gaagaatcag 480

gaaaccttcg gcgccctgga cctgggcgga gcttctaccc aagtgacctt cgtgccccag 540

aatcagacca tcgagagccc cgacaacgcc ctgcagttcc ggctgtacgg caaggactac 600

aatgtgtaca cccacagctt tctgtgctac ggaaaggacc aggctctgtg gcagaagctg 660

gccaaggaca tccaggtggc cagcaacgag atcctgcggg acccttgctt ccaccccggc 720

tacaagaaag tcgtgaacgt gtccgacctg tacaagaccc cctgcaccaa gagattcgag 780

atgaccctgc ccttccagca gttcgagatc cagggcatcg gcaattacca gcagtgccac 840

cagagcatcc tggaactgtt caacaccagc tactgcccct acagccagtg cgccttcaac 900

ggcatcttcc tgccacctct gcaggggggat ttcggcgcct tcagcgcctt ctactccgtg 960

atgaagttcc tgaacctgac cagcgagaag gtgtcccagg aaaaagtgac agagatgatg 1020

aagaagttct gcgcccagcc ctgggaggaa atcaagacct cctacgctgg cgtgaaagag 1080

aagtacctga gcgagtactg cttcagcggc acctacatcc tgagcctgct gcagcagggc 1140

taccacttca ccgccgatag ctgggagcac atccacttca tcggcaagat tcagggcagc 1200

gacgccggct ggacactggg ctacatgctg aatctgacca acatgatccc cgccgagcag 1260

cccctgagca cacctctgag ccacagcacc 1290

<210> 235
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 235
Ala Pro Thr Ser Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val

```
1               5                   10                  15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
            20                  25                  30

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
        35                  40                  45

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
    50                  55                  60

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
65                  70                  75                  80

Ala Met Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
                85                  90                  95

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
            100                 105                 110

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
        115                 120                 125

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
    130                 135                 140

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
145                 150                 155                 160

Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr
                165                 170                 175

Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn
            180                 185                 190

Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His
        195                 200                 205

Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala
    210                 215                 220

Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe
```

225 230 235 240

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

Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu
260 265 270

Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu
275 280 285

Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly
290 295 300

Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe
305 310 315 320

Tyr Ser Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln
325 330 335

Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu
340 345 350

Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu
355 360 365

Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr
370 375 380

His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile
385 390 395 400

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

Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser
420 425 430

Thr

<210> 236

<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 236
gcccctacca gcagcagcac ccagaacaag gccctgcccg agaacgtgaa gtacggcatc 60

gtgctggatg ccggcagcag ccacaccagc ctgtacatct acaagtggcc tgccgagaaa 120

gaaaacgaca ccggcgtggt gcatcaggtg gaagagtgca gagtgaaggg ccctggcatc 180

agcaagttcg tgcagaaagt gaacgagatc ggcatctacc tgaccgactg catggaacgg 240

gccatggaag tgatccccag aagccagcac caggaaaccc ccgtgtatct gggagccacc 300

gccggcatga gactgctgag aatggaaagc gaggaactgg ccgaccgggt gctggacgtg 360

gtggaaagaa gcctgagcaa ctacccattc gattttcaag gcgccagaat catcaccggc 420

caggaagaag gcgcctacgg ctggatcacc atcaactacc tgctgggcaa gttcagccag 480

aagaatcagg aaaccttcgg cgccctggac ctgggcggag cttctaccca agtgaccttc 540

gtgccccaga atcagaccat cgagagcccc gacaacgccc tgcagttccg gctgtacggc 600

aaggactaca atgtgtacac ccacagcttt ctgtgctacg gaaaggacca ggctctgtgg 660

cagaagctgg ccaaggacat ccaggtggcc agcaacgaga tcctgcggga cccttgcttc 720

caccccggct acaagaaagt cgtgaacgtg tccgacctgt acaagacccc ctgcaccaag 780

agattcgaga tgaccctgcc cttccagcag ttcgagatcc agggcatcgg caattaccag 840

cagtgccacc agagcatcct ggaactgttc aacaccagct actgccccta cagccagtgc 900

gccttcaacg gcatcttcct gccacctctg caggggggatt tcggcgcctt cagcgccttc 960

tactccgtga tgaagttcct gaacctgacc agcgagaagg tgtcccagga aaaagtgaca 1020

gagatgatga agaagttctg cgcccagccc tgggaggaaa tcaagacctc ctacgctggc 1080

gtgaaagaga agtacctgag cgagtactgc ttcagcggca cctacatcct gagcctgctg 1140

cagcagggct accacttcac cgccgatagc tgggagcaca tccacttcat cggcaagatt 1200

cagggcagcg acgccggctg gacactgggc tacatgctga atctgaccaa catgatcccc 1260

gccgagcagc ccctgagcac acctctgagc cacagcacc 1299

<210> 237

<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 237
Ala Pro Thr Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
1 5 10 15

