SEQUENCE LISTING

<110> VOYAGER THERAPEUTICS, INC.

<120> COMPOSITIONS AND METHODS OF TREATING AMYOTROPHIC LATERAL SCLEROSIS (ALS)

<130> 14482-164-228

<140> TBA
<141> On even date herewith

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<151> 2017-05-05

<150> US 62/507,927
<151> 2017-05-18

<150> US 62/520,100
<151> 2017-06-15

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<151> 2017-10-02

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Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


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


Thr Gly Glu Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190
```

```
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
```

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Ala Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620
```

```
Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 7
<211> 738
<212> PRT
<213> Adeno-associated virus 10

<400> 7

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
```

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270
```

```
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
```

```
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 8
<211> 258
<212> DNA
<213> Adeno-associated virus 11

<400> 8
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc 60

accagcaccc gaacctgggc cctgccaacc tacaacaacc acctctacaa acaaatctcc 120

agcgcttcaa cgggggccag caacgacaac cactactttg gctacagcac cccctggggg 180

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatc 240

aacaacaact ggggattc 258

<210> 9
<211> 255
<212> DNA
<213> Adeno-associated virus 12

<400> 9
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgaccg agtcattacc 60

accagcaccc ggacttgggc cctgcccacc tacaacaacc acctctacaa gcaaatctcc 120

agccaatcgg gtgccaccaa cgacaaccac tacttcggct acagcacccc ttgggggtat 180

tttgatttca acagattcca ctgccatttc tcaccacgtg actggcagcg actcatcaac 240

aacaactggg gattc 255

<210> 10
<211> 2208
<212> DNA
<213> Adeno-associated virus 2

<400> 10
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

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caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 11
<211> 735
<212> PRT
<213> Adeno-associated virus 2

<400> 11

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
```

```
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540
```

```
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 12
<211> 621
<212> PRT
<213> Adeno-associated virus 2

<400> 12

```
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                  10                  15

Gly His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85                  90                  95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165                 170                 175

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205
```

```
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275                 280                 285

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290                 295                 300

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

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430
```

```
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465                 470                 475                 480

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                 490                 495

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500                 505                 510

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515                 520                 525

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530                 535                 540

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545                 550                 555                 560

Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565                 570                 575

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
            580                 585                 590

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
        595                 600                 605

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
    610                 615                 620
```

<210> 13
<211> 4675
<212> DNA
<213> Adeno-associated virus 2

<400> 13
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag 180

ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat 240

gtggtcacgc tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga 300

ggtttgaacg cgcagccgcc atgccggggt tttacgagat tgtgattaag gtccccagcg 360

accttgacgg gcatctgccc ggcatttctg acagctttgt gaactgggtg gccgagaagg 420

aatgggagtt gccgccagat tctgacatgg atctgaatct gattgagcag gcacccctga 480

ccgtggccga gaagctgcag cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc 540

cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc 600

tcgtggaaac caccggggtg aaatccatgg ttttgggacg tttcctgagt cagattcgcg 660

aaaaactgat tcagagaatt taccgcggga tcgagccgac tttgccaaac tggttcgcgg 720

tcacaaagac cagaaatggc gccggaggcg ggaacaaggt ggtggatgag tgctacatcc 780

ccaattactt gctccccaaa acccagcctg agctccagtg ggcgtggact aatatggaac 840

agtatttaag cgcctgtttg aatctcacgg agcgtaaacg gttggtggcg cagcatctga 900

cgcacgtgtc gcagacgcag gagcagaaca aagagaatca gaatcccaat tctgatgcgc 960

cggtgatcag atcaaaaact tcagccaggt acatggagct ggtcgggtgg ctcgtggaca 1020

aggggattac ctcggagaag cagtggatcc aggaggacca ggcctcatac atctccttca 1080

atgcggcctc caactcgcgg tcccaaatca aggctgcctt ggacaatgcg ggaaagatta 1140

tgagcctgac taaaaccgcc cccgactacc tggtgggcca gcagcccgtg gaggacattt 1200

ccagcaatcg gatttataaa attttggaac taaacgggta cgatccccaa tatgcggctt 1260

ccgtctttct gggatgggcc acgaaaaagt tcggcaagag gaacaccatc tggctgtttg 1320

ggcctgcaac taccgggaag accaacatcg cggaggccat agcccacact gtgcccttct 1380

acgggtgcgt aaactggacc aatgagaact ttcccttcaa cgactgtgtc gacaagatgg 1440

tgatctggtg ggaggagggg aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc 1500

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ctcccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg aactcaacga 1620

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<212> PRT
<213> Adeno-associated virus 5

<400> 15

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


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


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg
    130                 135                 140


Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145                 150                 155                 160


Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
                165                 170                 175


Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
            180                 185                 190


Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
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        195                 200                 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
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Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225                 230                 235                 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
                245                 250                 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305                 310                 315                 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
                325                 330                 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
            340                 345                 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
        355                 360                 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
    370                 375                 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
                405                 410                 415
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Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
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Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
        435                 440                 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
    450                 455                 460

Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465                 470                 475                 480

Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met
                485                 490                 495

Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met
            500                 505                 510

Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met
        515                 520                 525

Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu
    530                 535                 540

Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn
545                 550                 555                 560

Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser
                565                 570                 575

Ser Thr Thr Ala Pro Thr Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val
            580                 585                 590

Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile
        595                 600                 605

Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala
    610                 615                 620

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys
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625 630 635 640

Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val
645 650 655

Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met
660 665 670

Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
675 680 685

Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro
690 695 700

Asp Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr
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Leu Thr Arg Pro Leu
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<210> 16
<211> 644
<212> PRT
<213> Artificial Sequence

<220>
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<400> 16

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Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
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Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

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

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
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            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

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

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
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Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Xaa Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480
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Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
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Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
500 505 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
515 520 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
530 535 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545 550 555 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
565 570 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
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Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
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Tyr Ser Glu Pro

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ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttctccc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacgccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 18
<211> 644
<212> PRT
<213> Artificial Sequence

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

<400> 18

Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Cys Leu Gln Glu Asp Thr
20 25 30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

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

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65 70 75 80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
85 90 95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
100 105 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Val Ala Gly Gly Gly
115 120 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
130 135 140

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

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

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Ser Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575
```

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

Tyr Ser Glu Pro

<210> 19
<211> 1933
<212> DNA
<213> Adeno-associated virus

<400> 19
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gccagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca cggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctgggccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gaatgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 20
<211> 644
<212> PRT
<213> Artificial Sequence

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

<400> 20

Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

```
Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20                  25                  30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35                  40                  45

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

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95

Gly Asp Ser Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
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225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

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

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445
```

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Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
            580                 585                 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625                 630                 635                 640

Tyr Ser Glu Pro
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<210> 21

<211> 1933
<212> DNA
<213> Adeno-associated virus

<400> 21
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gccagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca cggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctgggccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gaatgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 22
<211> 644
<212> PRT
<213> Artificial Sequence

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

<400> 22

Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
20 25 30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

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

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65 70 75 80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
85 90 95

Gly Asp Ser Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
100 105 110

```
Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320
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Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

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

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540
```

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545 550 555 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
565 570 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

Tyr Ser Glu Pro

<210> 23
<211> 1933
<212> DNA
<213> Adeno-associated virus

<400> 23
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aatagcgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggtgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

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ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagc ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 24
<211> 644
<212> PRT
<213> Artificial Sequence

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

<400> 24

Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1   5   10   15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20   25   30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35   40   45

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

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65   70   75   80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85   90   95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100   105   110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115   120   125

Ala Pro Met Ala Asp Asn Ser Glu Gly Ala Asp Gly Val Gly Asn Ala
    130   135   140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145   150   155   160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165   170   175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180   185   190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe

```
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

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

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415
```

```
Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Leu Ala Ser Phe Ile Thr
            580                 585                 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
```

625 630 635 640

Tyr Ser Glu Pro

<210> 25
<211> 1933
<212> DNA
<213> Adeno-associated virus

<400> 25
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggacc cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

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ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaaga ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 26
<211> 644
<212> PRT
<213> Artificial Sequence

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

<400> 26

Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
20 25 30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

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

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65 70 75 80

```
Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Pro Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

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

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510
```

```
Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Ile Ala Ser Phe Ile Thr
            580                 585                 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625                 630                 635                 640

Tyr Ser Glu Pro
```

<210> 27
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 27

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Thr Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
```

```
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala Arg Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460
```

```
Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Gly Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670
```

```
Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 28
<211> 3121
<212> DNA
<213> Adeno-associated virus

<400> 28

```
gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgactg       60

tgtcgacaag atggtgatct ggtgggagga ggggaagatg accgccaagg tcgtggagtc      120

ggccaaagcc attctcggag gaagcaaggt gcgcgtggac cagaaatgca agtcctcggc      180

ccagatagac ccgactcccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga      240

cgggaactca acgaccttcg aacaccagca gccgttgcaa gaccggatgt tcaaatttga      300

actcacccgc cgtctggatc atgactttgg gaaggtcacc aagcaggaag tcaaagactt      360

tttccggtgg gcaaaggatc acgtggttga ggtggagcac gaattctacg tcaaaaaggg      420

tggagccaag aaaagacccg cccccagtga cgcagatata agtgagccca aacgggtgcg      480

cgagtcagtt gcgcagccat cgacgtcaga cgcggaagct tcgatcaact acgcagacag      540

gtaccaaaac aaatgttctc gtcacgcggg catgaatctg atgctgtttc cctgcagaca      600

atgcgagaga atgaatcaga attcaaatat ctgcttcact cacggacaga aagactgttt      660

agagtgcttt cccgtgtcag aatctcaacc cgtttctgtc gtcaaaaagg cgtatcagaa      720

actgtgctac attcatcata tcatgggaaa ggtgccagac gcttgcactg cctgcgatct      780

ggtcgatgtg gatttggatg actgcatctt tgaacaataa atgatttaaa tcaggtatgg      840
```

ctgccgatgg ttatcttcca gattggctcg aggacaacct ctctgagggc attcgcgagt 900

ggtgggcgct gaaacctgga gccccgaagc ccaaagccaa ccagcaaaag caggacggcg 960

gccggggtct ggtgcttcct ggctacaagt acctcggacc cttcaacgga ctcgacaagg 1020

gggagcccgt caacgcggcg gacgcagcgg ccctcgagca cgacaaggcc tacgaccagc 1080

agctcaaagc gggtgacaat ccgtacctgc ggtataacca cgccgacgcc gagtttcagg 1140

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agaagagacc ggtagagcca tcaccccagc gttctccaga ctcctctacg ggcatcggca 1320

agaaaggcca gcagcccgcg aaaaagagac tcaactttgg gcagactggc gactcagagt 1380

cagtgcccga ccctcaacca atcggagaac cccccgcagg cccctctggt ctgggatctg 1440

gtacaatggc tgcaggcggt ggcgctccaa tggcagacaa taacgaaggc gccgacggag 1500

tgggtagttc ctcaggaaat tggcattgcg attccacatg gctgggcgac tgagtcatca 1560

ccaccagcac ccgaacctgg gccctcccca cctacaacaa ccacctctac aagcaaatct 1620

ccaacgggac ttcgggagga agcaccaacg acaacaccta cttcggctac agcacccccт 1680

gggggtattt tgactttaac agattccact gccacttctc accacgtgac tggcagcgac 1740

tcatcaacaa caactgggga ttccggccca agagactcaa cttcaagctc ttcaacatcc 1800

aggtcaagga ggtcacgcag aatgaaggca ccaagaccat cgccaataac cttaccagca 1860

cgattcaggt ctttacggac tcggaatacc agctcccgta cgtcctcggc tctgcgcacc 1920

agggctgcct gcctccgttc ccggcggacg tcttcatgat tcctcagtac gggtacctga 1980

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accagtacct gtactacctg tctcggactc agtccacggg aggtaccgca ggaactcagc 2220

agttgctatt ttctcaggcc gggcctaata acatgtcggc tcaggccaaa aactggctac 2280

ccgggccctg ctaccggcag taacgcgtct ccacgacact gtcgcaaaat aacaacagca 2340

actttgtctg gaccggtgcc accaagtatc atctgaatgg cagagactct ctggtagatc 2400

ccggtgtcgc tatggcaacc cacaaggacg acgaagagcg atttttccg tccagcggag 2460

tcataatgtt tgggaaacag ggagctggaa aagacaacgt ggactatagc agcgtcatgc 2520

taaccagtga ggaagaaatt aaaaccacca acccagtggc cacagaacag tacggcgtgg 2580

tggccgataa cctgcaacag caaaacgccg ctcctattgt aggggccgtc aacagtcaag 2640

gagccttacc tggcatggtc tggcagaacc gggacgtgta cctgcagggt cctacctggg 2700

ccaagattcc tcacacggac ggaaactttc atccctcgcc gctgatggga ggctttggac 2760

tgaaacaccc gcctcctcag atcctgatta agaatacacc tgttcccgcg gatcctccaa 2820

ctaccttcag tcaagctaag ctggcgtcgt tcatcacgca gtacagcacc ggacaggtca 2880

gcgtggaaat tgaatgggag ctgcaggaag aaaacagcaa acgctggaac ccagagattc 2940

aatacacttc caactactac aaatctacaa atgtggactt tgctgttaac acagatggca 3000

cttattctga gcctcgcccc atcggcaccc gttacctcac ccgtaatctg taattgcttg 3060

ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctctgcga agggcgaatt 3120

c 3121

<210> 29
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 29

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Gly Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
```

```
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Ser Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asp Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
```

```
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
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Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
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Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
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725 730 735

Asn Leu

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<211> 3121
<212> DNA
<213> Adeno-associated virus

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<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 31
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<211> 736
<212> PRT
<213> Adeno-associated virus 3

<400> 32

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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

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

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

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

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
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Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
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Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
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Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
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Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
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Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
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Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
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<211> 4726
<212> DNA
<213> Adeno-associated virus 3

<400> 33
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<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 34

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20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Asn Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Glu Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
```

```
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asp Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540
```

```
Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asp Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 35

<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 35
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaagg gggctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg agactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

agaggggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tcctttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgactg gaactgtcaa tcatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 36
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 36

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

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

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
```

```
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 37
<211> 736
<212> PRT
<213> Adeno-associated virus 3A

<400> 37

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

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

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145 150 155 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

```
Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  38
<211>  624
<212>  PRT
<213>  Adeno-associated virus 3A

<400>  38

Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15


Glu Arg Leu Pro Gly Ile Ser Asn Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30


Lys Glu Trp Asp Val Pro Pro Asp Ser Asp Met Asp Pro Asn Leu Ile
        35                  40                  45


Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60


Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
```

```
65                  70                  75                  80

Gln Phe Glu Lys Gly Glu Thr Tyr Phe His Leu His Val Leu Ile Glu
                85                  90                  95

Thr Ile Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110

Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Leu
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Ser Asn
        275                 280                 285
```

```
Pro Pro Glu Asp Ile Thr Lys Asn Arg Ile Tyr Gln Ile Leu Glu Leu
    290                 295                 300

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

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Glu Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Glu Phe
        435                 440                 445

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Asp Val
465                 470                 475                 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                 490                 495

Ser Asn Asp Ala Asp Val Ser Glu Pro Lys Arg Glu Cys Thr Ser Leu
```

```
            500                 505                 510

Ala Gln Pro Thr Thr Ser Asp Ala Glu Ala Pro Ala Asp Tyr Ala Asp
        515                 520                 525

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530                 535                 540

Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Ile Ser Asn Val Cys
545                 550                 555                 560

Phe Thr His Gly Gln Arg Asp Cys Gly Glu Cys Phe Pro Gly Met Ser
                565                 570                 575

Glu Ser Gln Pro Val Ser Val Val Lys Lys Lys Thr Tyr Gln Lys Leu
            580                 585                 590

Cys Pro Ile His His Ile Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser
        595                 600                 605

Ala Cys Asp Leu Ala Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610                 615                 620
```

<210> 39
<211> 736
<212> PRT
<213> Adeno-associated virus 3B

<400> 39

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720
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Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
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Glu His Leu Pro Gly Ile Ser Asn Ser Phe Val Asn Trp Val Ala Glu
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Pro Asn Leu Ile
        35                  40                  45


Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60


Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80


Gln Phe Glu Lys Gly Glu Thr Tyr Phe His Leu His Val Leu Ile Glu
                85                  90                  95


Thr Ile Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110


Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125


Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140


Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160


Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Leu
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Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Ser Asn
        275                 280                 285

Pro Pro Glu Asp Ile Thr Lys Asn Arg Ile Tyr Gln Ile Leu Glu Leu
    290                 295                 300

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

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380
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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400


Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Glu Pro Thr Pro Val
                405                 410                 415


Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430


Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445


Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460


Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Asp Val
465                 470                 475                 480


Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                 490                 495


Ser Asn Asp Ala Asp Val Ser Glu Pro Lys Arg Gln Cys Thr Ser Leu
            500                 505                 510


Ala Gln Pro Thr Thr Ser Asp Ala Glu Ala Pro Ala Asp Tyr Ala Asp
        515                 520                 525


Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530                 535                 540


Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Ile Ser Asn Val Cys
545                 550                 555                 560


Phe Thr His Gly Gln Arg Asp Cys Gly Glu Cys Phe Pro Gly Met Ser
                565                 570                 575


Glu Ser Gln Pro Val Ser Val Val Lys Lys Lys Thr Tyr Gln Lys Leu
            580                 585                 590


Cys Pro Ile His His Ile Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser
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595 600 605

Ala Cys Asp Leu Ala Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
610 615 620

<210> 41
<211> 4722
<212> DNA
<213> Adeno-associated virus 3B

<400> 41
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ccaactccat cactagaggt atggcagtga cgtaacgcga agcgcgcgaa gcgagaccac 180

gcctaccagc tgcgtcagca gtcaggtgac ccttttgcga cagtttgcga caccacgtgg 240

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<211> 1800
<212> DNA
<213> Adeno-associated virus 4

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<221> misc_feature
<222> (342)..(342)
<223> n is a, c, t, or g

<400> 42
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<210> 43
<211> 2208
<212> DNA
<213> Adeno-associated virus 4

<220>
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<222> (750)..(750)
<223> n is a, c, t, or g

<400> 43
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<211> 1872
<212> DNA
<213> Adeno-associated virus 4

<400> 44
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<210> 45
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<213> Adeno-associated virus 4

<400> 45
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ggcatttctg actcttttgt gagctgggtg gccgagaagg aatgggagct gccgccggat 120

tctgacatgg acttgaatct gattgagcag gcacccctga ccgtggccga aaagctgcaa 180

cgcgagttcc tggtcgagtg gcgccgcgtg agtaaggccc cggaggccct cttctttgtc 240

cagttcgaga agggggacag ctacttccac ctgcacatcc tggtggagac cgtgggcgtc 300

aaatccatgg tggtgggccg ctacgtgagc cagattaaag agaagctggt gacccgcatc 360

taccgcgggg tcgagccgca gcttccgaac tggttcgcgg tgaccaagac gcgtaatggc 420

gccggaggcg ggaacaaggt ggtggacgac tgctacatcc ccaactacct gctccccaag 480

acccagcccg agctccagtg ggcgtggact aacatggacc agtatataag cgcctgtttg 540

aatctcgcgg agcgtaaacg gctggtggcg cagcatctga cgcacgtgtc gcagacgcag 600

gagcagaaca aggaaaacca gaaccccaat tctgacgcgc cggtcatcag gtcaaaaacc 660

tccgccaggt acatggagct ggtcgggtgg ctggtggacc gcgggatcac gtcagaaaag 720

caatggatcc aggaggacca ggcgtcctac atctccttca acgccgcctc caactcgcgg 780

tcacaaatca aggccgcgct ggacaatgcc tccaaaatca tgagcctgac aaagacggct 840

ccggactacc tggtgggcca gaacccgccg gaggacattt ccagcaaccg catctaccga 900

atcctcgaga tgaacgggta cgatccgcag tacgcggcct ccgtcttcct gggctgggcg 960

caaaagaagt tcgggaagag gaacaccatc tggctctttg ggccggccac gacgggtaaa 1020

accaacatcg cggaagccat cgcccacgcc gtgcccttct acggctgcgt gaactggacc 1080

aatgagaact ttccgttcaa cgattgcgtc gacaagatgg tgatctggtg ggaggagggc 1140

aagatgacgg ccaaggtcgt agagagcgcc aaggccatcc tgggcggaag caaggtgcgc 1200

gtggaccaaa agtgcaagtc atcggcccag atcgacccaa ctcccgtgat cgtcacctcc 1260

aacaccaaca tgtgcgcggt catcgacgga aactcgacca ccttcgagca ccaacaacca 1320

ctccaggacc ggatgttcaa gttcgagctc accaagcgcc tggagcacga ctttggcaag 1380

gtcaccaagc aggaagtcaa agacttttc cggtgggcgt cagatcacgt gaccgaggtg 1440

actcacgagt tttacgtcag aaagggtgga gctagaaaga ggcccgcccc caatgacgca 1500

gatataagtg agcccaagcg ggcctgtccg tcagttgcgc agccatcgac gtcagacgcg 1560

gaagctccgg tggactacgc ggacagattg gctagaggac aacctctctg a 1611

<210> 46
<211> 1872
<212> DNA
<213> Adeno-associated virus 4

<400> 46
atgccggggt tctacgagat cgtgctgaag gtgcccagcg acctggacga gcacctgccc 60

ggcatttctg actcttttgt gagctgggtg gccgagaagg aatgggagct gccgccggat 120

tctgacatgg acttgaatct gattgagcag gcacccctga ccgtggccga aaagctgcaa 180

cgcgagttcc tggtcgagtg gcgccgcgtg agtaaggccc cggaggccct cttctttgtc 240

cagttcgaga agggggacag ctacttccac ctgcacatcc tggtggagac cgtgggcgtc 300

aaatccatgg tggtgggccg ctacgtgagc cagattaaag agaagctggt gacccgcatc 360

taccgcgggg tcgagccgca gcttccgaac tggttcgcgg tgaccaagac gcgtaatggc 420

gccggaggcg ggaacaaggt ggtggacgac tgctacatcc ccaactacct gctccccaag 480

acccagcccg agctccagtg ggcgtggact aacatggacc agtatataag cgcctgtttg 540

aatctcgcgg agcgtaaacg gctggtggcg cagcatctga cgcacgtgtc gcagacgcag 600

gagcagaaca aggaaaacca gaaccccaat tctgacgcgc cggtcatcag gtcaaaaacc 660

tccgccaggt acatggagct ggtcgggtgg ctggtggacc gcgggatcac gtcagaaaag 720

caatggatcc aggaggacca ggcgtcctac atctccttca acgccgcctc caactcgcgg 780

tcacaaatca aggccgcgct ggacaatgcc tccaaaatca tgagcctgac aaagacggct 840

ccggactacc tggtgggcca gaacccgccg gaggacattt ccagcaaccg catctaccga 900

atcctcgaga tgaacgggta cgatccgcag tacgcggcct ccgtcttcct gggctgggcg 960

caaaagaagt tcgggaagag gaacaccatc tggctctttg ggccggccac gacgggtaaa 1020

accaacatcg cggaagccat cgcccacgcc gtgcccttct acggctgcgt gaactggacc 1080

aatgagaact ttccgttcaa cgattgcgtc gacaagatgg tgatctggtg ggaggagggc 1140

aagatgacgg ccaaggtcgt agagagcgcc aaggccatcc tgggcggaag caaggtgcgc 1200

gtggaccaaa agtgcaagtc atcggcccag atcgacccaa ctcccgtgat cgtcacctcc 1260

aacaccaaca tgtgcgcggt catcgacgga aactcgacca ccttcgagca ccaacaacca 1320

ctccaggacc ggatgttcaa gttcgagctc accaagcgcc tggagcacga ctttggcaag 1380

gtcaccaagc aggaagtcaa agacttttтc cggtgggcgt cagatcacgt gaccgaggtg 1440

actcacgagt tttacgtcag aaagggtgga gctagaaaga ggcccgcccc caatgacgca 1500

gatataagtg agcccaagcg ggcctgtccg tcagttgcgc agccatcgac gtcagacgcg 1560

gaagctccgg tggactacgc ggacaggtac caaaacaaat gttctcgtca cgtgggtatg 1620

aatctgatgc ttttтccctg ccggcaatgc gagagaatga atcagaatgt ggacatttgc 1680

ttcacgcacg gggtcatgga ctgtgccgag tgcttccccg tgtcagaatc tcaacccgtg 1740

tctgtcgtca gaaagcggac gtatcagaaa ctgtgtccga ttcatcacat catggggagg 1800

gcgcccgagg tggcctgctc ggcctgcgaa ctggccaatg tggacttgga tgactgtgac 1860

atggaacaat aa 1872

<210> 47
<211> 1617
<212> DNA
<213> Adeno-associated virus 4

<220>
<221> misc_feature
<222> (162)..(162)
<223> n is a, c, t, or g

<400> 47
atgcgtgcag cagctggcgg agctgcagtc gagggsggac aaggtgccga tggagtgggt 60

aatgcctcgg gtgattggca ttgcgattcc acctggtctg agggccacgt cacgaccacc 120

agcaccagaa cctgggtctt gcccacctac aacaaccacc tntacaagcg actcggagag 180

agcctgcagt ccaacaccta caacggattc tccacccccc ggggatactt tgacttcaac 240

cgcttccact gccacttctc accacgtgac tggcagcgac tcatcaacaa caactggggc 300

atgcgaccca aagccatgcg ggtcaaaatc ttcaacatcc aggtcaagga ggtcacgacg 360

tcgaacggcg agacaacggt ggctaataac cttaccagca cggttcagat ctttgcggac 420

tcgtcgtacg aactgccgta cgtgatggat gcgggtcaag agggcagcct gcctcctttt 480

cccaacgacg tctttatggt gccccagtac ggctactgtg gactggtgac cggcaacact 540

tcgcagcaac agactgacag aaatgccttc tactgcctgg agtactttcc ttcgcagatg 600

ctgcggactg gcaacaactt tgaaattacg tacagttttg agaaggtgcc tttccactcg 660

atgtacgcgc acagccagag cctggaccgg ctgatgaacc ctctcatcga ccagtacctg 720

tggggactgc aatcgaccac caccggaacc accctgaatg ccgggactgc caccaccaac 780

tttaccaagc tgcggcctac caacttttcc aactttaaaa agaactggct gcccgggcct 840

tcaatcaagc agcagggctt ctcaaagact gccaatcaaa actacaagat ccctgccacc 900

gggtcagaca gtctcatcaa atacgagacg cacagcactc tggacggaag atggagtgcc 960

ctgacccccg gacctccaat ggccacggct ggacctgcgg acagcaagtt cagcaacagc 1020

cagctcatct ttgcggggcc taaacagaac ggcaacacgg ccaccgtacc cgggactctg 1080

atcttcacct ctgaggagga gctggcagcc accaacgcca ccgatacgga catgtggggc 1140

aacctacctg gcggtgacca gagcaacagc aacctgccga ccgtggacag actgacagcc 1200

ttgggagccg tgcctggaat ggtctggcaa aacagagaca tttactacca gggtcccatt 1260

tgggccaaga ttcctcatac cgatggacac tttcacccct caccgctgat tggtgggttt 1320

gggctgaaac acccgcctcc tcaaattttt atcaagaaca ccccggtacc tgcgaatcct 1380

gcaacgacct tcagctctac tccggtaaac tccttcatta ctcagtacag cactggccag 1440

gtgtcggtgc agattgactg ggagatccag aaggagcggt ccaaacgctg gaaccccgag 1500

gtccagttta cctccaacta cggacagcaa aactctctgt tgtgggctcc cgatgcggct 1560

gggaaataca ctgagcctag ggctatcggt acccgctacc tcacccacca cctgtaa 1617

<210> 48
<211> 939
<212> DNA
<213> Adeno-associated virus 4

<400> 48
atggagctgg tcgggtggct ggtggaccgc gggatcacgt cagaaaagca atggatccag 60

gaggaccagg cgtcctacat ctccttcaac gccgcctcca actcgcggtc acaaatcaag 120

gccgcgctgg acaatgcctc caaaatcatg agcctgacaa agacggctcc ggactacctg 180

gtgggccaga acccgccgga ggacatttcc agcaaccgca tctaccgaat cctcgagatg 240

aacgggtacg atccgcagta cgcggcctcc gtcttcctgg gctgggcgca aaagaagttc 300

gggaagagga acaccatctg gctctttggg ccggccacga cgggtaaaac caacatcgcg 360

gaagccatcg cccacgccgt gcccttctac ggctgcgtga actggaccaa tgagaacttt 420

ccgttcaacg attgcgtcga caagatggtg atctggtggg aggagggcaa gatgacggcc 480

aaggtcgtag agagcgccaa ggccatcctg ggcggaagca aggtgcgcgt ggaccaaaag 540

tgcaagtcat cggcccagat cgacccaact cccgtgatcg tcacctccaa caccaacatg 600

tgcgcggtca tcgacggaaa ctcgaccacc ttcgagcacc aacaaccact ccaggaccgg 660

atgttcaagt tcgagctcac caagcgcctg gagcacgact ttggcaaggt caccaagcag 720

gaagtcaaag actttttccg gtgggcgtca gatcacgtga ccgaggtgac tcacgagttt 780

tacgtcagaa agggtggagc tagaaagagg cccgccccca atgacgcaga tataagtgag 840

cccaagcggg cctgtccgtc agttgcgcag ccatcgacgt cagacgcgga agctccggtg 900

gactacgcgg acagattggc tagaggacaa cctctctga 939

<210> 49
<211> 1197
<212> DNA
<213> Adeno-associated virus 4

<400> 49
atggagctgg tcgggtggct ggtggaccgc gggatcacgt cagaaaagca atggatccag 60

gaggaccagg cgtcctacat ctccttcaac gccgcctcca actcgcggtc acaaatcaag 120

gccgcgctgg acaatgcctc caaaatcatg agcctgacaa agacggctcc ggactacctg 180

gtgggccaga acccgccgga ggacatttcc agcaaccgca tctaccgaat cctcgagatg 240

aacgggtacg atccgcagta cgcggcctcc gtcttcctgg gctgggcgca aaagaagttc 300

gggaagagga acaccatctg gctctttggg ccggccacga cgggtaaaac caacatcgcg 360

gaagccatcg cccacgccgt gcccttctac ggctgcgtga actggaccaa tgagaacttt 420

ccgttcaacg attgcgtcga caagatggtg atctggtggg aggagggcaa gatgacggcc 480

aaggtcgtag agagcgccaa ggccatcctg ggcggaagca aggtgcgcgt ggaccaaaag 540

tgcaagtcat cggcccagat cgacccaact cccgtgatcg tcacctccaa caccaacatg 600

tgcgcggtca tcgacggaaa ctcgaccacc ttcgagcacc aacaaccact ccaggaccgg 660

atgttcaagt tcgagctcac caagcgcctg gagcacgact ttggcaaggt caccaagcag 720

gaagtcaaag actttttccg gtgggcgtca gatcacgtga ccgaggtgac tcacgagttt 780

tacgtcagaa agggtggagc tagaaagagg cccgccccca atgacgcaga tataagtgag 840

cccaagcggg cctgtccgtc agttgcgcag ccatcgacgt cagacgcgga agctccggtg 900

gactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggtatgaa tctgatgctt 960

tttccctgcc ggcaatgcga gagaatgaat cagaatgtgg acatttgctt cacgcacggg 1020

gtcatggact gtgccgagtg cttccccgtg tcagaatctc aacccgtgtc tgtcgtcaga 1080

aagcggacgt atcagaaact gtgtccgatt catcacatca tggggagggc gcccgaggtg 1140

gcctgctcgg cctgcgaact ggccaatgtg gacttggatg actgtgacat ggaacaa 1197

<210> 50
<211> 245
<212> DNA
<213> Adeno-associated virus 4

<400> 50
ctccatcatc taggtttgcc cactgacgtc aatgtgacgt cctagggtta gggaggtccc 60

tgtattagca gtcacgtgag tgtcgtattt cgcggagcgt agcggagcgc ataccaagct 120

gccacgtcac agccacgtgg tccgtttgcg acagtttgcg acaccatgtg gtcaggaggg 180

tatataaccg cgagtgagcc agcgaggagc tccattttgc ccgcgaattt tgaacgagca 240

gcagc 245

<210> 51
<211> 313
<212> PRT
<213> Adeno-associated virus 4

<220>
<221> MOD_RES
<222> (313)..(313)
<223> Xaa = any amino acid

<400> 51

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
1 5 10 15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20 25 30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
35 40 45

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
50 55 60

Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
65 70 75 80

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
115 120 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160

```
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180                 185                 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195                 200                 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210                 215                 220

Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225                 230                 235                 240

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

Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
            260                 265                 270

Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
        275                 280                 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
    290                 295                 300

Arg Leu Ala Arg Gly Gln Pro Leu Xaa
305                 310
```

<210> 52
<211> 399
<212> PRT
<213> Adeno-associated virus 4

<400> 52

```
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
1               5                   10                  15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
```

```
            20                  25                  30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
        35                  40                  45

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
    50                  55                  60

Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
65                  70                  75                  80

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85                  90                  95

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100                 105                 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
        115                 120                 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145                 150                 155                 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180                 185                 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195                 200                 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210                 215                 220

Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225                 230                 235                 240
```

```
Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
                245                 250                 255

Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
            260                 265                 270

Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
        275                 280                 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
    290                 295                 300

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305                 310                 315                 320

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Val Asp Ile Cys
                325                 330                 335

Phe Thr His Gly Val Met Asp Cys Ala Glu Cys Phe Pro Val Ser Glu
            340                 345                 350

Ser Gln Pro Val Ser Val Val Arg Lys Arg Thr Tyr Gln Lys Leu Cys
        355                 360                 365

Pro Ile His His Ile Met Gly Arg Ala Pro Glu Val Ala Cys Ser Ala
    370                 375                 380

Cys Glu Leu Ala Asn Val Asp Leu Asp Asp Cys Asp Met Glu Gln
385                 390                 395
```

<210> 53
<211> 623
<212> PRT
<213> Adeno-associated virus 4

<400> 53

```
Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30
```

```
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60

Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Asp Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

Thr Val Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110

Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240
```

```
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
        275                 280                 285

Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
    290                 295                 300

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

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460
```

```
Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480


Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
                485                 490                 495


Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510


Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
        515                 520                 525


Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530                 535                 540


Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Val Asp Ile Cys
545                 550                 555                 560


Phe Thr His Gly Val Met Asp Cys Ala Glu Cys Phe Pro Val Ser Glu
                565                 570                 575


Ser Gln Pro Val Ser Val Val Arg Lys Arg Thr Tyr Gln Lys Leu Cys
            580                 585                 590


Pro Ile His His Ile Met Gly Arg Ala Pro Glu Val Ala Cys Ser Ala
        595                 600                 605


Cys Glu Leu Ala Asn Val Asp Leu Asp Asp Cys Asp Met Glu Gln
    610                 615                 620


<210>  54
<211>  537
<212>  PRT
<213>  Adeno-associated virus 4


<220>
<221>  MOD_RES
<222>  (537)..(537)
<223>  Xaa = any amino acid

<400>  54
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```
Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1               5                  10                  15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60

Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Asp Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

Thr Val Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110

Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
```

```
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
        275                 280                 285

Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
    290                 295                 300

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

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430
```

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445

Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465 470 475 480

Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
485 490 495

Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
500 505 510

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
515 520 525

Arg Leu Ala Arg Gly Gln Pro Leu Xaa
530 535

<210> 55
<211> 623
<212> PRT
<213> Adeno-associated virus 4

<400> 55

Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1 5 10 15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
20 25 30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
50 55 60

Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80

```
Gln Phe Glu Lys Gly Asp Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

Thr Val Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110

Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
        275                 280                 285
```

```
Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
    290                 295                 300

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

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480

Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
                485                 490                 495

Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510
```

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
515 520 525

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 535 540

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Val Asp Ile Cys
545 550 555 560

Phe Thr His Gly Val Met Asp Cys Ala Glu Cys Phe Pro Val Ser Glu
565 570 575

Ser Gln Pro Val Ser Val Val Arg Lys Arg Thr Tyr Gln Lys Leu Cys
580 585 590

Pro Ile His His Ile Met Gly Arg Ala Pro Glu Val Ala Cys Ser Ala
595 600 605

Cys Glu Leu Ala Asn Val Asp Leu Asp Asp Cys Asp Met Glu Gln
610 615 620

<210> 56
<211> 544
<212> PRT
<213> Adeno-associated virus 4

<400> 56

Met Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val
1 5 10 15

Glu Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp
20 25 30

His Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr
35 40 45

Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu
50 55 60

Gly Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp

65 70 75 80

Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
85 90 95

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met
100 105 110

Arg Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
115 120 125

Gly Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe
130 135 140

Ala Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
145 150 155 160

Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
165 170 175

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

Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
195 200 205

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

His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
225 230 235 240

Leu Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr
245 250 255

Thr Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro
260 265 270

Thr Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile
275 280 285

```
Lys Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro
    290                 295                 300

Ala Thr Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu
305                 310                 315                 320

Asp Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala
                325                 330                 335

Gly Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly
            340                 345                 350

Pro Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe
        355                 360                 365

Thr Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met
    370                 375                 380

Trp Gly Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr
385                 390                 395                 400

Val Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln
                405                 410                 415

Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
            420                 425                 430

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
        435                 440                 445

Lys His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
    450                 455                 460

Asn Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr
465                 470                 475                 480

Gln Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln
                485                 490                 495

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
```

500 505 510

Tyr Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys
515 520 525

Tyr Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
530 535 540

<210> 57
<211> 734
<212> PRT
<213> Adeno-associated virus 4

<400> 57

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
115 120 125

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

```
Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

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

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365
```

```
Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575
```

```
Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730
```

<210> 58
<211> 598
<212> PRT
<213> Adeno-associated virus 4

<400> 58

```
Thr Ala Pro Gly Lys Lys Arg Pro Leu Ile Glu Ser Pro Gln Gln Pro
1               5                   10                  15

Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Lys Gln Pro Ala Lys Lys
            20                  25                  30
```

```
Lys Leu Val Phe Glu Asp Glu Thr Gly Ala Gly Asp Gly Pro Pro Glu
        35                  40                  45

Gly Ser Thr Ser Gly Ala Met Ser Asp Asp Ser Glu Met Arg Ala Ala
    50                  55                  60

Ala Gly Gly Ala Ala Val Glu Gly Gly Gln Gly Ala Asp Gly Val Gly
65                  70                  75                  80

Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Ser Glu Gly His
                85                  90                  95

Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn
            100                 105                 110

His Leu Tyr Lys Arg Leu Gly Glu Ser Leu Gln Ser Asn Thr Tyr Asn
        115                 120                 125

Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
    130                 135                 140

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
145                 150                 155                 160

Met Arg Pro Lys Ala Met Arg Val Lys Ile Phe Asn Ile Gln Val Lys
                165                 170                 175

Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ala Asn Asn Leu Thr
            180                 185                 190

Ser Thr Val Gln Ile Phe Ala Asp Ser Ser Tyr Glu Leu Pro Tyr Val
        195                 200                 205

Met Asp Ala Gly Gln Glu Gly Ser Leu Pro Pro Phe Pro Asn Asp Val
    210                 215                 220

Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Leu Val Thr Gly Asn Thr
225                 230                 235                 240

Ser Gln Gln Gln Thr Asp Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe
```

```
                245                 250                 255

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

Phe Glu Lys Val Pro Phe His Ser Met Tyr Ala His Ser Gln Ser Leu
        275                 280                 285

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Trp Gly Leu Gln
    290                 295                 300

Ser Thr Thr Thr Gly Thr Thr Leu Asn Ala Gly Thr Ala Thr Thr Asn
305                 310                 315                 320

Phe Thr Lys Leu Arg Pro Thr Asn Phe Ser Asn Phe Lys Lys Asn Trp
                325                 330                 335

Leu Pro Gly Pro Ser Ile Lys Gln Gln Gly Phe Ser Lys Thr Ala Asn
            340                 345                 350

Gln Asn Tyr Lys Ile Pro Ala Thr Gly Ser Asp Ser Leu Ile Lys Tyr
        355                 360                 365

Glu Thr His Ser Thr Leu Asp Gly Arg Trp Ser Ala Leu Thr Pro Gly
    370                 375                 380

Pro Pro Met Ala Thr Ala Gly Pro Ala Asp Ser Lys Phe Ser Asn Ser
385                 390                 395                 400

Gln Leu Ile Phe Ala Gly Pro Lys Gln Asn Gly Asn Thr Ala Thr Val
                405                 410                 415

Pro Gly Thr Leu Ile Phe Thr Ser Glu Glu Glu Leu Ala Ala Thr Asn
            420                 425                 430

Ala Thr Asp Thr Asp Met Trp Gly Asn Leu Pro Gly Gly Asp Gln Ser
        435                 440                 445

Asn Ser Asn Leu Pro Thr Val Asp Arg Leu Thr Ala Leu Gly Ala Val
    450                 455                 460
```

```
Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile
465                 470                 475                 480

Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
                485                 490                 495

Ile Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Phe Ile Lys
            500                 505                 510

Asn Thr Pro Val Pro Ala Asn Pro Ala Thr Thr Phe Ser Ser Thr Pro
        515                 520                 525

Val Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Gln
    530                 535                 540

Ile Asp Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu
545                 550                 555                 560

Val Gln Phe Thr Ser Asn Tyr Gly Gln Gln Asn Ser Leu Leu Trp Ala
                565                 570                 575

Pro Asp Ala Ala Gly Lys Tyr Thr Glu Pro Arg Ala Ile Gly Thr Arg
            580                 585                 590