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
20 25 30

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
35 40 45

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
50 55 60

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu
65 70 75 80

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
85 90 95

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

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
115 120 125

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
130 135 140

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln
145 150 155 160

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
165 170 175

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
180 185 190

```
Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
        195                 200                 205

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
    210                 215                 220

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
225                 230                 235                 240

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
                245                 250                 255

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

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
        275                 280                 285

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
    290                 295                 300

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

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
                325                 330                 335

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
            340                 345                 350

Thr Ser Tyr Ala Gly Val Asn Glu Lys Tyr Leu Ser Glu Phe Cys Phe
        355                 360                 365

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
    370                 375                 380

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
385                 390                 395                 400

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
                405                 410                 415
```

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
420 425 430

<210> 238
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 238
gcccctacca cccagaacaa ggccctgccc gagaacgtga agtacggcat cgtgctggat 60

gccggcagca gccacaccag cctgtacatc tacaagtggc ctgccgagaa agaaaacgac 120

accggcgtgg tgcatcaggt ggaagagtgc agagtgaagg gccctggcat cagcaagttc 180

gtgcagaaag tgaacgagat cggcatctac ctgaccgact gcatggaacg ggccagggaa 240

gtgatcccca gaagccagca ccaggaaacc cccgtgtatc tgggagccac cgccggcatg 300

agactgctga gaatggaaag cgaggaactg gccgaccggg tgctggacgt ggtggaaaga 360

agcctgagca actacccatt cgattttcaa ggcgccagaa tcatcaccgg ccaggaagaa 420

ggcgcctacg gctggatcac catcaactac ctgctgggca agttcagcca gaagaatcag 480

gaaaccttcg gcgccctgga cctgggcgga gcttctaccc aagtgacctt cgtgccccag 540

aatcagacca tcgagagccc cgacaacgcc ctgcagttcc ggctgtacgg caaggactac 600

aatgtgtaca cccacagctt tctgtgctac ggaaaggacc aggctctgtg gcagaagctg 660

gccaaggaca tccaggtggc cagcaacgag atcctgcggg acccttgctt ccaccccggc 720

tacaagaaag tcgtgaacgt gtccgacctg tacaagaccc cctgcaccaa gagattcgag 780

atgaccctgc ccttccagca gttcgagatc cagggcatcg gcaattacca gcagtgccac 840

cagagcatcc tggaactgtt caacaccagc tactgcccct acagccagtg cgccttcaac 900

ggcatcttcc tgccacctct gcaggggggat ttcggcgcct tcagcgcctt ctacttcgtg 960

atgaagttcc tgaacctgac cagcgagaag gtgtcccagg aaaaagtgac agagatgatg 1020

aagaagttct gcgcccaacc ctgggaggaa atcaagacct cctacgctgg cgtgaacgag 1080

aagtacctga gcgagttttg cttcagcggc acctacatcc tgagcctgct gctgcagggc 1140

taccacttca ccgccgatag ctgggagcac atccacttca tcggcaagat tcagggcagc 1200

gacgccggct ggacactggg ctacatgctg aatctgacca acatgatccc cgccgagcag 1260

cccctgagca cacctctgag ccacagcacc 1290

<210> 239
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 239
Ala Pro Thr Ser Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val
1 5 10 15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
20 25 30

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
35 40 45

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
50 55 60

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
65 70 75 80

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
85 90 95

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
100 105 110

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
115 120 125

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
130 135 140

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
145 150 155 160

```
Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr
                165                 170                 175

Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn
            180                 185                 190

Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His
        195                 200                 205

Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala
    210                 215                 220

Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe
225                 230                 235                 240

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

Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu
            260                 265                 270

Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu
        275                 280                 285

Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly
    290                 295                 300

Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe
305                 310                 315                 320

Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln
                325                 330                 335

Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu
            340                 345                 350

Glu Ile Lys Thr Ser Tyr Ala Gly Val Asn Glu Lys Tyr Leu Ser Glu
        355                 360                 365

Phe Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr
    370                 375                 380
```

```
His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile
385                 390                 395                 400


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


Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser
            420                 425                 430


Thr
```