Tyr Leu Thr His His Leu
        595
```

<210> 59
<211> 129
<212> DNA
<213> Adeno-associated virus 4

<400> 59
ttggccactc cctctatgcg cgctcgctca ctcactcggc cctgcggcca gaggccggca 60

gtctggagac ctttggtgtc cagggcaggg ccgagtgagt gagcgagcgc gcatagaggg 120

agtggccaa 129

<210> 60
<211> 125
<212> DNA
<213> Adeno-associated virus 4

<400> 60
ttggccactc cctctatgcg cgctcgctca ctcactcggc cctggagacc aaaggtctcc 60

agactgccgg cctctggccg gcagggccga gtgagtgagc gagcgcgcat agagggagtg 120

gccaa 125

<210> 61
<211> 4768
<212> DNA
<213> Adeno-associated virus 4

<220>
<221> misc_feature
<222> (3009)..(3009)
<223> n is a, c, t, or g

<400> 61
ttggccactc cctctatgcg cgctcgctca ctcactcggc cctggagacc aaaggtctcc 60

agactgccgg cctctggccg gcagggccga gtgagtgagc gagcgcgcat agagggagtg 120

gccaactcca tcatctaggt ttgcccactg acgtcaatgt gacgtcctag ggttagggag 180

gtccctgtat tagcagtcac gtgagtgtcg tatttcgcgg agcgtagcgg agcgcatacc 240

aagctgccac gtcacagcca cgtggtccgt ttgcgacagt ttgcgacacc atgtggtcag 300

gagggtatat aaccgcgagt gagccagcga ggagctccat tttgcccgcg aattttgaac 360

gagcagcagc catgccgggg ttctacgaga tcgtgctgaa ggtgcccagc gacctggacg 420

agcacctgcc cggcatttct gactcttttg tgagctgggt ggccgagaag gaatgggagc 480

tgccgccgga ttctgacatg gacttgaatc tgattgagca ggcacccctg accgtggccg 540

aaaagctgca acgcgagttc ctggtcgagt ggcgccgcgt gagtaaggcc ccggaggccc 600

tcttctttgt ccagttcgag aaggggggaca gctacttcca cctgcacatc ctggtggaga 660

ccgtgggcgt caaatccatg gtggtgggcc gctacgtgag ccagattaaa gagaagctgg 720

tgacccgcat ctaccgcggg gtcgagccgc agcttccgaa ctggttcgcg gtgaccaaga 780

cgcgtaatgg cgccggaggc gggaacaagg tggtggacga ctgctacatc cccaactacc 840

tgctccccaa gacccagccc gagctccagt gggcgtggac taacatggac cagtatataa 900

gcgcctgttt gaatctcgcg gagcgtaaac ggctggtggc gcagcatctg acgcacgtgt 960

cgcagacgca ggagcagaac aaggaaaacc agaaccccaa ttctgacgcg ccggtcatca 1020

ggtcaaaaac ctccgccagg tacatggagc tggtcgggtg gctggtggac cgcgggatca 1080

cgtcagaaaa gcaatggatc caggaggacc aggcgtccta catctccttc aacgccgcct 1140

ccaactcgcg gtcacaaatc aaggccgcgc tggacaatgc ctccaaaatc atgagcctga 1200

caaagacggc tccggactac ctggtgggcc agaacccgcc ggaggacatt tccagcaacc 1260

gcatctaccg aatcctcgag atgaacgggt acgatccgca gtacgcggcc tccgtcttcc 1320

tgggctgggc gcaaaagaag ttcgggaaga ggaacaccat ctggctcttt gggccggcca 1380

cgacgggtaa aaccaacatc gcggaagcca tcgcccacgc cgtgcccttc tacggctgcg 1440

tgaactggac caatgagaac tttccgttca acgattgcgt cgacaagatg gtgatctggt 1500

gggaggaggg caagatgacg gccaaggtcg tagagagcgc caaggccatc ctgggcggaa 1560

gcaaggtgcg cgtggaccaa aagtgcaagt catcggccca gatcgaccca actcccgtga 1620

tcgtcacctc caacaccaac atgtgcgcgg tcatcgacgg aaactcgacc accttcgagc 1680

accaacaacc actccaggac cggatgttca agttcgagct caccaagcgc ctggagcacg 1740

actttggcaa ggtcaccaag caggaagtca aagacttttt ccggtgggcg tcagatcacg 1800

tgaccgaggt gactcacgag ttttacgtca gaaagggtgg agctagaaag aggcccgccc 1860

ccaatgacgc agatataagt gagcccaagc gggcctgtcc gtcagttgcg cagccatcga 1920

cgtcagacgc ggaagctccg gtggactacg cggacaggta ccaaaacaaa tgttctcgtc 1980

acgtgggtat gaatctgatg ctttttccct gccggcaatg cgagagaatg aatcagaatg 2040

tggacatttg cttcacgcac ggggtcatgg actgtgccga gtgcttcccc gtgtcagaat 2100

ctcaacccgt gtctgtcgtc agaaagcgga cgtatcagaa actgtgtccg attcatcaca 2160

tcatggggag ggcgcccgag gtggcctgct cggcctgcga actggccaat gtggacttgg 2220

atgactgtga catggaacaa taaatgactc aaaccagata tgactgacgg ttaccttcca 2280

gattggctag aggacaacct ctctgaaggc gttcgagagt ggtgggcgct gcaacctgga 2340

gcccctaaac ccaaggcaaa tcaacaacat caggacaacg ctcggggtct tgtgcttccg 2400

ggttacaaat acctcggacc cggcaacgga ctcgacaagg gggaacccgt caacgcagcg 2460

gacgcggcag ccctcgagca cgacaaggcc tacgaccagc agctcaaggc cggtgacaac 2520

ccctacctca agtacaacca cgccgacgcg gagttccagc agcggcttca gggcgacaca 2580

ccgtttgggg gcaacctcgg cagagcagtc ttccaggcca aaaagagggt tcttgaacct 2640

cttggtctgg ttgagcaagc gggtgagacg gctcctggaa agaagagacc gttgattgaa 2700

tccccccagc agcccgactc ctccacgggt atcggcaaaa aaggcaagca gccggctaaa 2760

aagaagctcg ttttcgaaga cgaaactgga gcaggcgacg gacccctga gggatcaact 2820

tccggagcca tgtctgatga cagtgagatg cgtgcagcag ctggcggagc tgcagtcgag 2880

ggsggacaag gtgccgatgg agtgggtaat gcctcgggtg attggcattg cgattccacc 2940

tggtctgagg gccacgtcac gaccaccagc accagaacct gggtcttgcc cacctacaac 3000

aaccacctnt acaagcgact cggagagagc ctgcagtcca acacctacaa cggattctcc 3060

acccctggg gatactttga cttcaaccgc ttccactgcc acttctcacc acgtgactgg 3120

cagcgactca tcaacaacaa ctggggcatg cgacccaaag ccatgcgggt caaaatcttc 3180

aacatccagg tcaaggaggt cacgacgtcg aacggcgaga caacggtggc taataacctt 3240

accagcacgg ttcagatctt tgcggactcg tcgtacgaac tgccgtacgt gatggatgcg 3300

ggtcaagagg gcagcctgcc tccttttccc aacgacgtct ttatggtgcc ccagtacggc 3360

tactgtggac tggtgaccgg caacacttcg cagcaacaga ctgacagaaa tgccttctac 3420

tgcctggagt actttccttc gcagatgctg cggactggca acaactttga aattacgtac 3480

agttttgaga aggtgccttt ccactcgatg tacgcgcaca gccagagcct ggaccggctg 3540

atgaaccctc tcatcgacca gtacctgtgg ggactgcaat cgaccaccac cggaaccacc 3600

ctgaatgccg ggactgccac caccaacttt accaagctgc ggcctaccaa cttttccaac 3660

tttaaaaaga actggctgcc cgggccttca atcaagcagc agggcttctc aaagactgcc 3720

aatcaaaact acaagatccc tgccaccggg tcagacagtc tcatcaaata cgagacgcac 3780

agcactctgg acggaagatg gagtgccctg acccccggac ctccaatggc cacggctgga 3840

cctgcggaca gcaagttcag caacagccag ctcatctttg cggggcctaa acagaacggc 3900

aacacggcca ccgtacccgg gactctgatc ttcacctctg aggaggagct ggcagccacc 3960

aacgccaccg atacggacat gtggggcaac ctacctggcg gtgaccagag caacagcaac 4020

ctgccgaccg tggacagact gacagccttg ggagccgtgc ctggaatggt ctggcaaaac 4080

agagacattt actaccaggg tcccatttgg gccaagattc ctcataccga tggacacttt 4140

cacccctcac cgctgattgg tgggtttggg ctgaaacacc cgcctcctca aatttttatc 4200

aagaacaccc cggtacctgc gaatcctgca acgaccttca gctctactcc ggtaaactcc 4260

ttcattactc agtacagcac tggccaggtg tcggtgcaga ttgactggga gatccagaag 4320

gagcggtcca aacgctggaa ccccgaggtc cagtttacct ccaactacgg acagcaaaac 4380

tctctgttgt gggctcccga tgcggctggg aaatacactg agcctagggc tatcggtacc 4440

cgctacctca cccaccacct gtaataacct gttaatcaat aaaccggttt attcgtttca 4500

gttgaacttt ggtctccgtg tccttcttat cttatctcgt ttccatggct actgcgtaca 4560

taagcagcgg cctgcggcgc ttgcgcttcg cggtttacaa ctgccggtta atcagtaact 4620

tctggcaaac catgatgatg gagttggcca ctccctctat gcgcgctcgc tcactcactc 4680

ggccctggag accaaaggtc tccagactgc cggcctctgg ccggcagggc cgagtgagtg 4740

agcgagcgcg catagaggga gtggccaa 4768

<210> 62
<211> 3098
<212> PRT
<213> Adeno-associated virus

<400> 62

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

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

Ala Cys Cys Ala Ala Thr Gly Ala Gly Ala Ala Cys Thr Thr Thr Cys
35 40 45

Cys Cys Thr Thr Cys Ala Ala Cys Gly Ala Thr Thr Gly Cys Gly Thr
50 55 60

Cys Gly Ala Cys Ala Ala Gly Ala Thr Gly Gly Thr Gly Ala Thr Cys
65 70 75 80

Thr Gly Gly Thr Gly Gly Gly Ala Gly Gly Ala Gly Gly Gly Cys Ala
85 90 95

Ala Gly Ala Thr Gly Ala Cys Gly Gly Cys Cys Ala Ala Gly Gly Thr
100 105 110

```
Cys Gly Thr Gly Gly Ala Gly Thr Cys Cys Gly Cys Cys Ala Ala Gly
        115                 120                 125

Gly Cys Cys Ala Thr Thr Cys Thr Cys Gly Gly Cys Gly Gly Cys Ala
    130                 135                 140

Gly Cys Ala Ala Gly Gly Thr Gly Cys Gly Cys Gly Thr Gly Gly Ala
145                 150                 155                 160

Cys Cys Ala Ala Ala Ala Gly Thr Gly Cys Ala Ala Gly Thr Cys Thr
                165                 170                 175

Thr Cys Cys Gly Cys Cys Cys Ala Gly Ala Thr Cys Gly Ala Thr Cys
            180                 185                 190

Cys Cys Ala Cys Cys Cys Cys Cys Gly Thr Gly Ala Thr Cys Gly Thr
        195                 200                 205

Cys Ala Cys Thr Thr Cys Cys Ala Ala Cys Ala Cys Cys Ala Ala Cys
    210                 215                 220

Ala Thr Gly Thr Gly Cys Gly Cys Thr Gly Thr Gly Ala Thr Thr Gly
225                 230                 235                 240

Ala Cys Gly Gly Gly Ala Ala Cys Ala Gly Cys Ala Cys Cys Ala Cys
                245                 250                 255

Cys Thr Thr Cys Gly Ala Gly Cys Ala Cys Cys Ala Gly Cys Ala Gly
            260                 265                 270

Cys Cys Gly Thr Thr Ala Cys Ala Ala Gly Ala Cys Cys Gly Gly Ala
        275                 280                 285

Thr Gly Thr Thr Cys Ala Ala Ala Thr Thr Thr Gly Ala Ala Cys Thr
    290                 295                 300

Cys Ala Cys Cys Cys Gly Cys Cys Gly Thr Cys Thr Gly Gly Ala Gly
305                 310                 315                 320

Cys Ala Cys Gly Ala Cys Thr Thr Thr Gly Gly Cys Ala Ala Gly Gly
```

```
                325                 330                 335

Thr Gly Ala Cys Ala Ala Ala Gly Cys Ala Gly Gly Ala Ala Gly Thr
            340                 345                 350

Cys Ala Ala Ala Gly Ala Gly Thr Thr Cys Thr Thr Cys Cys Gly Cys
        355                 360                 365

Thr Gly Gly Gly Cys Gly Cys Ala Gly Gly Ala Thr Cys Ala Cys Gly
    370                 375                 380

Thr Gly Ala Cys Cys Gly Ala Gly Gly Thr Gly Gly Cys Gly Cys Ala
385                 390                 395                 400

Thr Gly Ala Gly Thr Thr Cys Thr Ala Cys Gly Thr Cys Ala Gly Ala
                405                 410                 415

Ala Ala Gly Gly Gly Thr Gly Gly Ala Gly Cys Cys Ala Ala Cys Ala
            420                 425                 430

Ala Gly Ala Gly Ala Cys Cys Cys Gly Cys Cys Cys Cys Cys Gly Ala
        435                 440                 445

Thr Gly Ala Cys Gly Cys Gly Gly Ala Thr Ala Ala Ala Ala Gly Cys
    450                 455                 460

Gly Ala Gly Cys Cys Cys Ala Ala Gly Cys Gly Gly Gly Cys Cys Thr
465                 470                 475                 480

Gly Cys Cys Cys Cys Thr Cys Ala Gly Thr Cys Gly Cys Gly Gly Ala
                485                 490                 495

Thr Cys Cys Ala Thr Cys Gly Ala Cys Gly Thr Cys Ala Gly Ala Cys
            500                 505                 510

Gly Cys Gly Gly Ala Ala Gly Gly Ala Gly Cys Thr Cys Cys Gly Gly
        515                 520                 525

Thr Gly Gly Ala Cys Thr Thr Thr Gly Cys Cys Gly Ala Cys Ala Gly
    530                 535                 540
```

```
Gly Thr Ala Cys Cys Ala Ala Ala Ala Cys Ala Ala Ala Thr Gly Thr
545                 550                 555                 560


Thr Cys Thr Cys Gly Thr Cys Ala Cys Gly Cys Gly Gly Gly Cys Ala
                565                 570                 575


Thr Gly Cys Thr Thr Cys Ala Gly Ala Thr Gly Cys Thr Gly Thr Thr
            580                 585                 590


Thr Cys Cys Cys Thr Gly Cys Ala Ala Gly Ala Cys Ala Thr Gly Cys
        595                 600                 605


Gly Ala Gly Ala Gly Ala Ala Thr Gly Ala Ala Thr Cys Ala Gly Ala
    610                 615                 620


Ala Thr Thr Thr Cys Ala Ala Cys Ala Thr Thr Thr Gly Cys Thr Thr
625                 630                 635                 640


Cys Ala Cys Gly Cys Ala Cys Gly Gly Gly Ala Cys Cys Ala Gly Ala
                645                 650                 655


Gly Ala Cys Thr Gly Thr Thr Cys Ala Gly Ala Ala Thr Gly Thr Thr
            660                 665                 670


Thr Cys Cys Cys Cys Gly Gly Cys Gly Thr Gly Thr Cys Ala Gly Ala
        675                 680                 685


Ala Thr Cys Thr Cys Ala Ala Cys Cys Gly Gly Thr Cys Gly Thr Cys
    690                 695                 700


Ala Gly Ala Ala Ala Gly Ala Gly Gly Ala Cys Gly Thr Ala Thr Cys
705                 710                 715                 720


Gly Gly Ala Ala Ala Cys Thr Cys Thr Gly Thr Gly Cys Cys Ala Thr
                725                 730                 735


Thr Cys Ala Thr Cys Ala Thr Cys Thr Gly Cys Thr Gly Gly Gly Gly
            740                 745                 750


Cys Gly Gly Gly Cys Thr Cys Cys Cys Gly Ala Gly Ala Thr Thr Gly
```

```
        755                 760                 765

Cys Thr Thr Gly Cys Thr Cys Gly Gly Cys Cys Thr Gly Cys Gly Ala
    770                 775                 780

Thr Cys Thr Gly Gly Thr Cys Ala Ala Cys Gly Thr Gly Gly Ala Cys
785                 790                 795                 800

Cys Thr Gly Gly Ala Thr Gly Ala Cys Cys Gly Thr Gly Thr Thr Thr
                805                 810                 815

Cys Thr Gly Ala Gly Cys Ala Ala Thr Ala Ala Ala Thr Gly Ala Cys
            820                 825                 830

Thr Thr Ala Ala Ala Cys Cys Ala Gly Gly Thr Ala Thr Gly Gly Cys
        835                 840                 845

Thr Gly Cys Cys Gly Ala Thr Gly Gly Thr Thr Ala Thr Cys Thr Thr
    850                 855                 860

Cys Cys Ala Gly Ala Thr Thr Gly Gly Cys Thr Cys Gly Ala Gly Gly
865                 870                 875                 880

Ala Cys Ala Ala Cys Cys Thr Cys Thr Cys Thr Gly Ala Gly Gly Gly
                885                 890                 895

Cys Ala Thr Thr Cys Gly Cys Gly Ala Gly Thr Gly Gly Thr Gly Gly
            900                 905                 910

Gly Ala Cys Thr Thr Gly Ala Ala Ala Cys Cys Thr Gly Gly Ala Gly
        915                 920                 925

Cys Cys Cys Cys Gly Ala Ala Ala Cys Cys Cys Ala Ala Ala Gly Cys
    930                 935                 940

Cys Ala Ala Cys Cys Ala Gly Cys Ala Ala Ala Ala Gly Cys Ala Gly
945                 950                 955                 960

Gly Ala Cys Gly Ala Cys Gly Gly Cys Cys Gly Gly Gly Gly Thr Cys
                965                 970                 975
```

```
Thr Gly Gly Thr Gly Cys Thr Thr Cys Cys Thr Gly Gly Cys Thr Ala
            980                 985                 990


Cys Ala Ala Gly Thr Ala Cys Cys  Thr Cys Gly Gly Ala  Cys Cys Cys
        995                 1000                1005


Thr Thr  Cys Ala Ala Cys Gly  Gly Ala Cys Thr Cys  Gly Ala Cys
    1010                1015                1020


Ala Ala  Gly Gly Gly Ala Gly  Ala Gly Cys Cys Gly  Gly Thr Cys
    1025                1030                1035


Ala Ala  Cys Gly Ala Gly Gly  Cys Ala Gly Ala Cys  Gly Cys Cys
    1040                1045                1050


Gly Cys  Gly Gly Cys Cys Cys  Thr Cys Gly Ala Gly  Cys Ala Cys
    1055                1060                1065


Gly Ala  Cys Ala Ala Gly Gly  Cys Cys Thr Ala Cys  Gly Ala Cys
    1070                1075                1080


Ala Ala  Gly Cys Ala Gly Cys  Thr Cys Gly Ala Gly  Cys Ala Gly
    1085                1090                1095


Gly Gly  Gly Gly Ala Cys Ala  Ala Cys Cys Cys Gly  Thr Ala Cys
    1100                1105                1110


Cys Thr  Cys Ala Ala Gly Thr  Ala Cys Ala Ala Cys  Cys Ala Cys
    1115                1120                1125


Gly Cys  Cys Gly Ala Cys Gly  Cys Cys Gly Ala Gly  Thr Thr Thr
    1130                1135                1140


Cys Ala  Gly Gly Ala Gly Cys  Gly Thr Cys Thr Thr  Cys Ala Ala
    1145                1150                1155


Gly Ala  Ala Gly Ala Thr Ala  Cys Gly Thr Cys Thr  Thr Thr Thr
    1160                1165                1170


Gly Gly  Gly Gly Gly Cys Ala  Ala Cys Cys Thr Cys  Gly Gly Gly
```

```
    1175                1180                1185

Cys Gly  Ala Gly Cys Ala Gly  Thr Cys Thr Thr Cys  Cys Ala Gly
    1190                1195                1200

Gly Cys  Cys Ala Ala Gly Ala  Ala Gly Cys Gly Gly  Gly Thr Thr
    1205                1210                1215

Cys Thr  Cys Gly Ala Ala Cys  Cys Thr Cys Thr Cys  Gly Gly Thr
    1220                1225                1230

Cys Thr  Gly Gly Thr Thr Gly  Ala Gly Gly Ala Ala  Gly Gly Cys
    1235                1240                1245

Gly Cys  Thr Ala Ala Gly Ala  Cys Gly Gly Cys Thr  Cys Cys Thr
    1250                1255                1260

Gly Gly  Ala Ala Ala Gly Ala  Ala Gly Ala Gly Ala  Cys Cys Cys
    1265                1270                1275

Ala Thr  Ala Gly Ala Ala Thr  Cys Cys Cys Cys Cys  Gly Ala Cys
    1280                1285                1290

Thr Cys  Cys Thr Cys Cys Ala  Cys Gly Gly Gly Cys  Ala Thr Cys
    1295                1300                1305

Gly Gly  Cys Ala Ala Gly Ala  Ala Ala Gly Gly Cys  Cys Ala Gly
    1310                1315                1320

Cys Ala  Gly Cys Cys Cys Gly  Cys Thr Ala Ala Ala  Ala Ala Gly
    1325                1330                1335

Ala Ala  Gly Cys Thr Cys Ala  Ala Cys Thr Thr Thr  Gly Gly Gly
    1340                1345                1350

Cys Ala  Gly Ala Cys Thr Gly  Gly Cys Gly Ala Cys  Thr Cys Ala
    1355                1360                1365

Gly Ala  Gly Thr Cys Ala Gly  Thr Gly Cys Cys Cys  Gly Ala Cys
    1370                1375                1380
```

```
Cys Cys  Cys Cys Ala Ala Cys  Cys Thr Cys Thr Cys  Gly Gly Ala
    1385                1390                1395

Gly Ala  Ala Cys Cys Thr Cys  Cys Cys Gly Cys Cys  Gly Cys Gly
    1400                1405                1410

Cys Cys  Cys Thr Cys Ala Gly  Gly Thr Cys Thr Gly  Gly Gly Ala
    1415                1420                1425

Thr Cys  Thr Gly Gly Thr Ala  Cys Ala Ala Thr Gly  Gly Cys Thr
    1430                1435                1440

Gly Cys  Ala Gly Gly Cys Gly  Gly Thr Gly Gly Cys  Gly Cys Ala
    1445                1450                1455

Cys Cys  Ala Ala Thr Gly Gly  Cys Ala Gly Ala Cys  Ala Ala Thr
    1460                1465                1470

Ala Ala  Cys Gly Ala Ala Gly  Gly Cys Gly Cys Cys  Gly Ala Cys
    1475                1480                1485

Gly Gly  Ala Gly Thr Gly Gly  Gly Thr Ala Ala Thr  Gly Cys Cys
    1490                1495                1500

Thr Cys  Cys Gly Gly Ala Ala  Ala Thr Thr Gly Gly  Cys Ala Thr
    1505                1510                1515

Thr Gly  Cys Gly Ala Thr Thr  Cys Cys Ala Cys Ala  Thr Gly Gly
    1520                1525                1530

Cys Thr  Gly Gly Gly Cys Gly  Ala Cys Ala Gly Ala  Gly Thr Cys
    1535                1540                1545

Ala Thr  Cys Ala Cys Cys Ala  Cys Cys Ala Gly Cys  Ala Cys Cys
    1550                1555                1560

Cys Gly  Cys Ala Cys Cys Thr  Gly Gly Gly Cys Cys  Cys Thr Gly
    1565                1570                1575

Cys Cys  Cys Ala Cys Cys Thr  Ala Cys Ala Ala Cys  Ala Ala Cys
```

```
    1580                1585                1590

Cys Ala  Cys Cys Thr Cys Thr  Ala Cys Ala Ala Gly  Cys Ala Gly
    1595                1600                1605

Ala Thr  Ala Thr Cys Ala Ala  Gly Thr Cys Ala Gly  Ala Gly Cys
    1610                1615                1620

Gly Gly  Gly Gly Cys Thr Ala  Cys Cys Ala Ala Cys  Gly Ala Cys
    1625                1630                1635

Ala Ala  Cys Cys Ala Cys Thr  Thr Cys Thr Thr Cys  Gly Gly Cys
    1640                1645                1650

Thr Ala  Cys Ala Gly Cys Ala  Cys Cys Cys Cys Cys  Thr Gly Gly
    1655                1660                1665

Gly Gly  Cys Thr Ala Thr Thr  Thr Thr Gly Ala Cys  Thr Thr Cys
    1670                1675                1680

Ala Ala  Cys Ala Gly Ala Thr  Thr Cys Cys Ala Cys  Thr Gly Cys
    1685                1690                1695

Cys Ala  Cys Thr Thr Cys Thr  Cys Ala Cys Cys Ala  Cys Gly Thr
    1700                1705                1710

Gly Ala  Cys Thr Gly Gly Cys  Ala Gly Cys Gly Ala  Cys Thr Cys
    1715                1720                1725

Ala Thr  Cys Ala Ala Cys Ala  Ala Cys Ala Ala Cys  Thr Gly Gly
    1730                1735                1740

Gly Gly  Ala Thr Thr Cys Cys  Gly Gly Cys Cys Cys  Ala Gly Ala
    1745                1750                1755

Ala Ala  Gly Cys Thr Gly Cys  Gly Gly Thr Thr Cys  Ala Ala Gly
    1760                1765                1770

Thr Thr  Gly Thr Thr Cys Ala  Ala Cys Ala Thr Cys  Cys Ala Gly
    1775                1780                1785
```

```
Gly Thr  Cys Ala Ala Gly Gly  Ala Gly Gly Thr Cys  Ala Cys Gly
    1790                1795                1800

Ala Cys  Gly Ala Ala Cys Gly  Ala Cys Gly Gly Cys  Gly Thr Thr
    1805                1810                1815

Ala Cys  Gly Ala Cys Cys Ala  Thr Cys Gly Cys Thr  Ala Ala Thr
    1820                1825                1830

Ala Ala  Cys Cys Thr Thr Ala  Cys Cys Ala Gly Cys  Ala Cys Gly
    1835                1840                1845

Ala Thr  Thr Cys Ala Gly Gly  Thr Cys Thr Thr Cys  Thr Cys Gly
    1850                1855                1860

Gly Ala  Cys Thr Cys Gly Gly  Ala Gly Thr Ala Cys  Cys Ala Ala
    1865                1870                1875

Cys Thr  Gly Cys Cys Gly Thr  Ala Cys Gly Thr Cys  Cys Thr Cys
    1880                1885                1890

Gly Gly  Cys Thr Cys Thr Gly  Cys Gly Cys Ala Cys  Cys Ala Gly
    1895                1900                1905

Gly Gly  Cys Thr Gly Cys Cys  Thr Cys Cys Cys Thr  Cys Cys Gly
    1910                1915                1920

Thr Thr  Cys Cys Cys Thr Gly  Cys Gly Gly Ala Cys  Gly Thr Gly
    1925                1930                1935

Thr Thr  Cys Ala Thr Gly Ala  Thr Thr Cys Cys Thr  Cys Ala Gly
    1940                1945                1950

Thr Ala  Cys Gly Gly Ala Thr  Ala Thr Cys Thr Gly  Ala Cys Thr
    1955                1960                1965

Cys Thr  Ala Ala Ala Cys Ala  Ala Cys Gly Gly Cys  Ala Gly Thr
    1970                1975                1980

Cys Ala  Gly Thr Cys Thr Gly  Thr Gly Gly Gly Ala  Cys Gly Thr
```

```
    1985                1990                1995

Thr Cys  Cys Thr Cys Cys Thr  Thr Cys Thr Ala Cys  Thr Gly Cys
    2000                2005                2010

Cys Thr  Gly Gly Ala Gly Thr  Ala Cys Thr Thr Thr  Cys Cys Thr
    2015                2020                2025

Thr Cys  Thr Cys Ala Gly Ala  Thr Gly Cys Thr Gly  Ala Gly Ala
    2030                2035                2040

Ala Cys  Gly Gly Gly Cys Ala  Ala Thr Ala Ala Cys  Thr Thr Thr
    2045                2050                2055

Gly Ala  Ala Thr Thr Cys Ala  Gly Cys Thr Ala Cys  Ala Cys Cys
    2060                2065                2070

Thr Thr  Thr Gly Ala Gly Gly  Ala Ala Gly Thr Gly  Cys Cys Thr
    2075                2080                2085

Thr Thr  Cys Cys Ala Cys Ala  Gly Cys Ala Gly Cys  Thr Ala Thr
    2090                2095                2100

Gly Cys  Gly Cys Ala Cys Ala  Gly Cys Cys Ala Gly  Ala Gly Cys
    2105                2110                2115

Cys Thr  Gly Gly Ala Cys Cys  Gly Gly Cys Thr Gly  Ala Thr Gly
    2120                2125                2130

Ala Ala  Thr Cys Cys Cys Cys  Thr Cys Ala Thr Cys  Gly Ala Cys
    2135                2140                2145

Cys Ala  Gly Thr Ala Cys Cys  Thr Gly Thr Ala Cys  Thr Ala Cys
    2150                2155                2160

Cys Thr  Gly Gly Cys Cys Cys  Gly Gly Ala Cys Cys  Cys Ala Gly
    2165                2170                2175

Ala Gly  Cys Ala Cys Thr Ala  Cys Gly Gly Gly Gly  Thr Cys Cys
    2180                2185                2190
```

```
Ala Cys  Ala Ala Gly Gly Gly  Ala Gly Cys Thr Gly  Cys Ala Gly
    2195                 2200                 2205

Thr Thr  Cys Cys Ala Thr Cys  Ala Gly Gly Cys Thr  Gly Gly Gly
    2210                 2215                 2220

Cys Cys  Cys Ala Ala Cys Ala  Cys Cys Ala Thr Gly  Gly Cys Cys
    2225                 2230                 2235

Gly Ala  Gly Cys Ala Ala Thr  Cys Ala Ala Ala Gly  Ala Ala Cys
    2240                 2245                 2250

Thr Gly  Gly Cys Thr Gly Cys  Cys Cys Gly Gly Ala  Cys Cys Cys
    2255                 2260                 2265

Thr Gly  Thr Thr Ala Thr Cys  Gly Gly Cys Ala Gly  Cys Ala Gly
    2270                 2275                 2280

Ala Gly  Ala Cys Thr Gly Thr  Cys Ala Ala Ala Ala  Ala Ala Cys
    2285                 2290                 2295

Ala Thr  Ala Gly Ala Cys Ala  Gly Cys Ala Ala Cys  Ala Ala Cys
    2300                 2305                 2310

Ala Ala  Cys Ala Gly Thr Ala  Ala Cys Thr Thr Thr  Gly Cys Cys
    2315                 2320                 2325

Thr Gly  Gly Ala Cys Cys Gly  Gly Gly Gly Cys Cys  Ala Cys Thr
    2330                 2335                 2340

Ala Ala  Ala Thr Ala Cys Cys  Ala Thr Cys Thr Gly  Ala Ala Thr
    2345                 2350                 2355

Gly Gly  Thr Ala Gly Ala Ala  Ala Thr Thr Cys Ala  Thr Thr Ala
    2360                 2365                 2370

Ala Cys  Cys Ala Ala Cys Cys  Cys Gly Gly Gly Cys  Gly Thr Ala
    2375                 2380                 2385

Gly Cys  Cys Ala Thr Gly Gly  Cys Cys Ala Cys Cys  Ala Ala Cys
```

```
    2390                2395                2400

Ala Ala  Gly Gly Ala Cys Gly  Ala Cys Gly Ala Gly  Gly Ala Cys
    2405                2410                2415

Cys Ala  Gly Thr Thr Cys Thr  Thr Thr Cys Cys Cys  Ala Thr Cys
    2420                2425                2430

Ala Ala  Cys Gly Gly Ala Gly  Thr Gly Cys Thr Gly  Gly Thr Thr
    2435                2440                2445

Thr Thr  Thr Gly Gly Cys Gly  Ala Ala Ala Cys Gly  Gly Gly Gly
    2450                2455                2460

Gly Cys  Thr Gly Cys Cys Ala  Ala Cys Ala Ala Gly  Ala Cys Ala
    2465                2470                2475

Ala Cys  Gly Cys Thr Gly Gly  Ala Ala Ala Ala Cys  Gly Thr Gly
    2480                2485                2490

Cys Thr  Ala Ala Thr Gly Ala  Cys Cys Ala Gly Cys  Gly Ala Gly
    2495                2500                2505

Gly Ala  Gly Gly Ala Gly Ala  Thr Cys Ala Ala Ala  Ala Cys Cys
    2510                2515                2520

Ala Cys  Cys Ala Ala Thr Cys  Cys Cys Gly Thr Gly  Gly Cys Thr
    2525                2530                2535

Ala Cys  Ala Gly Ala Ala Gly  Ala Ala Thr Ala Cys  Gly Gly Thr
    2540                2545                2550

Gly Thr  Gly Gly Thr Cys Thr  Cys Cys Ala Gly Cys  Ala Ala Cys
    2555                2560                2565

Cys Thr  Gly Cys Ala Ala Thr  Cys Gly Thr Cys Thr  Ala Cys Gly
    2570                2575                2580

Gly Cys  Cys Gly Gly Ala Cys  Cys Cys Cys Ala Gly  Ala Cys Ala
    2585                2590                2595
```

```
Cys Ala  Gly Ala Cys Thr Gly  Thr Cys Ala Ala Cys  Ala Gly Cys
    2600                 2605                 2610

Cys Ala  Gly Gly Gly Gly Gly  Cys Thr Cys Thr Gly  Cys Cys Cys
    2615                 2620                 2625

Gly Gly  Cys Ala Thr Gly Gly  Thr Cys Thr Gly Gly  Cys Ala Gly
    2630                 2635                 2640

Ala Ala  Cys Cys Gly Gly Gly  Ala Cys Gly Thr Gly  Thr Ala Cys
    2645                 2650                 2655

Cys Thr  Gly Cys Ala Gly Gly  Gly Thr Cys Cys Cys  Ala Thr Cys
    2660                 2665                 2670

Thr Gly  Gly Gly Cys Cys Ala  Ala Ala Ala Thr Thr  Cys Cys Thr
    2675                 2680                 2685

Cys Ala  Cys Ala Cys Gly Gly  Ala Cys Gly Gly Cys  Ala Ala Cys
    2690                 2695                 2700

Thr Thr  Thr Cys Ala Cys Cys  Cys Gly Thr Cys Thr  Cys Cys Cys
    2705                 2710                 2715

Cys Thr  Gly Ala Thr Gly Gly  Gly Cys Gly Gly Ala  Thr Thr Thr
    2720                 2725                 2730

Gly Gly  Ala Cys Thr Cys Ala  Ala Ala Cys Ala Cys  Cys Cys Gly
    2735                 2740                 2745

Cys Cys  Thr Cys Cys Thr Cys  Ala Ala Ala Thr Thr  Cys Thr Cys
    2750                 2755                 2760

Ala Thr  Cys Ala Ala Ala Ala  Ala Cys Ala Cys Cys  Cys Cys Gly
    2765                 2770                 2775

Gly Thr  Ala Cys Cys Thr Gly  Cys Thr Ala Ala Thr  Cys Cys Thr
    2780                 2785                 2790

Cys Cys  Ala Gly Ala Gly Gly  Thr Gly Thr Thr Thr  Ala Cys Thr
```

```
    2795                2800                2805

Cys Cys  Thr Gly Cys Cys Ala  Ala Gly Thr Thr Thr  Gly Cys Cys
    2810                2815                2820

Thr Cys  Ala Thr Thr Thr Ala  Thr Cys Ala Cys Gly  Cys Ala Gly
    2825                2830                2835

Thr Ala  Cys Ala Gly Cys Ala  Cys Cys Gly Gly Cys  Cys Ala Gly
    2840                2845                2850

Gly Thr  Cys Ala Gly Cys Gly  Thr Gly Gly Ala Gly  Ala Thr Cys
    2855                2860                2865

Gly Ala  Gly Thr Gly Gly Gly  Ala Ala Cys Thr Gly  Cys Ala Gly
    2870                2875                2880

Ala Ala  Ala Gly Ala Ala Ala  Ala Cys Ala Gly Cys  Ala Ala Ala
    2885                2890                2895

Cys Gly  Cys Thr Gly Gly Ala  Ala Thr Cys Cys Ala  Gly Ala Gly
    2900                2905                2910

Ala Thr  Thr Cys Ala Gly Thr  Ala Cys Ala Cys Cys  Thr Cys Ala
    2915                2920                2925

Ala Ala  Thr Thr Ala Thr Gly  Cys Cys Ala Ala Gly  Thr Cys Thr
    2930                2935                2940

Ala Ala  Thr Ala Ala Thr Gly  Thr Gly Gly Ala Ala  Thr Thr Thr
    2945                2950                2955

Gly Cys  Thr Gly Thr Cys Ala  Ala Cys Ala Ala Cys  Gly Ala Ala
    2960                2965                2970

Gly Gly  Gly Gly Thr Thr Thr  Ala Thr Ala Cys Thr  Gly Ala Gly
    2975                2980                2985

Cys Cys  Thr Cys Gly Cys Cys  Cys Cys Ala Thr Thr  Gly Gly Cys
    2990                2995                3000
```

Ala Cys Cys Cys Gly Thr Thr Ala Cys Cys Thr Cys Ala Cys Cys
    3005   3010   3015

Cys Gly Thr Ala Ala Cys Cys Thr Gly Thr Ala Ala Thr Thr Gly
    3020   3025   3030

Cys Cys Thr Gly Thr Thr Ala Ala Thr Cys Ala Ala Thr Ala Ala
    3035   3040   3045

Ala Cys Cys Gly Gly Thr Thr Ala Ala Thr Thr Cys Gly Thr Thr
    3050   3055   3060

Thr Cys Ala Gly Thr Thr Gly Ala Ala Cys Thr Thr Thr Gly Gly
    3065   3070   3075

Thr Cys Thr Cys Thr Gly Cys Gly Ala Ala Gly Gly Gly Cys Gly
    3080   3085   3090

Ala Ala Thr Thr Cys
    3095

<210> 63
<211> 728
<212> PRT
<213> Artificial Sequence

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

<400> 63

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
```

```
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495
```

```
Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Glu Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
```

705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 64
<211> 2495
<212> DNA
<213> Adeno-associated virus

<400> 64
gaattcgccc tttctacggc tgcgtcaact agaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattcatcat ctgctggggc gggctcccga gattgcttgc tcggcctgcg 180

atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt 240

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 300

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 360

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 420

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 480

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 540

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 600

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 660

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaaaggccag 720

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 780

cctcaaccaa tcggagaacc ccccgcaggc ccctctggtc tgggatctgg tacaatggct 840

gcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 900

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 960

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 1020

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 1080

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 1140

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 1200

acgaacgacg gcgttacgac catcgctaat aaccttacca gcacgattca ggtcttctcg 1260

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1320

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1380

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1440

acgggcaata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1500

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1560

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1620

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1680

agactgtcaa aaaacataga cagcaacaac accagtaact ttgcctggac cggggccact 1740

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1800

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1860

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1920

accaatcccg tggctacaga acagtacggt gtggtctcca gcaacctgca atcgtctacg 1980

gccggacccc agacacagac tgtcaacagc caggggggctc tgcccggcat ggtctggcag 2040

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atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 2220

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2280

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2340

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2400

acccgttacc tcacccgtaa cctgtaattg cctgttaatc aataaaccgg ttaattcgtt 2460

tcagttgaac tttggtctct gcgaagggcg aattc 2495

<210> 65
<211> 728
<212> PRT
<213> Artificial Sequence

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

<400> 65

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220
```

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His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430
```

```
Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Thr Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655
```

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 66
<211> 2504
<212> DNA
<213> Adeno-associated virus

<400> 66
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gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattcatcat ctgctggggc gggctcccga gattgcttgc tcggcctgcg 180

atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt 240

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 300

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 360

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 420

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 480

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 540

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 600

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 660

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaaaggccag 720

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 780

cctcaaccaa tcggagaacc ccccgcaggc ccctctggtc tgggatctgg tacaatggct 840

gcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 900

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 960

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 1020

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 1080

aacagattcc actgccactt ctcatcacgt gactggcagc gactcatcaa caacaactgg 1140

ggattccggc ccaagagact caacttcaag ctcttcaaca tccaggtcaa ggaggtcacg 1200

cagaatgaag gcaccaagac catcgccaat aaccttacca gcacgattca ggtctttacg 1260

gactcggaat accggctccc gtacgtcctc ggctctgcgc accagggctg cctgcctccg 1320

ttcccggcgg acgtcttcat gattcctcag tacgggtacc tgactctgaa caacggcagt 1380

caggccgtgg gccgttcctc cttctactgc ctggagtact ttccttctca aatgctgaga 1440

acgggcaaca actttgagtt cagctaccag tttgaggacg tgccttttca cagcagctac 1500

gcgcacagcc aaagcctgga ccggctgatg aacccccctca tcgaccagta cctgtactac 1560

ctgtctcgga ctcagtccac gggaggtacc gcaggaactc agcagttgct attttctcag 1620

gccgggccta ataacatgtc ggctcaggcc aaaaactggc tacccgggcc ctgctaccgg 1680

cagcaacgcg tctccacgac actgtcgcaa aataacaaca gcaactttgc ttggaccggt 1740

gccaccaagt atcatctgaa tggcagagac tctctggtaa atcccggtgt cgctatggca 1800

acgcacaagg acgacgaaga gcgatttttt ccatccagcg gagtcttgat gtttgggaaa 1860

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atcaaaacca ccaacccagt ggccacagaa cagtacggcg tggtggccga taacctgcaa 1980

cagcaaaacg ccgctcctat tgtaggggcc gtcaacagtc aaggagcctt acctggcatg 2040

gtctggcaga accgggacgt gtacctgcag ggtcctatct gggccaagat tcctcacacg 2100

gacggcaact ttcatccttc gccgctgatg ggaggctttg gactgaaaca cccgcctcct 2160

cagatcctga ttaagaatac acctgttccc gcggatcctc caactacctt cagtcaagcc 2220

aagccggcgt cgttcatcac gcagtacagc accggacagg tcagcgtgga aattgaatgg 2280

gagctgcaga aagagaacag caagcgctgg aacccagaga ttcagtatac ttccaactac 2340

tacaaatcta caaatgtgga ctttgctgtc aatactgagg gtacttattc agagcctcgc 2400

cccattggca cccgttacct cacccgtaac ctgtaattgc ctgttaatca ataaaccggt 2460

taattcgttt cagttgaact ttggtctctg cgaagggcga attc 2504

<210> 67
<211> 731
<212> PRT
<213> Artificial Sequence

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

<400> 67

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

```
Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
               165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
               245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Ser Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
               325                 330                 335

Gln Val Phe Thr Asp Ser Glu Tyr Arg Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly
```

```
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser Thr Gly
        435                 440                 445

Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly Pro Asn
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540

Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575

Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590
```

```
Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Thr
                645                 650                 655

Phe Ser Gln Ala Lys Pro Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            660                 665                 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        675                 680                 685

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr
    690                 695                 700

Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu Pro Arg
705                 710                 715                 720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730
```