<210> 240
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 240
gcccctacca gcagcagcac ccagaacaag gccctgcccg agaacgtgaa gtacggcatc 60

gtgctggatg ccggcagcag ccacaccagc ctgtacatct acaagtggcc tgccgagaaa 120

gaaaacgaca ccggcgtggt gcatcaggtg gaagagtgca gagtgaaggg ccctggcatc 180

agcaagttcg tgcagaaagt gaacgagatc ggcatctacc tgaccgactg catggaacgg 240

gccagggaag tgatccccag aagccagcac caggaaaccc ccgtgtatct gggagccacc 300

gccggcatga gactgctgag aatggaaagc gaggaactgg ccgaccgggt gctggacgtg 360

gtggaaagaa gcctgagcaa ctacccattc gattttcaag gcgccagaat catcaccggc 420

caggaagaag gcgcctacgg ctggatcacc atcaactacc tgctgggcaa gttcagccag 480

aagaatcagg aaaccttcgg cgccctggac ctgggcggag cttctaccca agtgaccttc 540

gtgccccaga atcagaccat cgagagcccc gacaacgccc tgcagttccg gctgtacggc 600

aaggactaca atgtgtacac ccacagcttt ctgtgctacg gaaaggacca ggctctgtgg 660

cagaagctgg ccaaggacat ccaggtggcc agcaacgaga tcctgcggga cccttgcttc 720

caccccggct acaagaaagt cgtgaacgtg tccgacctgt acaagacccc ctgcaccaag 780

agattcgaga tgaccctgcc cttccagcag ttcgagatcc agggcatcgg caattaccag 840

cagtgccacc agagcatcct ggaactgttc aacaccagct actgccccta cagccagtgc 900

gccttcaacg gcatcttcct gccacctctg cagggggatt tcggcgcctt cagcgccttc 960

tacttcgtga tgaagttcct gaacctgacc agcgagaagg tgtcccagga aaaagtgaca 1020

gagatgatga agaagttctg cgcccaaccc tgggaggaaa tcaagacctc ctacgctggc 1080

gtgaacgaga agtacctgag cgagttttgc ttcagcggca cctacatcct gagcctgctg 1140

ctgcagggct accacttcac cgccgatagc tgggagcaca tccacttcat cggcaagatt 1200

cagggcagcg acgccggctg gacactgggc tacatgctga atctgaccaa catgatcccc 1260

gccgagcagc ccctgagcac acctctgagc cacagcacc 1299

<210> 241
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 241
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr
1 5 10 15

Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20 25 30

Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
35 40 45

Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
50 55 60

Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
65 70 75 80

Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg
85 90 95

Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
100 105 110

```
Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp
        115                 120                 125

Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
    130                 135                 140

Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile
145                 150                 155                 160

Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln Glu Thr Phe Gly
                165                 170                 175

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

Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr
        195                 200                 205

Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys
    210                 215                 220

Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser
225                 230                 235                 240

Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val
                245                 250                 255

Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu
            260                 265                 270

Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr
        275                 280                 285

Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys
    290                 295                 300

Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln
305                 310                 315                 320

Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu
                325                 330                 335
```

```
Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met
            340                 345                 350


Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala
        355                 360                 365


Gly Val Asn Glu Lys Tyr Leu Ser Glu Phe Cys Phe Ser Gly Thr Tyr
    370                 375                 380


Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp
385                 390                 395                 400


Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp
                405                 410                 415


Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln
            420                 425                 430


Pro Leu Ser Thr Pro Leu Ser His Ser Thr
        435                 440


<210> 242
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 242
gcccctacca gcagcagcac caagaaaacc cagctgacca gcagcaccca gaacaaggcc       60

ctgcccgaga acgtgaagta cggcatcgtg ctggatgccg gcagcagcca caccagcctg      120

tacatctaca agtggcctgc cgagaaagaa aacgacaccg gcgtggtgca tcaggtggaa      180

gagtgcagag tgaagggccc tggcatcagc aagttcgtgc agaaagtgaa cgagatcggc      240

atctacctga ccgactgcat ggaacgggcc agggaagtga tccccagaag ccagcaccag      300

gaaaccccg tgtatctggg agccaccgcc ggcatgagac tgctgagaat ggaaagcgag       360

gaactggccg accgggtgct ggacgtggtg gaaagaagcc tgagcaacta cccattcgat      420

tttcaaggcg ccagaatcat caccggccag gaagaaggcg cctacggctg gatcaccatc      480

aactacctgc tgggcaagtt cagccagaag aatcaggaaa ccttcggcgc cctggacctg      540
```