<210> 68
<211> 3128
<212> DNA
<213> Adeno-associated virus

<400> 68

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gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt       60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt      120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcttccg      180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg      240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg      300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt      360
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tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

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ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

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cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

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gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

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aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460

agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

ttgcctgtta atcaataaac cggctaattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> 69
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 69

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220
```

```
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


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


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415


Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
```

```
Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655
```

```
Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 70
<211> 3084
<212> DNA
<213> Adeno-associated virus

<400> 70

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gaattcgccc tttctacggc tgcatcaact ggaccaatga gaactttccc ttcaacgatt       60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt      120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg      180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg      240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagttcg      300

aactcacccg ccgtctggag cacgactttg gcaaggtgac caagcaggaa gtcaaagagt      360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg      420

gcggagccag caaaagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct      480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg      540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca      600

aaacgtgcga gaaaatgaat cagaatttca acatttgctt cacgcacggg gtcagagact      660

gctcagaatg tttccccggt gcatcagaat ctcaaccggt cgtcagaaaa aaaacgtatc      720
```

agaaactgtg tgccattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggacgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggcttgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacctgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca cctcagcgtt cccccgactc ctccacgggc 1320

atcggcaaga aaggccacca gcccgcgaga aagagactga actttgggca gactggcgac 1380

tcggagtcag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaacca tctctacaag 1620

caaatctcca acgggacatc gggaggaagc actaacgaca acacctactt tggctacagc 1680

acccccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaataa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtgtt tacggactcg gaataccagc tcccgtacgt ccccggctct 1920

gcgcaccagg gctgcctccc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tatctgaccc taaacaatgg cagtcaggct gtgggccgtt cctccttcta ctgcctggaa 2040

tacttccctt ctcaaatgct gaggacgggc aacaactttg aattcagcta caccttcgag 2100

gacgtgcctt tccacagcag ctacgcgcac agccagagcc tggaccggct gatgaaccct 2160

ctcatcgacc agtacctgta ttacttatcc agaactcagt ccacaggagg aactcaaggt 2220

actcagcaat tgttattttc tcaagccggg cccgcaaaca tgtcggctca ggccaagaac 2280

tggctacctg gaccgtgtta ccgtcagcaa cgagtttcca cgacactgtc gcaaaacaac 2340

aacagcaatt ttgcttggac cggtgccacc aagtatcacc tgaatggcag agactccctg 2400

gttaatcccg gcgttgccat ggctacccac aaggacgacg aggagcgctt cttcccgtca 2460

agcggagttc taatgtttgg caagcagggg gctggaaaag acaatgtgga ctacagcagc 2520

gtgatgctca ccagcgaaga agaaattaaa actactaacc cagtggctac agagcagtat 2580

ggtgtggtgg cagacaacct gcagcagacc aacggagctc ccattgtggg aactgtcaac 2640

agccaggggg ccttacctgg tatggtctgg caaaaccggg acgtgtacct gcagggcccc 2700

atctgggcca aaattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctggtgaaaa acactcctgt tcctgcggat 2820

cctccgacca ccttcagcca ggccaagctg gcttctttta tcacgcagta cagcaccgga 2880

caggtcagcg tggaaatcga atgggagctg cagaaagaaa acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcactcgtt atctcacccg taatctgtaa 3060

ttgcttgtta atcaataaac cggt 3084

<210> 71
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 71

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
```

```
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
```

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            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720
```

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 72
<211> 3123
<212> DNA
<213> Adeno-associated virus

<400> 72
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gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc 120

aaggccattc tcggcggcag caaggtgcgc gtggaccaaa agtgcaagtc gtccgcccag 180

atcgacccca cccccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg 240

aacagcacca ccttcgagca ccagcagccg ttgcaggacc ggatgttcaa gttcgaactc 300

acccgccgtc tggagcacga ctttggcaag gtgaccaagc aggaagtcaa agagttcttc 360

cgctgggcgc aggatcacgt gaccgaggtg gcgcatgagt tctacgtcag aaagggcgga 420

gccagcaaaa gacccgcccc cgatgacgcg gatataagcg agcccaagcg ggcctgcccc 480

tcagtcgcgg atccatcgac gtcagacgcg gaaggagctc cggtggactt tgccgacagg 540

taccaaaaca aatgttctcg tcacgcgggc atgctccaga tgctgtttcc ctgcaaaacg 600

tgcgagagaa tgaatcagaa tttcaacatt tgcttcacgc acggggtcag agactgctca 660

gaatgtttcc ccggtgcatc agaatctcaa ccggtcgtca gaaaaaaaac gtatcagaaa 720

ctgtgtgcca ttcatcatct gctggggcgg gcacccgaga ttgcttgctc ggcctgcgat 780

ctggtcaacg tggacctgga cgactgtgtt tctgagcaat aaatgactta aaccaggtat 840

ggctgccgat ggttatcttc cagattggct tgaggacaac ctctctgagg gcattcgcga 900

gtggtgggac ctgaaacctg gagccccgaa acccaaagcc aaccagcaaa agcaggacga 960

cggccggggt ctggtgcttc ctggctacaa gtacctcgga cccttcaacg gactcgacaa 1020

gggggagccc gtcaacgcgg cggacgcagc ggccctcgag cacgacaagg cctacgacca 1080

gcagctcaaa gcgggtgaca atccgtacct gcggtataac cacgccgacg ccgagtttca 1140

ggagcgtctg caagaagata cgtcttttgg gggcaacctc gggcgagcag tcttccaggc 1200

caagaagcgg gttctcgaac ctctcggtct ggttgaggaa ggcgctaaga cggctcctgg 1260

aaagaagaga ccggtagagc catcacctca gcgttccccc gactcctcca cgggcatcgg 1320

caagaaaggc caccagcccg cgagaaagag actgaacttt gggcagactg gcgactcgga 1380

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 1440

tggtacaatg gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg 1500

agtgggtagt tcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 1560

caccaccagc acccgaacct gggccctgcc cacctacaac aaccatctct acaagcaaat 1620

ctccaacggg acatcgggag gaagcactaa cgacaacacc tactttggct acagcacccc 1680

ctgggggtat tttgacttca acagattcca ctgccacttc tcaccacgtg actggcagcg 1740

actcatcaac aataactggg gattccggcc caagagactc aacttcaagc tcttcaacat 1800

ccaggtcaag gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag 1860

cacgattcag gtgtttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca 1920

ccagggctgc ctccctccgt tcccggcgga cgtcttcatg attcctcagt acgggtatct 1980

gaccctaaac aatggcagtc aggctgtggg ccgttcctcc ttctactgcc tggaatactt 2040

cccttctcaa atgctgagga cgggcaacaa ctttgaattc agctacacct tcgaggacgt 2100

gcctttccac agcagctacg cgcacagcca gagcctggac cggctgatga accctctcat 2160

cgaccagtac ctgtattact tatccagaac tcagtccaca ggaggaactc aaggtactca 2220

gcaattgtta ttttctcaag ccgggcccgc aaacatgtcg gctcaggcca agaactggct 2280

acctggaccg tgttaccgtc agcaacgagt ttccacgaca ctgtcgcaaa acaacaacag 2340

caattttgct tggaccggtg ccaccaagta tcacctgaat ggcagagact ccctggttaa 2400

tcccggcgtt gccatggcta cccacaagga cgacgaggag cgcttcttcc cgtcaagcgg 2460

agttctaatg tttggcaagc agggggctgg aaaagacaat gtggactaca gcagcgtgat 2520

gctcaccagc gaagaagaaa ttaaaactac taacccagtg gctacagagc agtatggtgt 2580

ggtggcagac aacctgcagc agaccaacgg agctcccatt gtgggaactg tcaacagcca 2640

gggggcctta cctggtatgg tctggcaaaa ccgggacgtg tacctgcagg gccccatctg 2700

ggccaaaatt cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg 2760

actgaaacac ccgcctcctc agatcctggt gaaaaacact cctgttcctg cggatcctcc 2820

gaccaccttc agccaggcca agctggcttc ttttatcacg cagtacagca ccggacaggt 2880

cagcgtggaa atcgaatggg agctgcagaa agaaaacagc aagcgctgga acccagagat 2940

tcagtatact tccaactact acaaatctac aaatgtggac tttgctgtca atactgaggg 3000

tacttattca gagcctcgcc ccattggcac tcgttatctc acccgtaatc tgtaattgct 3060

tgttaatcaa taaaccggtt aattcgtttc agttgaactt tggtctctgc gaagggcgaa 3120

ttc 3123

<210> 73
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 73

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560
```

```
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 74
<211> 3122
<212> DNA
<213> Adeno-associated virus

<400> 74
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgtgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag cgccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac gaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttccac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

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agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

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cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

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cgactcatca acaacaattg gggattccgg cccaaaagac tcaacttcaa gctgttcaac 1800

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gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaattacat 3060

gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctctgcg aagggcgaat 3120

tc 3122

<210> 75
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 75

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Leu Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

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

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Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Thr Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
```

385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
435 440 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
450 455 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
485 490 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
500 505 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
515 520 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
530 535 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
580 585 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 76
<211> 3117
<212> DNA
<213> Adeno-associated virus

<400> 76
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gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc 120

aaggccattc tcggcggcag caaggtgcgt gtggaccaaa agtgcaagtc ttccgcccag 180

atcgatccca cccccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg 240

aacagcacca ccttcgagca ccagcagccg ttgcaggacc ggatgttcaa atttgaactc 300

acccgccgtc tggagcatga ctttggcaag gtgacgaagc aggaagtcaa agagttcttc 360

cgctgggcgc aggatcacgt gaccgaggtg gcgcatgagt tccacgtcag aaagggtgga 420

gccaacaaga gacccgcccc cgatgacgcg gatataagcg agcccaagcg ggcctgcccc 480

tcagtcgcgg atccatcgac gtcagacgcg gaaggagctc cggtggactt tgccgacagg 540

taccaaaaca aatgttctcg tcacgcgggc atgcttcaga tgctgtttcc ctgcaagaca 600

tgcgagagaa tgaatcagaa tttcaacatt tgcttcacgc acgggaccag agactgttca 660

gaatgtttcc ccggcgtgtc agaatctcaa ccggtcgtca gaaagaggac gtatcggaaa 720

ctctgtgcga ttcatcatct gctggggcgg gctcccgaga ttgcttgctc ggcctgcgat 780

ctggtcaacg tggacctgga tgactgtgtt tctgagcaat aaatgactta aaccaggtat 840

ggctgccgat ggttatcttc cagattggct cgaggacaac ctctctgagg gcattcgcga 900

gtggtgggac ttgaaacctg gagccccgaa acccaaagcc aaccagcaaa agcaggacga 960

cggccggggt ctggtgcttc ctggctacaa gtacctcgga cccttcaacg gactcgacaa 1020

gggggagccc gtcaacgcgg cggacgcagc ggccctcgag cacgacaaag cctacgacca 1080

gcagctcaaa gcgggtgaca atccgtacct gcggtataat cacgccgacg ccgagtttca 1140

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caagaagcgg gttctcgaac ctctcggtct ggttgaggaa ggcgctaaga cggctcctgg 1260

aaagaagaga ccggtagagc agtcgccaca agagccagac tcctcctcgg gcatcggcaa 1320

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agtccccgac ccacaacctc tcggagaacc tccagcagcc ccctcaggtc tgggacctaa 1440

tacaatggct tcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt 1500

gggtaattcc tcgggaaatt ggcattgcga ttccacatgg ctgggggaca gagtcatcac 1560

caccagcacc cgaacctggg ccctgcccac ctacaacaac cacctctaca agcaaatctc 1620

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cgtgcgggtc tttacggact cggagtacca gttaccgtac gtgctaggat ccgctcacca 1920

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cacttccaac tactacaaat ctacaaatgt ggactttgct gtcaacacgg aaggagttta 3000

tagcgagcct cgccccattg gcacccgtta cctcacccgc aacctgtaat tacatgttaa 3060

tcaataaacc ggttaattcg tttcagttga actttggtct ctgcgaaggg cgaattc 3117

<210> 77
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 77

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Arg Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460
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Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Ser
                485                 490                 495


Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575


Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590


Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
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Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 78
<211> 3121
<212> DNA
<213> Adeno-associated virus

<400> 78
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cgtcgacaag atggtgatct ggtgggagga gggcaagatg acggccaagg tcgtggagtc 120

cgccaaggcc attctcggcg gcagcaaggt gcgtgtggac caaaagtgca agtcttccgc 180

ccagatcgat cccacccccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga 240

cgggaacagc accaccttcg agcaccagca gccgttgcag gaccggatgt tcaaatttga 300

actcacccgc cgtctggagc atgactttgg caaggtgacg aagcaggaag tcaaagagtt 360

cttccgctgg gcgcaggatc acgtgaccga ggtggcgcat gagttccacg tcagaaaggg 420

tggcgccaac aagagacccg cccccgatga cgcggatata agcgagccca agcgggcctg 480

cccctcagtc gcggatccat cgacgtcaga cgcggaagga gctccggtgg actttgccga 540

caggtaccaa aacaaatgtt ctcgtcacgc gggcatgctt cagatgctgt ttccctgcaa 600

gacatgcgag agaatgaatc agaatttcaa catttgcttc acgcacggga ccagagactg 660

ttcagaatgt ttccccggcg tgtcagaatc tcaaccggtc gtcagaaaga ggacgtatcg 720

gaaactctgt gcgattcatc atctgctggg gcgggctccc gagattgctt gctcggcctg 780

cgatctggtc aacgtggacc tggatgactg tgtttctgag caataaatga cttaaaccag 840

gtatggctgc cgatggttat cttccagatt ggctcgagga caacctctct gagggcattc 900

gcgagtggtg ggacttgaaa cctggagccc cgaaacccaa agccaaccag caaaagcagg 960

acgacggccg gggtctggtg cttcctggct acaagtacct cggacccttc aacggactcg 1020

acaaggggga gcccgtcaac gcggcggacg cagcggccct cgagcacgac aaagcctacg 1080

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ctggaaagaa gagaccggta gagcagtcgc cacaagagcc agactcctcc tcgggcatcg 1320

gcaagacagg ccagcagccc gctaaaaaga gactcaattt tggtcagact ggcgactcag 1380

agtcagtccc cgacccacaa cctctcggag aacctccagc agccccctca ggtctgggac 1440

ctaatacaat ggcttcaggc ggtggcgctc caatggcaga caataacgaa ggcgccgacg 1500

gagtgggtaa ttcctcggga aattggcatt gcgattccac atggctgggg gacagagtca 1560

tcaccaccag cacccgaacc tgggccctgc ccacctacaa caaccacctc tacaagcaaa 1620

tctccaacgg cacctcggga ggaagcacca acgacaacac ctattttggc tacagcaccc 1680

cctgggggta ttttgacttc aacagattcc actgtcactt ttcaccacgt gactggcaac 1740

gactcatcaa caacaattgg ggattccggc ccaaaagact caacttcaag ctgttcaaca 1800

tccaggtcaa ggaagtcacg acgaacgaag gcaccaagac catcgccaat aatctcacca 1860

gcaccgtgca ggtctttacg gacttggagt accagttacc gtacgtgcta ggatccgctc 1920

accagggatg tctgcctccg ttcccggcgg acgtcttcat ggttcctcag tacggctatt 1980

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ctctggcatt cagccaagcg ggtcctagct caatggccaa ccaggctaga aattgggtgc 2280

ccggaccttg ctaccggcag cagcgcgtct ccacgacaac caaccagaac aacaacagca 2340

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cgggcgtggc aatggcttcc cacaaggatg acgacgaccg cttcttccct tcgagcgggg 2460

tcctgatttt tggcaagcaa ggagccggga acgatggagt ggattacagc caagtgctga 2520

ttacagatga ggaagaaatc aaggctacca accccgtggc cacagaagaa tatggagcag 2580

tggccatcaa caaccaggcc gccaatacgc aggcgcagac cggactcgtg cacaaccagg 2640

gggtgattcc cggcatggtg tggcagaata gagacgtgta cctgcagggt cccatctggg 2700

ccaaaattcc tcacacggac ggcaactttc acccgtctcc cctgatgggc ggctttggac 2760

tgaagcaccc gcctcctcaa attctcatca agaacacacc ggttccagcg gacccgccgc 2820

ttaccttcaa ccaggccaag ctgaactctt tcatcacgca gtacagcacc ggacaggtca 2880

gcgtggaaat cgagtgggag ctgcagaaag aaaacagcaa acgctggaat ccagagattc 2940

aatacacttc caactactac aaatctacaa atgtggactt tgctgtcaac acggaaggag 3000

tttatagcga gcctcgcccc attggcaccc gttacctcac ccgcaacctg taattacatg 3060

ttaatcaata aaccggttaa ttcgtttcag ttgaactttg gtctctgcga agggcgaatt 3120

c 3121

<210> 79
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 79

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Pro Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
```

530 535 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
580 585 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 80
<211> 3122
<212> DNA

<213> Adeno-associated virus

<400> 80
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgtgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac gaagcaggaa gtcaaagggt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttccac gtgcgagccc 420

aagcgggcct gcccctcagt cgcggatcca tcgacgtcag accagaaagg gtggagccaa 480

caagagaccc gcccccgatg acgcggatat aagcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaagcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataatcacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagcagtcg ccacaagagc cagactcctc ctcgggcatc 1320

ggcaagacag gccagcagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 1380

gagtcagtcc ccgacccaca acctctcgga gaacctccag cagccccctc aggtctggga 1440

cctaatacaa tggcttcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 1500

ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg ggacagagtc 1560

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 1620

atctccaacg gcacctcggg aggaagcacc aacgacaaca cctattttgg ctacagcacc 1680

ccctgggggt attttgactt caacagattc cactgtcact tttcaccacg tgactggcaa 1740

cgactcatca acaacaattg gggattccgg cccaaaagac tcaacttcaa gctgttcaac 1800

atccaggtca aggaagtcac gacgaacgaa ggcaccaaga ccatcgccaa taatctcacc 1860

agcaccgtgc aggtctttac ggactcggag taccagttac cgtacgtgct aggatccgct 1920

caccagggat gtctgcctcc gttcccggcg gacgtcttca tggttcctca gtacggctat 1980

ttaactttaa acaatggaag ccaagccctg ggacgttcct ccttctactg tctggagtat 2040

ttcccatcgc agatgctgag aaccggcaac aactttcagt tcagctacac cttcgaggac 2100

gtgcctttcc acagcagcta cgcgcacagc cagagcctgg acaggctgat gaatcccctc 2160

atcgaccagt acctgtacta cctggtcaga acgcaaacga ctggaactgg agggacgcag 2220

actctggcat tcagccaagc gggtcctagc tcaatggcca accaggctag aaattgggtg 2280

cccggacctt gctaccggca gcagcgcgtc tccacgacaa ccaaccagaa caacaacagc 2340

aactttgcct ggacgggagc tgccaagttt aagctgaacg gccgagactc tctaatgaat 2400

ccgggcgtgg caatggcttc ccacaaggat gacgacgacc gcttcttccc ttcgagcggg 2460

gtcctgattt ttggcaagca aggagccggg aacgatggag tggattacag ccaagtgctg 2520

attacagatg aggaagaaat caaggctacc aaccccgtgg ccacagaaga atatggagca 2580

gtggccatca acaaccaggc cgccaatacg caggcgcaga ccggactcgt gcacaaccag 2640

ggggtgattc ccggcatggt gtggcagaat agagacgtgt acctgcaggg tcccatctgg 2700

gccaaaattc ctcacacgga cggcaacttt cacccgtctc ccctgatggg cggctttgga 2760

ctgaagcacc cgcctcctca aattctcatc aagaacacac cggttccagc ggacccgccg 2820

cttaccttca accaggccaa gctgaactct ttcatcacgc agtacagcac cggacaggtc 2880

agcgtggaaa tcgagtggga gctgcagaaa gaaaacagca aacgctggaa tccagagatt 2940

caatacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa cacggagggg 3000

gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaattacat 3060

gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctctgcg aagggcgaat 3120

tc 3122

<210> 81
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 81

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380
```

```
Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 82
<211> 2370
<212> DNA
<213> Adeno-associated virus

<400> 82
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagttcg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac caagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gcggagccag caaaagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagacgctg tttccctgca 600

aaacgtgcga gagaatgaat cagaatttca acatttgctt cacgcacggg gtcagagact 660

gctcagaatg tttccccggt gcatcagaat ctcaaccggt cgtcagaaaa aaaacgtatc 720

agaaactgtg tgccattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggacgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggcttgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacctgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca cctcagcgtt cccccgactc ctccacgggc 1320

atcggcaaga aaggccacca gcccgcgaga aagagactga actttgggca gactggcgac 1380

tcggagtcag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaacca tctctacaag 1620

caaatctcca acgggacatc gggaggaagc actaacgaca acacctactt tggctacagc 1680

acccccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaataa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtgtt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctccc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tatctgaccc taaacaatgg cagtcaggct gtgggccgtt cctccttcta ctgcctggaa 2040

tacttccctt ctcaaatgct gaggacgggc aacaactttg aattcagcta caccttcgag 2100

gacgtgcctt tccacagcag ctacgcgcac agccagagcc tggaccggct gatgaaccct 2160

ctcatcgacc agtacctgta ttacttatcc agaactcagt ccacaggagg aactcaaggt 2220

actcagcaat tgttattttc tcaagccggg cccgcaaaca tgtyggctca ggccaagaac 2280

tggctacctg gaccgtgtta ccgtcagcaa cgagtttcca cgacactgtc gcaaaacaac 2340

aacagcaatt ttgctggacc ggtgccacca 2370

<210> 83
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 83

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
```

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            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560
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```
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 84
<211> 2205
<212> DNA
<213> Adeno-associated virus

<400> 84
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tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggaccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

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cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc aacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 85
<211> 734
<212> PRT
<213> Adeno-associated virus

<400> 85

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn

```
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

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

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

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

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320
```

```
Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
```

530 535 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545 550 555 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
565 570 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
580 585 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
595 600 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
610 615 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
645 650 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
675 680 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
690 695 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705 710 715 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730

<210> 86
<211> 3128
<212> DNA

<213> Adeno-associated virus

<400> 86
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gcgtcgacaa gatgttgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagccgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgcg ggaccggatg ttcaagtttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcagagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaaa aagacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctagatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

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atcggcaaga aaggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacttc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaatgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

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aacagcaact gtaaatcccg gtgtcgctat ggcaacccac aaggacgacg aagagcgatt 2400

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gttatgctaa ccagtgagga agaaattaaa accaccaacc cagtggccac ggaacagtac 2580

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agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacgga aactttcatc cctcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agctaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaaa acagcaaacg ctggaaccca 2940

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gatggcactt attctgagcc tcgccccatt ggcacccgtt acctcacccg taatctgtaa 3060

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gcgaattc 3128

<210> 87
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 87

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


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

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
```

```
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

```
Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 88
<211> 3128
<212> DNA
<213> Adeno-associated virus

<400> 88

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gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt      120

ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagtcgtccg      180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg      240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagtttg      300
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tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt tgtcagaaaa aagacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctagatgact gtgtttctga gcaataaatg acttaaacca 840

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ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

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gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

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gatggcactt attctgagcc tcgccccatt ggcacccgtt acctcacccg taatctgtaa 3060

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<210> 89
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 89

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220
```

```
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Pro Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
```

```
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655
```

```
Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 90
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 90

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735
```

Asn Leu

<210> 91
<211> 2172
<212> DNA
<213> Artificial Sequence

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

<400> 91
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tt 2172

<210> 92
<211> 720
<212> PRT
<213> Artificial Sequence

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

<400> 92

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

```
Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255
```

```
Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480
```

```
Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685
```

```
Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720
```

<210> 93
<211> 724
<212> PRT
<213> Adeno-associated virus 5

<400> 93

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160
```

```
Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
```

```
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

```
Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 94
<211> 2175
<212> PRT
<213> Adeno-associated virus

<400> 94

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

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

Gly Gly Ala Ala Gly Ala Ala Gly Thr Thr Gly Gly Thr Gly Ala Ala
        35                  40                  45
```

```
Gly Gly Thr Cys Thr Thr Cys Gly Cys Gly Ala Gly Thr Thr Thr Thr
    50                  55                  60

Thr Gly Gly Gly Cys Cys Thr Thr Gly Ala Ala Gly Cys Gly Gly Gly
65                  70                  75                  80

Cys Cys Cys Ala Cys Cys Gly Ala Ala Ala Cys Cys Ala Ala Ala Ala
                85                  90                  95

Cys Cys Cys Ala Ala Thr Cys Ala Gly Cys Ala Gly Cys Ala Thr Cys
            100                 105                 110

Ala Ala Gly Ala Thr Cys Ala Ala Gly Cys Cys Cys Gly Thr Gly Gly
        115                 120                 125

Thr Cys Thr Thr Gly Thr Gly Cys Thr Gly Cys Cys Thr Gly Gly Thr
    130                 135                 140

Thr Ala Thr Ala Ala Cys Thr Ala Thr Cys Thr Cys Gly Gly Ala Cys
145                 150                 155                 160

Cys Cys Gly Gly Ala Ala Ala Cys Gly Gly Thr Cys Thr Cys Gly Ala
                165                 170                 175

Thr Cys Gly Ala Gly Gly Ala Gly Ala Gly Cys Cys Thr Gly Thr Cys
            180                 185                 190

Ala Ala Cys Ala Gly Gly Gly Cys Ala Gly Ala Cys Gly Ala Gly Gly
        195                 200                 205

Thr Cys Gly Cys Gly Cys Gly Ala Gly Ala Gly Cys Ala Cys Gly Ala
    210                 215                 220

Cys Ala Thr Cys Thr Cys Gly Thr Ala Cys Ala Ala Cys Gly Ala Gly
225                 230                 235                 240

Cys Ala Gly Cys Thr Thr Gly Ala Gly Gly Cys Gly Gly Gly Ala Gly
                245                 250                 255
```

```
Ala Cys Ala Ala Cys Cys Cys Cys Thr Ala Cys Cys Thr Cys Ala Ala
            260                 265                 270

Gly Thr Ala Cys Ala Ala Cys Cys Ala Cys Gly Cys Gly Gly Ala Cys
        275                 280                 285

Gly Cys Cys Gly Ala Gly Thr Thr Thr Cys Ala Gly Gly Ala Gly Ala
    290                 295                 300

Ala Gly Cys Thr Cys Gly Cys Cys Gly Ala Cys Gly Ala Cys Ala Cys
305                 310                 315                 320

Ala Thr Cys Cys Thr Thr Cys Gly Gly Gly Gly Gly Ala Ala Ala Cys
                325                 330                 335

Cys Thr Cys Gly Gly Ala Ala Ala Gly Gly Cys Ala Gly Thr Cys Thr
            340                 345                 350

Thr Thr Cys Ala Gly Gly Cys Cys Ala Ala Gly Ala Ala Ala Ala Gly
        355                 360                 365

Gly Gly Thr Thr Cys Thr Cys Gly Ala Ala Cys Cys Thr Thr Thr Thr
    370                 375                 380

Gly Gly Cys Cys Thr Gly Gly Thr Thr Gly Ala Ala Gly Ala Gly Gly
385                 390                 395                 400

Gly Thr Gly Cys Thr Ala Ala Gly Ala Cys Gly Gly Cys Cys Cys Cys
                405                 410                 415

Thr Ala Cys Cys Gly Gly Ala Ala Ala Gly Cys Gly Gly Ala Thr Ala
            420                 425                 430

Gly Ala Cys Gly Ala Cys Cys Ala Cys Thr Thr Thr Cys Cys Ala Ala
        435                 440                 445

Ala Ala Ala Gly Ala Ala Ala Gly Ala Ala Gly Gly Cys Thr Cys Gly
    450                 455                 460

Gly Ala Cys Cys Gly Ala Ala Gly Ala Gly Gly Ala Cys Thr Cys Cys
465                 470                 475                 480
```

```
Ala Ala Gly Cys Cys Thr Thr Cys Cys Ala Cys Cys Thr Cys Gly Thr
               485                 490                 495

Cys Ala Gly Ala Cys Gly Cys Cys Gly Ala Ala Gly Cys Thr Gly Gly
            500                 505                 510

Ala Cys Cys Cys Ala Gly Cys Gly Gly Ala Thr Cys Cys Cys Ala Gly
        515                 520                 525

Cys Ala Gly Cys Thr Gly Cys Ala Ala Ala Thr Cys Cys Cys Ala Gly
    530                 535                 540

Cys Cys Cys Ala Ala Cys Cys Ala Gly Cys Cys Thr Cys Ala Ala Gly
545                 550                 555                 560

Thr Thr Thr Gly Gly Gly Ala Gly Cys Thr Gly Ala Thr Ala Cys Ala
               565                 570                 575

Ala Thr Gly Thr Cys Thr Gly Cys Gly Gly Gly Ala Gly Gly Thr Gly
            580                 585                 590

Gly Cys Gly Gly Cys Cys Cys Ala Thr Thr Gly Gly Gly Cys Gly Ala
        595                 600                 605

Cys Ala Ala Thr Ala Ala Cys Cys Ala Ala Gly Gly Thr Gly Cys Cys
    610                 615                 620

Gly Ala Thr Gly Gly Ala Gly Thr Gly Gly Gly Cys Ala Ala Thr Gly
625                 630                 635                 640

Cys Cys Thr Cys Gly Gly Gly Ala Gly Ala Thr Thr Gly Gly Cys Ala
               645                 650                 655

Thr Thr Gly Cys Gly Ala Thr Thr Cys Cys Ala Cys Gly Thr Gly Gly
            660                 665                 670

Ala Thr Gly Gly Gly Gly Gly Ala Cys Ala Gly Ala Gly Thr Cys Gly
        675                 680                 685
```

```
Thr Cys Ala Cys Cys Ala Ala Gly Thr Cys Cys Ala Cys Cys Cys Gly
    690                 695                 700

Ala Ala Cys Cys Thr Gly Gly Gly Thr Gly Cys Thr Gly Cys Cys Cys
705                 710                 715                 720

Ala Gly Cys Thr Ala Cys Ala Ala Cys Ala Ala Cys Cys Ala Cys Cys
                725                 730                 735

Ala Gly Thr Ala Cys Cys Gly Ala Gly Ala Gly Ala Thr Cys Ala Ala
            740                 745                 750

Ala Ala Gly Cys Gly Gly Cys Thr Cys Cys Gly Thr Cys Gly Ala Cys
        755                 760                 765

Gly Gly Ala Ala Gly Cys Ala Ala Cys Gly Cys Cys Ala Ala Cys Gly
    770                 775                 780

Cys Cys Thr Ala Cys Thr Thr Thr Gly Gly Ala Thr Ala Cys Ala Gly
785                 790                 795                 800

Cys Ala Cys Cys Cys Cys Cys Thr Gly Gly Gly Gly Gly Thr Ala Cys
                805                 810                 815

Thr Thr Thr Gly Ala Cys Thr Thr Thr Ala Ala Cys Cys Gly Cys Thr
            820                 825                 830

Thr Cys Cys Ala Cys Ala Gly Cys Cys Ala Cys Thr Gly Gly Ala Gly
        835                 840                 845

Cys Cys Cys Cys Cys Gly Ala Gly Ala Cys Thr Gly Gly Cys Ala Ala
    850                 855                 860

Ala Gly Ala Cys Thr Cys Ala Thr Cys Ala Ala Cys Ala Ala Cys Thr
865                 870                 875                 880

Ala Cys Thr Gly Gly Gly Gly Cys Thr Thr Cys Ala Gly Ala Cys Cys
                885                 890                 895

Cys Cys Gly Gly Thr Cys Cys Cys Thr Cys Ala Gly Ala Gly Thr Cys
            900                 905                 910
```

```
Ala Ala Ala Ala Thr Cys Thr Thr Cys Ala Ala Cys Ala Thr Thr Cys
        915                 920                 925


Ala Ala Gly Thr Cys Ala Ala Ala Gly Ala Gly Gly Thr Cys Ala Cys
    930                 935                 940


Gly Gly Thr Gly Cys Ala Gly Gly Ala Cys Thr Cys Cys Ala Cys Cys
945                 950                 955                 960


Ala Cys Cys Ala Cys Cys Ala Thr Cys Gly Cys Cys Ala Ala Cys Ala
                965                 970                 975


Ala Cys Cys Thr Cys Ala Cys Cys Thr Cys Cys Ala Cys Cys Gly Thr
            980                 985                 990


Cys Cys Ala Ala Gly Thr Gly Thr  Thr Thr Ala Cys Gly  Gly Ala Cys
        995                 1000                1005


Gly Ala  Cys Gly Ala Cys Thr  Ala Cys Cys Ala Gly  Cys Thr Gly
    1010                1015                1020


Cys Cys  Cys Thr Ala Cys Gly  Thr Cys Gly Thr Cys  Gly Gly Cys
    1025                1030                1035


Ala Ala  Cys Gly Gly Gly Ala  Cys Cys Gly Ala Gly  Gly Gly Ala
    1040                1045                1050


Thr Gly  Cys Cys Thr Gly Cys  Cys Gly Gly Cys Cys  Thr Thr Cys
    1055                1060                1065


Cys Cys  Thr Cys Cys Gly Cys  Ala Gly Gly Thr Cys  Thr Thr Thr
    1070                1075                1080


Ala Cys  Gly Cys Thr Gly Cys  Cys Gly Cys Ala Gly  Thr Ala Cys
    1085                1090                1095


Gly Gly  Thr Thr Ala Cys Gly  Cys Gly Ala Cys Gly  Cys Thr Gly
    1100                1105                1110
```

```
Ala Ala  Cys Cys Gly Cys Gly  Ala Cys Ala Ala Cys  Ala Cys Ala
    1115                1120                1125


Gly Ala  Ala Ala Ala Thr Cys  Cys Cys Ala Cys Cys  Gly Ala Gly
    1130                1135                1140


Ala Gly  Gly Ala Gly Cys Ala  Gly Cys Thr Thr Cys  Thr Thr Cys
    1145                1150                1155


Thr Gly  Cys Cys Thr Ala Gly  Ala Gly Thr Ala Cys  Thr Thr Thr
    1160                1165                1170


Cys Cys  Cys Ala Gly Cys Ala  Ala Gly Ala Thr Gly  Cys Thr Gly
    1175                1180                1185


Ala Gly  Ala Ala Cys Gly Gly  Gly Cys Ala Ala Cys  Ala Ala Cys
    1190                1195                1200


Thr Thr  Thr Gly Ala Gly Thr  Thr Thr Ala Cys Cys  Thr Ala Cys
    1205                1210                1215


Ala Ala  Cys Thr Thr Thr Gly  Ala Gly Gly Ala Gly  Gly Thr Gly
    1220                1225                1230


Cys Cys  Cys Thr Thr Cys Cys  Ala Cys Thr Cys Cys  Ala Gly Cys
    1235                1240                1245


Thr Thr  Cys Gly Cys Thr Cys  Cys Cys Ala Gly Thr  Cys Ala Gly
    1250                1255                1260


Ala Ala  Cys Cys Thr Gly Thr  Thr Cys Ala Ala Gly  Cys Thr Gly
    1265                1270                1275


Gly Cys  Cys Ala Ala Cys Cys  Cys Gly Cys Thr Gly  Gly Thr Gly
    1280                1285                1290


Gly Ala  Cys Cys Ala Gly Thr  Ala Cys Thr Thr Gly  Thr Ala Cys
    1295                1300                1305


Cys Gly  Cys Thr Thr Cys Gly  Thr Gly Ala Gly Cys  Ala Cys Ala
    1310                1315                1320
```

```
Ala Ala  Thr Ala Ala Cys Ala  Cys Thr Gly Gly Cys  Gly Gly Ala
    1325                1330                1335

Gly Thr  Cys Cys Ala Gly Thr  Thr Cys Ala Ala Cys  Ala Ala Gly
    1340                1345                1350

Ala Ala  Cys Cys Thr Gly Gly  Cys Cys Gly Gly Gly  Ala Gly Ala
    1355                1360                1365

Thr Ala  Cys Gly Cys Cys Ala  Ala Cys Ala Cys Cys  Thr Ala Cys
    1370                1375                1380

Ala Ala  Ala Ala Ala Cys Thr  Gly Gly Thr Thr Cys  Cys Cys Gly
    1385                1390                1395

Gly Gly  Gly Cys Cys Cys Ala  Thr Gly Gly Gly Cys  Cys Gly Ala
    1400                1405                1410

Ala Cys  Cys Cys Ala Gly Gly  Gly Cys Thr Gly Gly  Ala Ala Cys
    1415                1420                1425

Cys Thr  Gly Gly Gly Cys Thr  Cys Cys Gly Gly Gly  Gly Thr Cys
    1430                1435                1440

Ala Ala  Cys Cys Gly Cys Gly  Cys Cys Ala Gly Thr  Gly Thr Cys
    1445                1450                1455

Ala Gly  Cys Gly Cys Cys Thr  Thr Cys Gly Cys Cys  Ala Cys Gly
    1460                1465                1470

Ala Cys  Cys Ala Ala Thr Ala  Gly Gly Ala Thr Gly  Gly Ala Gly
    1475                1480                1485

Cys Thr  Cys Gly Ala Gly Gly  Gly Cys Gly Cys Gly  Ala Gly Thr
    1490                1495                1500

Thr Ala  Cys Cys Ala Gly Gly  Thr Gly Cys Cys Cys  Cys Cys Gly
    1505                1510                1515
```

```
Cys Ala  Gly Cys Cys Gly Ala  Ala Cys Gly Gly Cys  Ala Thr Gly
    1520                1525                1530

Ala Cys  Cys Ala Ala Cys Ala  Ala Cys Cys Thr Cys  Cys Ala Gly
    1535                1540                1545

Gly Gly  Cys Ala Gly Cys Ala  Ala Cys Ala Cys Cys  Thr Ala Thr
    1550                1555                1560

Gly Cys  Cys Cys Thr Gly Gly  Ala Gly Ala Ala Cys  Ala Cys Thr
    1565                1570                1575

Ala Thr  Gly Ala Thr Cys Thr  Thr Cys Ala Ala Cys  Ala Gly Cys
    1580                1585                1590

Cys Ala  Gly Cys Cys Gly Gly  Cys Gly Ala Ala Cys  Cys Cys Gly
    1595                1600                1605

Gly Gly  Cys Ala Cys Cys Ala  Cys Cys Gly Cys Cys  Ala Cys Gly
    1610                1615                1620

Thr Ala  Cys Cys Thr Cys Gly  Ala Gly Gly Gly Cys  Ala Ala Cys
    1625                1630                1635

Ala Thr  Gly Cys Thr Cys Ala  Thr Cys Ala Cys Cys  Ala Gly Cys
    1640                1645                1650

Gly Ala  Gly Ala Gly Cys Gly  Ala Gly Ala Cys Gly  Cys Ala Gly
    1655                1660                1665

Cys Cys  Gly Gly Thr Gly Ala  Ala Cys Cys Gly Cys  Gly Thr Gly
    1670                1675                1680

Gly Cys  Gly Thr Ala Cys Ala  Ala Cys Gly Thr Cys  Gly Gly Cys
    1685                1690                1695

Gly Gly  Gly Cys Ala Gly Ala  Thr Gly Gly Cys Cys  Ala Cys Cys
    1700                1705                1710

Ala Ala  Cys Ala Ala Cys Cys  Ala Gly Ala Gly Cys  Thr Cys Cys
    1715                1720                1725
```

```
Ala Cys  Cys Ala Cys Thr Gly  Cys Cys Cys Cys Cys  Gly Cys Gly
    1730                1735                1740

Ala Cys  Cys Gly Gly Cys Ala  Cys Gly Thr Ala Cys  Ala Ala Cys
    1745                1750                1755

Cys Thr  Cys Cys Ala Gly Gly  Ala Ala Ala Thr Cys  Gly Thr Gly
    1760                1765                1770

Cys Cys  Cys Gly Gly Cys Ala  Gly Cys Gly Thr Gly  Thr Gly Gly
    1775                1780                1785

Ala Thr  Gly Gly Ala Gly Ala  Gly Gly Gly Ala Cys  Gly Thr Gly
    1790                1795                1800

Thr Ala  Cys Cys Thr Cys Cys  Ala Ala Gly Gly Ala  Cys Cys Cys
    1805                1810                1815

Ala Thr  Cys Thr Gly Gly Gly  Cys Cys Ala Ala Gly  Ala Thr Cys
    1820                1825                1830

Cys Cys  Ala Gly Ala Gly Ala  Cys Gly Gly Gly Gly  Gly Cys Gly
    1835                1840                1845

Cys Ala  Cys Thr Thr Thr Cys  Ala Cys Cys Cys Cys  Thr Cys Thr
    1850                1855                1860

Cys Cys  Gly Gly Cys Cys Ala  Thr Gly Gly Gly Cys  Gly Gly Ala
    1865                1870                1875

Thr Thr  Cys Gly Gly Ala Cys  Thr Cys Ala Ala Ala  Cys Ala Cys
    1880                1885                1890

Cys Cys  Ala Cys Cys Gly Cys  Cys Cys Ala Thr Gly  Ala Thr Gly
    1895                1900                1905

Cys Thr  Cys Ala Thr Cys Ala  Ala Gly Ala Ala Cys  Ala Cys Gly
    1910                1915                1920
```

```
Cys Cys  Thr Gly Thr Gly Cys  Cys Cys Gly Gly Ala  Ala Ala Thr
    1925                1930                1935

Ala Thr  Cys Ala Cys Cys Ala  Gly Cys Thr Thr Cys  Thr Cys Gly
    1940                1945                1950

Gly Ala  Cys Gly Thr Gly Cys  Cys Cys Gly Thr Cys  Ala Gly Cys
    1955                1960                1965

Ala Gly  Cys Thr Thr Cys Ala  Thr Cys Ala Cys Cys  Cys Ala Gly
    1970                1975                1980

Thr Ala  Cys Ala Gly Cys Ala  Cys Cys Gly Gly Gly  Cys Ala Gly
    1985                1990                1995

Gly Thr  Cys Ala Cys Cys Gly  Thr Gly Gly Ala Gly  Ala Thr Gly
    2000                2005                2010

Gly Ala  Gly Thr Gly Gly Gly  Ala Gly Cys Thr Cys  Ala Ala Gly
    2015                2020                2025

Ala Ala  Gly Gly Ala Ala Ala  Ala Cys Thr Cys Cys  Ala Ala Gly
    2030                2035                2040

Ala Gly  Gly Thr Gly Gly Ala  Ala Cys Cys Cys Ala  Gly Ala Gly
    2045                2050                2055

Ala Thr  Cys Cys Ala Gly Thr  Ala Cys Ala Cys Ala  Ala Ala Cys
    2060                2065                2070

Ala Ala  Cys Thr Ala Cys Ala  Ala Cys Gly Ala Cys  Cys Cys Cys
    2075                2080                2085

Cys Ala  Gly Thr Thr Thr Gly  Thr Gly Gly Ala Cys  Thr Thr Thr
    2090                2095                2100

Gly Cys  Cys Cys Cys Gly Gly  Ala Cys Ala Gly Cys  Ala Cys Cys
    2105                2110                2115

Gly Gly  Gly Gly Ala Ala Thr  Ala Cys Ala Gly Ala  Ala Cys Cys
    2120                2125                2130
```