ggcggagctt ctacccaagt gaccttcgtg ccccagaatc agaccatcga gagccccgac 600

aacgccctgc agttccggct gtacggcaag gactacaatg tgtacaccca cagctttctg 660

tgctacggaa aggaccaggc tctgtggcag aagctggcca aggacatcca ggtggccagc 720

aacgagatcc tgcgggaccc ttgcttccac cccggctaca agaaagtcgt gaacgtgtcc 780

gacctgtaca agacccccctg caccaagaga ttcgagatga ccctgccctt ccagcagttc 840

gagatccagg gcatcggcaa ttaccagcag tgccaccaga gcatcctgga actgttcaac 900

accagctact gcccctacag ccagtgcgcc ttcaacggca tcttcctgcc acctctgcag 960

ggggatttcg gcgccttcag cgccttctac ttcgtgatga agttcctgaa cctgaccagc 1020

gagaaggtgt cccaggaaaa agtgacagag atgatgaaga agttctgcgc ccaaccctgg 1080

gaggaaatca agacctccta cgctggcgtg aacgagaagt acctgagcga gttttgcttc 1140

agcggcacct acatcctgag cctgctgctg cagggctacc acttcaccgc cgatagctgg 1200

gagcacatcc acttcatcgg caagattcag ggcagcgacg ccggctggac actgggctac 1260

atgctgaatc tgaccaacat gatccccgcc gagcagcccc tgagcacacc tctgagccac 1320

agcacc 1326

<210> 243
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 243
Ala Pro Thr Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
1 5 10 15

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
20 25 30

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
35 40 45

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
50 55 60

```
Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu
65                  70                  75                  80

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
                85                  90                  95

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

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
        115                 120                 125

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
    130                 135                 140

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Asn Gln
145                 150                 155                 160

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
                165                 170                 175

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
            180                 185                 190

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
        195                 200                 205

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
    210                 215                 220

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
225                 230                 235                 240

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
                245                 250                 255

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

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
        275                 280                 285
```

```
Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
    290                 295                 300

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

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
                325                 330                 335

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
            340                 345                 350

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
        355                 360                 365

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr His Phe Thr
    370                 375                 380

Ala Asp Ser Trp Glu Asp Ile His Phe Ile Gly Lys Ile Gln Gly Ser
385                 390                 395                 400

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
                405                 410                 415

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
            420                 425                 430
```

<210> 244
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 244
gcccctacca cccagaacaa ggccctgccc gagaacgtga agtacggcat cgtgctggat 60