Ala Cys Cys Ala Gly Ala Cys Cys Thr Ala Thr Cys Gly Gly Ala
    2135   2140   2145

Ala Cys Cys Cys Gly Ala Thr Ala Cys Cys Thr Thr Ala Cys Cys
    2150   2155   2160

Cys Gly Ala Cys Cys Cys Cys Thr Thr Thr Ala Ala
    2165   2170   2175

<210> 95
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 95
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctg 2208

<210> 96
<211> 736
<212> PRT
<213> Adeno-associated virus 6

<400> 96

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460
```

```
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210>  97
<211>  623
<212>  PRT
<213>  Adeno-associated virus 6

<400>  97

Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15


Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30


Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45


Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60


Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80


Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95


Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110


Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125
```

```
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala His Asp
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
        275                 280                 285

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
```

```
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465                 470                 475                 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
                485                 490                 495

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
        515                 520                 525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
    530                 535                 540

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545                 550                 555                 560
```

```
Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
                565                 570                 575

Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
            580                 585                 590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
        595                 600                 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610                 615                 620
```

<210> 98
<211> 4683
<212> DNA
<213> Adeno-associated virus 6

<400> 98

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ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc       60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg      120

gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag      180

ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat      240

gtggtcacgc tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga      300

ggtttgaacg cgcagcgcca tgccggggtt ttacgagatt gtgattaagg tccccagcga      360

ccttgacgag catctgcccg gcatttctga cagctttgtg aactgggtgg ccgagaagga      420

atgggagttg ccgccagatt ctgacatgga tctgaatctg attgagcagg cacccctgac      480

cgtggccgag aagctgcagc gcgacttcct ggtccagtgg cgccgcgtga gtaaggcccc      540

ggaggccctc ttctttgttc agttcgagaa gggcgagtcc tacttccacc tccatattct      600

ggtggagacc acgggggtca aatccatggt gctgggccgc ttcctgagtc agattaggga      660

caagctggtg cagaccatct accgcgggat cgagccgacc ctgcccaact ggttcgcggt      720

gaccaagacg cgtaatggcg ccggaggggg gaacaaggtg gtggacgagt gctacatccc      780

caactacctc ctgcccaaga ctcagcccga gctgcagtgg gcgtggacta acatggagga      840

gtatataagc gcgtgtttaa acctggccga gcgcaaacgg ctcgtggcgc acgacctgac      900

ccacgtcagc cagacccagg agcagaacaa ggagaatctg aaccccaatt ctgacgcgcc      960
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tgtcatccgg tcaaaaacct ccgcacgcta catggagctg gtcgggtggc tggtggaccg 1020

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gaatcagaat ttcaacattt gcttcacgca cgggaccaga gactgttcag aatgtttccc 2040

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gcaaccggtt acacattaac tgcttagttg cgcttcgcga ataccctag tgatggagtt 4560

gcccactccc tctatgcgcg ctcgctcgct cggtggggcc ggcagagcag agctctgccg 4620

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caa 4683

<210> 99
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 99
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

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actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

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gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

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aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 100
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 100

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 101
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 101

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
```

530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 102
<211> 736
<212> PRT

<213> Adeno-associated virus

<400> 102

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


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


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
               645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
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<210> 103
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 103

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
```

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
```

```
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 104
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 104
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

aacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtcattt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

gcaaagaaga gaccggtaga gccgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacag tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

attaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccagtg aaactgcagg tagtaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagaagctgc ggttcaagct cttcaacatc 960

caggtcaagg aggtcacgac gaatgacggc gttacgacca tcgctaataa ccttaccagc 1020

acgattcagg tattctcgga ctcggaatac cagctgccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg 1140

actctcaaca atggcagtca gtctgtggga cgttcctcct tctactgcct ggagtacttc 1200

ccctctcaga tgctgagaac gggcaacaac tttgagttca gctacagctt cgaggacgtg 1260

cctttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcccctcatc 1320

gaccagtact tgtactacct ggccagaaca cagagtaacc caggaggcac agctggcaat 1380

cgggaactgc agttttacca gggcgggcct tcaactatgg ccgaacaagc caagaattgg 1440

ttacctggac cttgcttccg gcaacaaaga gtctccaaaa cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggcagaaa ctcgttggtt 1560

aatcccggcg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc 1620

ggagtcctga tttttggaaa aactggagca actaacaaaa ctacattgga aaatgtgtta 1680

atgacaaatg aagaagaaat tcgtcctact aatcctgtag ccacggaaga atacgggata 1740

gtcagcagca acttacaagc ggctaatact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga tggcaacttt cacccgtctc ctttgatggg cggctttgga 1920

cttaaacatc cgcctcctca gatcctgatc aagaacactc ccgttcccgc taatcctccg 1980

gaggtgttta ctcctgccaa gtttgcttcg ttcatcacac agtacagcac cggacaagtc 2040

agcgtggaaa tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatt 2100

cagtacacct ccaactttga aaagcagact ggtgtggact ttgccgttga cagccagggt 2160

gtttactctg agcctcgccc tattggcact cgttacctca cccgtaatct gtaa 2214

<210> 105
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 105

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
```

```
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510
```

```
Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
```

725 730 735

Asn Leu

<210> 106
<211> 737
<212> PRT
<213> Adeno-associated virus 7

<400> 106

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380
```

```
Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590
```

```
Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 107
<211> 623
<212> PRT
<213> Artificial Sequence

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

<400> 107

```
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15
```

```
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Val Leu Val Glu
                85                  90                  95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

Arg Glu Lys Leu Val Gln Thr Ile Tyr Arg Gly Val Glu Pro Thr Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240
```

```
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ser
        275                 280                 285

Leu Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445
```

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465 470 475 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Ser Lys Arg Pro Ala
485 490 495

Pro Asp Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
500 505 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
515 520 525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Ile Gln Met
530 535 540

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545 550 555 560

Cys Phe Thr His Gly Val Arg Asp Cys Leu Glu Cys Phe Pro Gly Val
565 570 575

Ser Glu Ser Gln Pro Val Val Arg Lys Lys Thr Tyr Arg Lys Leu Cys
580 585 590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
595 600 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
610 615 620

<210> 108
<211> 4721
<212> DNA
<213> Adeno-associated virus 7

<400> 108
ttggccactc cctctatgcg cgctcgctcg ctcggtgggg cctgcggacc aaaggtccgc 60

agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgcat agagggagtg 120

gccaactcca tcactagggg taccgcgaag cgcctcccac gctgccgcgt cagcgctgac 180

gtaaatcacg tcatagggga gtggtcctgt attagctgtc acgtgagtgc ttttgcgaca 240

ttttgcgaca ccacgtggcc atttgaggta tatatggccg agtgagcgag caggatctcc 300

attttgaccg cgaaatttga acgagcagca gccatgccgg gtttctacga gatcgtgatc 360

aaggtgccga gcgacctgga cgagcacctg ccgggcattt ctgactcgtt tgtgaactgg 420

gtggccgaga aggaatggga gctgcccccg gattctgaca tggatctgaa tctgatcgag 480

caggcacccc tgaccgtggc cgagaagctg cagcgcgact tcctggtcca atggcgccgc 540

gtgagtaagg ccccggaggc cctgttcttt gttcagttcg agaagggcga gagctacttc 600

caccttcacg ttctggtgga gaccacgggg gtcaagtcca tggtgctagg ccgcttcctg 660

agtcagattc gggagaagct ggtccagacc atctaccgcg gggtcgagcc cacgctgccc 720

aactggttcg cggtgaccaa gacgcgtaat ggcgccggcg gggggaacaa ggtggtggac 780

gagtgctaca tccccaacta cctcctgccc aagacccagc ccgagctgca gtgggcgtgg 840

actaacatgg aggagtatat aagcgcgtgt ttgaacctgg ccgaacgcaa acggctcgtg 900

gcgcagcacc tgacccacgt cagccagacg caggagcaga acaaggagaa tctgaacccc 960

aattctgacg cgcccgtgat caggtcaaaa acctccgcgc gctacatgga gctggtcggg 1020

tggctggtgg accggggcat cacctccgag aagcagtgga tccaggagga ccaggcctcg 1080

tacatctcct tcaacgccgc ctccaactcg cggtcccaga tcaaggccgc gctggacaat 1140

gccggcaaga tcatggcgct gaccaaatcc gcgcccgact acctggtggg gccctcgctg 1200

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atctggctgt ttgggcccgc caccaccggc aagaccaaca ttgcggaagc catcgcccac 1380

gccgtgccct tctacggctg cgtcaactgg accaatgaga actttccctt caacgattgc 1440

gtcgacaaga tggtgatctg gtgggaggag ggcaagatga cggccaaggt cgtggagtcc 1500

gccaaggcca ttctcggcgg cagcaaggtg cgcgtggacc aaaagtgcaa gtcgtccgcc 1560

cagatcgacc ccacccccgt gatcgtcacc tccaacacca acatgtgcgc cgtgattgac 1620

gggaacagca ccaccttcga gcaccagcag ccgttgcagg accggatgtt caaatttgaa 1680

ctcacccgcc gtctggagca cgactttggc aaggtgacga agcaggaagt caaagagttc 1740

ttccgctggg ccagtgatca cgtgaccgag gtggcgcatg agttctacgt cagaaagggc 1800

ggagccagca aaagacccgc ccccgatgac gcggatataa gcgagcccaa gcgggcctgc 1860

ccctcagtcg cggatccatc gacgtcagac gcggaaggag ctccggtgga ctttgccgac 1920

aggtaccaaa acaaatgttc tcgtcacgcg ggcatgattc agatgctgtt tccctgcaaa 1980

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<210> 109
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 109
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<210> 110
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 110

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

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

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540
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Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
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Leu
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<210> 111

<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 111
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

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<210> 112
<211> 2213
<212> DNA
<213> Adeno-associated virus 8

<400> 112
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<211> 4393
<212> DNA
<213> Adeno-associated virus 8

<400> 113
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gttttacgtc agaaagggcg gagccagcaa aagacccgcc cccgatgacg cggataaaag 1740

cgagcccaag cgggcctgcc cctcagtcgc ggatccatcg acgtcagacg cggaaggagc 1800

tccggtggac tttgccgaca ggtaccaaaa caaatgttct cgtcacgcgg gcatgcttca 1860

gatgctgttt ccctgcaaaa cgtgcgagag aatgaatcag aatttcaaca tttgcttcac 1920

acacggggtc agagactgct cagagtgttt ccccggcgtg tcagaatctc aaccggtcgt 1980

cagaaagagg acgtatcgga aactctgtgc gattcatcat ctgctggggc gggctcccga 2040

gattgcttgc tcggcctgcg atctggtcaa cgtggacctg gatgactgtg tttctgagca 2100

ataaatgact taaaccaggt atggctgccg atggttatct tccagattgg ctcgaggaca 2160

acctctctga gggcattcgc gagtggtggg cgctgaaacc tggagccccg aagcccaaag 2220

ccaaccagca aaagcaggac gacggccggg gtctggtgct tcctggctac aagtacctcg 2280

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agcgtttttt tcccagtaac gggatcctga tttttggcaa acaaaatgct gccagagaca 3780

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ctccgctgat gggcggcttt ggcctgaaac atcctccgcc tcagatcctg atcaagaaca 4080

cgcctgtacc tgcggatcct ccgaccacct tcaaccagtc aaagctgaac tctttcatca 4140

cgcaatacag caccggacag gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca 4200

gcaagcgctg gaaccccgag atccagtaca cctccaacta ctacaaatct acaagtgtgg 4260

actttgctgt taatacagaa ggcgtgtact ctgaaccccg ccccattggc acccgttacc 4320

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tttggtctct gcg 4393

<210> 114
<211> 738
<212> PRT
<213> Adeno-associated virus 8

<400> 114

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220
```

```
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
```

```
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655
```

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 115
<211> 737
<212> PRT
<213> Adeno-associated virus 8

<400> 115

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Ile Gln Lys
705                 710                 715                 720

Ala Cys Thr Leu Asn Pro Ala Pro Leu Ala Pro Val Thr Ser Pro Val
                725                 730                 735
```

Ile

<210> 116
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 116
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

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ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

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gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 117
<211> 2214
<212> DNA
<213> Artificial Sequence

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

<400> 117
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

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caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgcc tgagcggacg gcgatgagtc ttccgggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctg 2214

<210> 118
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 118

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile

```
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
```

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Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Pro Glu Arg Thr Ala Met
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580 585 590

Ser Leu Pro Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 119
<211> 2214
<212> DNA
<213> Artificial Sequence

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

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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

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cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

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aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

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ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctg 2214

<210> 120
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 120

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

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            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320
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Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
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    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Ser Phe Ser Arg Ala Val
            580                 585                 590

Leu Cys Asp Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
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Asn Leu
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<210> 121
<211> 4385
<212> DNA
<213> Adeno-associated virus 9

<400> 121
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tccaatggcg ccgcgtgagt aaggccccgg aggccctctt ctttgttcag ttcgagaagg 480

gcgagagcta ctttcacctg cacgttctgg tcgagaccac gggggtcaag tccatggtgc 540

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<210> 122
<211> 4382
<212> DNA
<213> Adeno-associated virus 9

<400> 122

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aataacctta ccagcaccgt ccaggtcttt acggactcgg agtaccagct accgtacgtc 3180

ctaggctctg cccaccaagg atgcctgcca ccgtttcctg cagacgtctt catggttcct 3240

cagtacggct acctgacgct caacaatgga agtcaagcgt taggacgttc ttctttctac 3300

tgtctggaat acttcccttc tcagatgctg agaaccggca acaactttca gttcagctac 3360

actttcgagg acgtgccttt ccacagcagc tacgcacaca gccagagtct agatcgactg 3420

atgaaccccc tcatcgacca gtacctatac tacctggtca gaacacagac aactggaact 3480

gggggaactc aaactttggc attcagccaa gcaggcccta gctcaatggc caatcaggct 3540

agaaactggg tacccgggcc ttgctaccgt cagcagcgcg tctccacaac caccaaccaa 3600

aataacaaca gcaactttgc gtggacggga gctgctaaat tcaagctgaa cgggagagac 3660

tcgctaatga atcctggcgt ggctatggca tcgcacaaag acgacgagga ccgcttcttt 3720

ccatcaagtg gcgttctcat atttggcaag caaggagccg ggaacgatgg agtcgactac 3780

agccaggtgc tgattacaga tgaggaagaa attaaagcca ccaaccctgt agccacagag 3840

gaatacggag cagtggccat caacaaccag gccgctaaca cgcaggcgca aactggactt 3900

gtgcataacc agggagttat tcctggtatg gtctggcaga accgggacgt gtacctgcag 3960

ggccctattt gggctaaaat acctcacaca gatggcaact ttcacccgtc tcctctgatg 4020

ggtggatttg gactgaaaca cccacctcca cagattctaa ttaaaaatac accagtgccg 4080

gcagatcctc ctcttacctt caatcaagcc aagctgaact ctttcatcac gcagtacagc 4140

acgggacaag tcagcgtgga aatcgagtgg gagctgcaga aagaaaacag caagcgctgg 4200

aatccagaga tccagtatac ttcaaactac tacaaatcta caaatgtgga ctttgctgtc 4260

aataccgaag gtgtttactc tgagcctcgc cccattggta ctcgttacct cacccgtaat 4320

ttgtaattgc ctgttaatca ataaaccggt taattcgttt cagttgaact ttggtctctg 4380

cg 4382

<210> 123
<211> 736
<212> PRT
<213> Adeno-associated virus 9

<400> 123

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

```
Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 124
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 124

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Glu Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 125
<211> 623
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 125

```
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                  10                  15


Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30


Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Arg Asn Leu Ile
        35                  40                  45


Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60


Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80


Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Val Leu Val Glu
                85                  90                  95


Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110


Arg Glu Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125


Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140


Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160


Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175


Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190


Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205
```

```
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ser
        275                 280                 285

Leu Pro Val Asp Ile Thr Gln Asn Arg Ile Tyr Arg Ile Leu Gln Leu
    290                 295                 300

Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415
```

```
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Ser Lys Arg Pro Ala
                485                 490                 495

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
        515                 520                 525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
    530                 535                 540

Leu Leu Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545                 550                 555                 560

Cys Phe Thr His Gly Val Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
                565                 570                 575

Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
            580                 585                 590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
        595                 600                 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610                 615                 620
```

<210> 126
<211> 2211

<212> DNA
<213> Adeno-associated virus

<400> 126
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 127
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 127

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 128
<211> 2460
<212> DNA
<213> Adeno-associated virus

<400> 128
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgaccg agtcattacc 60

accagcaccc ggacttgggc cctgcccacc tacaacaacc acctctacaa gcaaatctcc 120

agccaatcgg gtgccaccaa cgacaaccac tacttcggct acagcacccc ttgggggtat 180

tttgatttca acagattcca ctgccatttc tcaccacgtg actggcagcg actcatcaac 240

aacaactggg gattcatggc tgccgatggt tatcttccag attggctcga ggacactctc 300

tctgaaggaa tcagacagtg gtggaagctc aaacctggcc caccaccgcc gaaacctaac 360

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aatcccgcga ccactttcac tcctggaaag tttgcttcgt tcattaccca gtattccacc 2280

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<210> 129
<211> 3123
<212> DNA
<213> Adeno-associated virus

<400> 129
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ctgccaaagc cattctgggt ggaggcaagg ttcgtgtgga ccagaaatgc aagtcttcgg 180

cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg 240

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aacttacccg ccgtttggat catgactttg ggaaggtcac caagcaggaa gtcaaagact 360

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<210> 130
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 130

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
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Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Gly Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Ala Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445
```

```
Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Val Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
            580                 585                 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

```
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 131
<211> 3123
<212> DNA
<213> Adeno-associated virus

<400> 131

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ctgccaaagc cattctgggt ggaagcaagg ttcgtgtgga ccagaaatgc aagtcttcgg      180

cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg      240

acggaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg      300

aacttacccg ccgtttggat catgactttg ggaaggtcac caagcaggaa gtcaaagact      360

ttttccggtg ggctcaagat cacgtgactg aggtggagca tgagttctac gtcaaaaagg      420

gtggagccaa gaaaaggccc gcccccgatg atgtatatat aaatgagccc aagcgggcgc      480

gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc ttcgataaac tacgcgggca      540

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aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt      660

tggaatgctt tcccgtgtca gaatctcaac ccgtttctgt cgtcagaaaa acgtatcaga      720

aactttgtta cattcatcat atcatgggaa aagaaccaga cgcctgcact gcctgcgacc      780

tggtaaatgt ggacttggat gactgtattt ctgagcaata aatgacttaa atcaggtatg      840

gctgctgacg gttatcttcc agattggctc gaggacactc tctctgaagg aatcagacag      900
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cta 3123

<210> 132
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 132

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asp Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
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        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asp Thr Thr Ala Ser Tyr
            580                 585                 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 133
<211> 3113
<212> DNA
<213> Adeno-associated virus