gccggcagca gccacaccag cctgtacatc tacaagtggc ctgccgagaa agaaaacgac 120

accggcgtgg tgcatcaggt ggaagagtgc agagtgaagg gccctggcat cagcaagttc 180

gtgcagaaag tgaacgagat cggcatctac ctgaccgact gcatggaacg ggccagggaa 240

gtgatcccca gaagccagca ccaggaaacc cccgtgtatc tgggagccac cgccggcatg 300

agactgctga gaatggaaag cgaggaactg gccgaccggg tgctggacgt ggtggaaaga 360

agcctgagca actacccatt cgattttcaa ggcgccagaa tcatcaccgg ccaggaagaa 420

ggcgcctacg gctggatcac catcaactac ctgctgggca agttcagcca gaagaatcag 480

gaaaccttcg gcgccctgga cctgggcgga gcttctaccc aagtgacctt cgtgccccag 540

aatcagacca tcgagagccc cgacaacgcc ctgcagttcc ggctgtacgg caaggactac 600

aatgtgtaca cccacagctt tctgtgctac ggaaaggacc aggctctgtg gcagaagctg 660

gccaaggaca tccaggtggc cagcaacgag atcctgcggg acccttgctt ccaccccggc 720

tacaagaaag tcgtgaacgt gtccgacctg tacaagaccc cctgcaccaa gagattcgag 780

atgaccctgc ccttccagca gttcgagatc cagggcatcg gcaattacca gcagtgccac 840

cagagcatcc tggaactgtt caacaccagc tactgcccct acagccagtg cgccttcaac 900

ggcatcttcc tgccacctct gcaggggggat ttcggcgcct tcagcgcctt ctacttcgtg 960

atgaagttcc tgaacctgac cagcgagaag gtgtcccagg aaaaagtgac agagatgatg 1020

aagaagttct gcgcccagcc ctgggaggaa atcaagacct cctacgctgg cgtgaaagag 1080

aagtacctga gcgagtactg cttcagcggc acctacatcc tgagcctgct gcagcagggc 1140

taccacttca ccgccgatag ctgggaggac atccacttca tcggcaagat tcagggcagc 1200

gacgccggct ggacactggg ctacatgctg aatctgacca acatgatccc cgccgagcag 1260

cccctgagca cacctctgag ccacagcacc 1290

<210> 245
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 245
Ala Pro Thr Ser Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val
1 5 10 15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
20 25 30

```
Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
        35                  40                  45

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
    50                  55                  60

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
65                  70                  75                  80

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
                85                  90                  95

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
            100                 105                 110

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
        115                 120                 125

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
    130                 135                 140

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
145                 150                 155                 160

Lys Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr
                165                 170                 175

Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn
            180                 185                 190

Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His
        195                 200                 205

Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala
    210                 215                 220

Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe
225                 230                 235                 240

His Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr
                245                 250                 255
```

```
Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu
            260                 265                 270

Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu
        275                 280                 285

Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly
    290                 295                 300

Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe
305                 310                 315                 320

Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln
                325                 330                 335

Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu
            340                 345                 350

Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu
        355                 360                 365

Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gln Gly Tyr
    370                 375                 380

His Phe Thr Ala Asp Ser Trp Glu Asp Ile His Phe Ile Gly Lys Ile
385                 390                 395                 400

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

Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser
            420                 425                 430

Thr
```

<210> 246
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 246
gcccctacca gcagcagcac ccagaacaag gccctgcccg agaacgtgaa gtacggcatc 60

gtgctggatg ccggcagcag ccacaccagc ctgtacatct acaagtggcc tgccgagaaa 120

gaaaacgaca ccggcgtggt gcatcaggtg gaagagtgca gagtgaaggg ccctggcatc 180

agcaagttcg tgcagaaagt gaacgagatc ggcatctacc tgaccgactg catggaacgg 240

gccagggaag tgatccccag aagccagcac caggaaaccc ccgtgtatct gggagccacc 300

gccggcatga gactgctgag aatggaaagc gaggaactgg ccgaccgggt gctggacgtg 360

gtggaaagaa gcctgagcaa ctacccattc gattttcaag gcgccagaat catcaccggc 420

caggaagaag gcgcctacgg ctggatcacc atcaactacc tgctgggcaa gttcagccag 480

aagaatcagg aaaccttcgg cgccctggac ctgggcggag cttctaccca agtgaccttc 540

gtgccccaga atcagaccat cgagagcccc gacaacgccc tgcagttccg gctgtacggc 600

aaggactaca atgtgtacac ccacagcttt ctgtgctacg gaaaggacca ggctctgtgg 660

cagaagctgg ccaaggacat ccaggtggcc agcaacgaga tcctgcggga cccttgcttc 720

caccccggct acaagaaagt cgtgaacgtg tccgacctgt acaagacccc ctgcaccaag 780

agattcgaga tgaccctgcc cttccagcag ttcgagatcc agggcatcgg caattaccag 840

cagtgccacc agagcatcct ggaactgttc aacaccagct actgccccta cagccagtgc 900

gccttcaacg gcatcttcct gccacctctg caggggggatt tcggcgcctt cagcgccttc 960

tacttcgtga tgaagttcct gaacctgacc agcgagaagg tgtcccagga aaaagtgaca 1020

gagatgatga agaagttctg cgcccagccc tgggaggaaa tcaagacctc ctacgctggc 1080

gtgaaagaga agtacctgag cgagtactgc ttcagcggca cctacatcct gagcctgctg 1140

cagcagggct accacttcac cgccgatagc tgggaggaca tccacttcat cggcaagatt 1200

cagggcagcg acgccggctg gacactgggc tacatgctga atctgaccaa catgatcccc 1260

gccgagcagc ccctgagcac acctctgagc cacagcacc 1299

<210> 247
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 247
Glu Phe Arg His Asp Ser
1 5

<210> 248
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 248
gaattccggc acgacagc 18

<210> 249
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic 6xHis tag"

<400> 249
His His His His His His
1 5

<210> 250
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 250
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peptide"

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1 5