<400> 133
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ctgccaaagc cattctgggt ggaagcaagg ttcgtgtgga ccagaaatgc aagtcttcgg 180

cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg 240

acggaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg 300

aacttacccg ccgtttggat catgactttg ggaaggtcac caagcaggaa gtcaaagact 360

ttttccggtg ggctcaagat cacgtgactg aggtggagca tgagttctac gtcaaaaagg 420

gtggagccaa gaaaaggccc gcccccgatg atgtatatat aaatgagccc aagcgggcgc 480

gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc ttcgataaac tacgcggaca 540

ggtaccaaaa caaatgttct cgtcacgtgg gcatgaatct gatgctgttt ccctgtcgac 600

aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt 660

tggaatgctt tcccgtgtca gaatctcaac ccgttcctgt cgtcagaaaa acgtatcaga 720

aactttgtta cattcatcat atcatgggaa aagtaccaga cgcctgcact gcctgcgacc 780

tggtaaatgt ggacttggat gactgtattt ctgagcaata aatgacttaa atcaggtatg 840

gctgctgacg gttatcttcc agattggctc gaggacactc tctctgaagg aatcagacag 900

tggtggaagc tcaaacctgg cccaccaccg ccgaaaccta accaacaaca ccgggacgac 960

agtaggggtc ttgtgcttcc tgggtacaag tacctcggac ccttcaacgg actcgacaaa 1020

ggagagccgg tcaacgaggc agacgccgcg gccctcgagc acgacaaagc ctacgaccac 1080

cagctcaagc aaggggacaa cccgtacctc aaatacaacc acgcggacgc tgaatttcag 1140

gagcgtcttc aagaagatac gtctttcggg ggcaacctcg ggcgagcagt cttccaggcc 1200

aaaaagaggg tactcgagcc tcttggtctg gttgaggaag ctgttaagac ggctcctgga 1260

aaaaagagac ctatagagca gtctcctgca gaaccggact cttcctcggg catcggcaaa 1320

tcaggccagc agcccgctaa gaaaagactc aattttggtc agactggcga cacagagtca 1380

gtcccagacc ctcaaccaat cggagaaccc cccgcagccc cctctggtgt gggatctaat 1440

acaatggctt caggcggtgg ggcaccaatg gcagacaata acgaaggcgc cgacggagtg 1500

ggtaattcct cgggaaattg gcattgcgat tccacatgga tgggcgacag agttatcacc 1560

accagcacaa gaacctgggc cctccccacc tacaataatc acctctacaa gcaaatctcc 1620

agcgaatcgg gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 1680

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gaggtcacgc agaatgatgg aaccacgacc atcgccaata accttaccag cacggtgcag 1860

gtcttcacag actctgagta ccagctgccc tacgtcctcg gttcggctca ccagggctgc 1920

cttccgccgt tcccagcaga cgtcttcatg attcctcagt acggctactt gactctgaac 1980

aatggcagcc aagcggtagg acgttcttca ttctactgtc tagagtattt tccctctcag 2040

atgctgagga cgggaaacaa cttcaccttc agctacactt ttgaagacgt gcctttccac 2100

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ctgtattacc tgagcaaaac tcagggtaca agtggaacaa cgcagcaatc gagactgcag 2220

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cctggaatgg tgtggcagga ccgcgatgtc tatcttcaag gtcccatttg ggccaaaact 2700

cctcacacgg acggacactt tcatccttct ccgctcatgg gaggctttgg actgaaacac 2760

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gaaccccgcc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa 3060

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<210> 134
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 134

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

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Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Asn Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Pro Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn Arg Gln Ser Gln Asn Thr Thr Ala Ser Tyr
            580                 585                 590
```

```
Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 135
<211> 3122
<212> DNA
<213> Adeno-associated virus

<400> 135
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tcaacgattg cgtcgacaag atggtgatct ggtgggagga gggaaagatg accgccaagg 120

tcgtggaatc tgccaaagcc attctgggtg gaagcaaggt tcgtgtggac cagaaatgca 180

ggtcttcggc ccagatcgac ccgactccgg tgattgtcac ctctaacacc aacatgtgcg 240

ccgtgattga cggaaactcg accaccttcg agcaccagca gccgttgcaa gaccggatgt 300

tcaaatttga acttacccgc cgtttggatc atgactttgg gaaggtcacc aagcaggaag 360

tcaaagactt tttccggtgg gctcaagatc acgtgactga ggtggagcat gagttctacg 420

tcaaaaaggg tggagccaag aaaaggcccg cccccgatga tgtatatata aatgagccca 480

agcgggcgcg cgagtcagtt gcgcagccat cgacgtcaga cgcggaagct tcgataaact 540

acgcggacag gtaccaaaac aaatgttctc gtcacgtggg catgaatctg atgctgtttc 600

cctgtcgaca atgcgaaaga atgaatcaga attcaaatat ctgcttcaca cacgggcaaa 660

aagactgttt ggaatgcttt cccgtgtcag aatctcaacc cgtttctgtc gtcagaaaaa 720

cgtatcagaa actttgttac attcatcata tcatgggaaa agtaccagac gcctgcactg 780

cctgcgacct ggtaaatgtg gacttggatg actgtatttc tgagcaataa atgacttaaa 840

tcaggtatgg ctgctgacgg ttatcttcca gattggctcg aggacactct ctctgaagga 900

atcagacagt ggtggaagct caaacctggc ccaccaccgc cgaaacctaa ccaacaacac 960

cgggacgaca gtaggggtct tgtgcttcct gggtacaagt acctcggacc cttcaacgga 1020

ctcgacaaag gagagccggt caacgaggca gacgccgcgg ccctcgagca cgacaaagcc 1080

tacgaccacc agctcaagca aggggacaac ccgtacctca aatacaacca cgcggacgct 1140

gaatttcagg agcgtcttca agaagatacg tctttcgggg gcaacctcgg gcgagcagtc 1200

ttccaggcca aaaagagggt actcgagcct cttggtctgg ttgaggaagc tgttaagacg 1260

gctcctggaa aaaagagacc tatagagcag tctcctgcag aaccggactc ttcctcgggc 1320

atcggcaaat caggccagca gcccgctaag aaaagactca attttggtca gactggcgac 1380

acagagtcag tcccagaccc tcaaccaatc ggagaacccc ccgcagcccc ctctggtgtg 1440

ggatctaata caatggcttc aggcggtggg gcaccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtaattcctc gggaaattgg cattgcgatt ccacatggat gggcgacaga 1560

gttatcacca ccagcacaag aacctgggcc ctccccacct acaataatcg cctctacaag 1620

caaatctcca gcgaatcggg agccaccaac gacaaccact acttcggcta cagcaccccc 1680

tgggggtatt ttgactttaa cagattccac tgtcacttct caccacgtga ctggcagcga 1740

ctcatcaaca acaactgggg atttagaccc aagaaactca atttcaagct cttcaacatc 1800

caagtcaagg aggtcacgca gaatgatgga accacgacca tcgccaataa ccttaccagc 1860

acggtgcagg tcttcacaga ctctgagtac cagctgccct acgtcctcgg ttcggctcac 1920

cagggctgcc ttccgccgtt cccagcagac gtcttcatga ttcctcagta cggctacttg 1980

actctgaaca atggcagcca agcggtagga cgttcttcat tctactgtct agagtatttt 2040

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cctttccaca gcagctacgc gcacagccag agtctggatc ggctgatgaa tcctctcatt 2160

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ggaatcttac ctggaatggt gtggcaggac cgcgatgtct atcttcaagg tcccatttgg 2700

gccaaaactc ctcacacgga cggacacttt catccttctc cgctcatggg aggctttgga 2760

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accactttca ctcctggaaa gtttgcttcg ttcattaccc agtattccac cggacaggtc 2880

agcgtggaaa tagagtggga gctgcagaaa gaaaacagca aacgctggaa cccagaaatt 2940

cagtacacct ccaactacaa caagtcggtg aatgtggagt ttaccgtgga cgcaaacggt 3000

gtttattctg aaccccgccc tattggcact cgttacctta cccggaactt gtaatttcct 3060

gttaatgaat aaaccgattt atgcgtttca gttgaacttt ggtctctgcg aagggcgaat 3120

tc 3122

<210> 136
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 136

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
```

```
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn Arg Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445
```

```
Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
            580                 585                 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
```

660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 137
<211> 3121
<212> DNA
<213> Adeno-associated virus

<400> 137
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acaagcaatt acagattacg ggtgaggtaa cgggtgccga tggggcgagg ctcagaataa 120

gtgccatctg tgttaacagc aaagtccaca tttgtagatt tgtagtagtt ggaagtgtat 180

tgaatctctg ggttccagcg tttgctgttt tctttctgca gctcccattc aatttccacg 240

ctgacctgtc cggtgctgta ctgcgtgatg aacgacgcca gcttagcttg actgaaggta 300

gttggaggat ccgcgggaac aggtgtattc ttaatcagga tctgaggagg cgggtgtttc 360

agtccaaagc cccccatcag cggcgaggga tgaaagtttc cgtccgtgtg aggaatcttg 420

gcccagatag gaccctgcag gtacacgtcc cggttctgcc agaccatgcc aggtaaggct 480

ccttgactgt tgacggcccc tacaatagga gcggcgtttt gctgttgcag gttatcggcc 540

accacgccgt actgttctgt ggccactggg ttggtggttt taatttcttc ctcactggtt 600

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ggaaagtact ccaggcagta gaaggaggaa cggcccacgg cctgactgcc attgttcaga 1140

gtcaggtacc cgtactgagg aatcatgaag acgtccgccg ggaacggagg caggcagccc 1200

tggcgcgcag agccgaggac gtacgggagc tggtattccg agtccgtaaa gacctgaatc 1260

gtgctggtaa ggttattggc gatggtcttg gtgccttcat tctgcgtgac ctccttgacc 1320

tggatgttga agagcttgaa gttgagtctc ttgggccgga atccccagtt gttgttgatg 1380

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caggggtgc tgtagccgaa gtaggtgttg tcgttggtgc ttcctcccga agtcccgttg 1500

gagatttgct tgtagaggtg gttgttgtag gtggggaggg cccaggttcg ggtgctggtg 1560

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actccgtcgg cgccttcgtt attgtctgcc attggagcgc caccgcctgc agccattgta 1680

ccagatccca gaccagaggg gcctgcgggg ggttctccga ttggttgagg gtcgggcact 1740

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tcctgaaact cggcgtcggc gtggttatac cgcaggtacg gattgtcacc cgctttgagc 2040

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gccatacctg atctaaatca tttattgttc aaagatgcag tcatccaaat ccacattgac 2340

cagatcgcag gcagtgcaag cgtctggcac ctttcccatg atatgatgaa tgtagcacag 2400

tttctgatac gccttttga cgacagaaac gggttgagat tctgacacgg gaaagcactc 2460

taaacagtct ttctgtccgt gagtgaagca gatatttgaa ttctgattca ttctctcgca 2520

ttgtctgcag ggaaacagca tcagattcat gcccacgtga cgagaacatt tgttttggta 2580

cctgtccgcg tagttgatcg aagcttccgc gtctgacgtc gatggctgcg caactgactc 2640

gcgcacccgt ttgggctcac ttatatctgc gtcactgggg gcgggtcttt tcttggctcc 2700

acccttttg acgtagaatt catgctccac ctcaaccacg tgatcctttg cccaccggaa 2760

aaagtctttg acttcctgct tggtgacctt cccaaagtca tgatccagac ggcgggtgag 2820

ttcaaatttg aacatccggt cttgcaacgg ctgctggtgt tcgaaggtcg ttgagttccc 2880

gtcaatcacg gcgcacatgt tggtgttgga ggtgacgatc acgggagtcg ggtctatctg 2940

ggccgaggac ttgcatttct ggtccacgcg caccttgctt cctccgagaa tggctttggc 3000

cgactccacg accttggcgg tcatcttccc ctcctcccac cagatcacca tcttgtcgac 3060

acagtcgttg aagggaaagt tctcattggt ccagttgacg cagccgtaga agggcgaatt 3120

c 3121

<210> 138
<211> 733
<212> PRT
<213> Artificial Sequence

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

<400> 138

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Leu
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe His Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300
```

```
Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510
```

```
Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Gly Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685

Ser Lys Arg Arg Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
    690                 695                 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705                 710                 715                 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730
```

<210> 139
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 139

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro

```
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
            580                 585                 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
```

610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 140
<211> 3127
<212> DNA
<213> Adeno-associated virus

<400> 140
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt 60

attgattaac atgcaattac agattacggg tgaggtaacg agtgccaata gggcgaggct 120

cagagtaaac accctggctg tcaacggcaa agtccacacc agtctgcttt tcaaagttgg 180

aggtgtactg aatctccggg tcccagcgct tgctgttttc cttctgcagc tcccactcga 240

tttccacgct gacttgtccg gtgctgtact gtgtgatgaa cgaagcaaac ttggcaggag 300

taaacacctc cggaggatta gcgggaacgg gagtgttctt gatcaggatc tgaggaggcg 360

gatgtttaag tccaaagccg cccatcaaag gagacgggtg aaagttgcca tccgtgtgag 420

gaatcttggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccag 480

gtaaggctcc ctggttgttg acaacttgtg tctgggctgc agtattagcc gcttgtaagt 540

tgctgctgac tatcccgtat tcttccgtgg ctacaggatt agtaggacga atttcttctt 600

catttgtcat taacacattt tccaatgtag ttttgttagt tgctccagtt tttccaaaaa 660

tcaggactcc gctggatggg aaaaagcggt cctcgtcgtc cttgtgagtt gccatggcga 720

cgccgggatt aaccaacgag tttctgccgt tcaggtgata tttggtggca ccagtccaag 780

caaagttgct gttgttgttt tgatccagcg ttttggagac cctttgttgc cggaagcagg 840

gtccaggtaa ccaattcttg gcttgttcgg ccatagttga aggcccgccc tggtaaaact 900

gcagttcccg attgccagct gtgcctcctg ggtcactctg tgttctggcc aggtagtaca 960

agtactggtc gatgagggga ttcatcagcc ggtccaggct ctggctgtgt gcgtagctgc 1020

tgtggaaagg cacgtcctcg aagctgtagc tgaactcaaa gttgttgccc gttctcagca 1080

tctgagaggg gaagtactcc aggcagtaga aggaggaacg tcccacagac tgactgccat 1140

tgttgagagt caggtagccg tactgaggaa tcatgaagac gtccgccggg aacggaggca 1200

ggcagccctg gtgcgcagag ccgaggacgt acggcagctg gtattccgag tccgagaata 1260

cctgaatcgt gctggtaagg ttattagcga tggtcgtaac gccgtcattc gtcgtgacct 1320

ccttgacctg gatgttgaag agcttgaacc gcagcttctt gggccggaat ccccagttgt 1380

tgttgatgag tcgctgccag tcacgtggtg agaagtggca gtggaatctg ttaaagtcaa 1440

aataccccca gggggtgctg tagccgaagt aggtgttgtc gttggtacta cctgcagttt 1500

cactggagat ttgctcgtag aggtggttgt tgtaggtggg cagggcccag gttcgggtgc 1560

tggtggtaat gactctgtcg cccagccatg tggaatcgca atgccaattt cctgaggcat 1620

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ctgtaccaga tcccacacta gagggcgctg ctggaggttc tccgagaggt tgagggtcgg 1740

ggactgactc tgagtcgcca gtctgaccga aattgagtct ctttctggcg ggctgctggc 1800

ccttcttgcc gatgcccgtg gaggagtcgg gggaacgctg aggtgacggc tctaccggtc 1860

tcttctttgc aggagccgtc ttagcgcctt cctcaaccag accgagaggt tcgagaaccc 1920

gcttcttggc ctggaagact gctcgcccga ggttgccccc aaatgacgta tcttcttgca 1980

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cccaccactc gcgaatgccc tcagagaggt tgtcctcgag ccaatctgga agataaccat 2280

cggcagccat acctgattta aatcatttat tgttcaaaga tgcagtcatc caaatccaca 2340

ttgaccagat cgcaggcagt gcaagcgtct ggcacctttc ccatgatatg atgaatgtag 2400

cacagtttct gatacgcctt tttgacgaca gaaacgggtt tagattctga cacgggaaag 2460

cactctaaac agtctttctg tccgtgagtg aagcagatat ttgaattctg attcattctc 2520

tcgcattgtc tgcagggaaa cagcatcaga ttcatgccca cgtgacgaga acatttgttt 2580

tggtacctgt ctgcgtagtt gatcgaagct tccgcgtctg acgtcgatgg ctgcgcaact 2640

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cggaaaaagt ctttgacttc ctgcttggtg accttcccaa agtcatgatc cagacggcgg 2820

gtgagttcaa atttgaacat ccggtcttgc aacggctgct ggtgttcgaa ggtcgttgag 2880

ttcccgtcga tcacggcgca catgttggtg ttggagatga cgatcgcggg agtcgggtct 2940

atctgggccg aggacttgca tttctggtcc acgcgcacct tgcttcctcc gagaatggct 3000

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tcgacacagt cgttgaaggg aaagttctca ttggtccagt tgacgcagcc gtagaaaggg 3120

cgaattc 3127

<210> 141
<211> 728
<212> PRT
<213> Artificial Sequence

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

<400> 141

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Arg Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Val Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255
```

```
Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Ser Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Val His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460
```

```
Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Cys Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685
```

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 142
<211> 3106
<212> DNA
<213> Adeno-associated virus

<400> 142
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt 60

attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct 120

cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg 180

aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga 240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag 300

taaacacctc tggaggatta gcaggtaccg gggtgttttt gatgagaatt tgaggaggcg 360

ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag 420

gaattttggc ccagatggga ccctgcaggc acacgtcccg gttctgccag accatgccgg 480

gcagagcccc ctggctgttg acagtctgtg tctggggtcc ggccgtagac gattgcaggt 540

tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct 600

cgctggtcat tagcacgttt tccagcgttg tcttgttggc agcccccgtt ttgccaaaaa 660

ccagcactcc gttgatggga aagaactggt cctcgtcgtc cttgttggtg gccatggcta 720

cgcccgggtt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg 780

caaagttact gttgttgttg ctgtctatgt tttttgacag tctctgctgc cgataacagg 840

gtccgggcag ccagttcttt gattgctcgg ccatggtgtt gggcccagcc tgatggaact 900

gcagctccct tgtggacccc gtagtgctct gggtccgggc caggtagtac aggtactggt 960

cgatgagggg attcatcagc cggtctaggc tctggctgtg cacatagctg ctgtggaaag 1020

gcacttcctc aaaggtgtag ctgaattcaa agttattgcc cgttctcagc atctgagaag 1080

gaaagtactc caggcagtag aaggaggaac gtcccacaga ctgactgccg ttgtttagag 1140

tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct 1200

ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg 1260

tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct 1320

ggatgttgaa caacttgaac cgcagctttc tgggccggaa tccccagttg ttgttgatga 1380

gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc 1440

agggggtgct gtagctgaag aagtggttgt cgttggtagc cccgctctga cttgatatct 1500

gcttgtagag gtggttgttg taggtgggca gggcccaggt gcgggtgctg gtggtgatga 1560

ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt 1620

cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc 1680

ccagacctga gggcgcggcg ggaggttctc cgagaggttg ggggtcgggc actgactctg 1740

agtcgccagt ctgcccaaag ttgagcttct ttttagcggg ctgctggcct ttcttgccga 1800

tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccaggagcc gtcttagcga 1860

cttcctcaac cagaccgaga ggttcgagaa cccgcttctt ggcctggaag actgctcgcc 1920

cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt 1980

ggttgtactt gaggtacggg ttgtcccccc gctcgagctg cttgtcgtag gccttgtcgt 2040

gctcgagggc cgcggcgtct gcctcgttga ccggctctcc cttgtcgagt ccgttgaagg 2100

gtctgaggta cttgtagcca ggaagcacca gaccccggcc gtcgtcctgc ttttgctggt 2160

tggctttggg tttcggggct ccaggtttca agtcccacca ctcgcgaatg ccctcagaga 2220

ggttgtcctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt 2280

tattgctcag aaacacagtc atccaggtcc acgttgacca gatcgcaggc cgagcaagca 2340

atctcgggag cccgccccag cagatgatga atggcacaga gtttccgata cgtcctcttt 2400

ctgacgaccg gttgagattc tgacacgccg gggaaacatt ctgaacagtc tctggtcccg 2460

tgcgtgaagc aaatgttgaa attctgattc actctctcgc atgtcttgca gggaaacagc 2520

atctgaagca tgcccgcgtg acgagaacat ttgttttggt acctgtcggc aaagtccacc 2580

ggagctcctt ccgcgtctga cgtcgatgga ttcgcgactg aggggcaggc ccgcttgggc 2640

tcgcttttat ccgcgtcatc gggggcgggt ctcttgttgg ccccaccctt tctgacgtag 2700

aacccatgcg ccacctcggt cacgtgatcc tgcgcccagc ggaagaacct tttgacttcc 2760

tgctttgtca ccttgccaaa gttatgctcc agacggcggg tgggttcaaa tttgaacatc 2820

cggtcctgca acggctgctg gtgctcgaag gtggcgctgt tcccgtcaat cacggcgcac 2880

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ttttggtcca cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg 3000

gccgtcatct tgccctcctc ccaccagatc accatcttgt cggcgcaatc gttgaaggga 3060

aagttctcat tggtccagtt gacgcagccg tagaaagggc gaattc 3106

<210> 143
<211> 728
<212> PRT
<213> Artificial Sequence

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

<400> 143

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Ser Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

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

```
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Cys Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Val
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Leu
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540
```

```
Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Arg Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Glu Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 144
<211> 3102
<212> DNA
<213> Adeno-associated virus

<400> 144
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt 60

attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct 120

cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg 180

aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga 240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag 300

taaacacctc tggaggatta gcaggtaccg gggtgttttt gatgagaatt tgaggaggcg 360

ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag 420

gaatttcggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccgg 480

gcagagcccc ctggctgttg acagtctgtg tccggggtcc ggccgtagac gattgcaggt 540

tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct 600

cgctggtcat tagcacgttt tccagcgttg tcttgttggc agcccccgtt ttgccaaaaa 660

ccagcactcc gttgatggga aggaactggt cctcgtcgtc cttgttggtg gccatggcta 720

cgcccgggtt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg 780

caaagttact gttgttgttg ctgtctatgt tttttgacag tctctgctgc cgataacagg 840

gtccgggcag ccagttcttt gattgctcgg ccacggtgtt gggcccagcc tgatggaact 900

gcagctccct tgtggacccc gtagtgctct gggtccgggc caggtagtac aggtactggt 960

cgatgagggg attcatcagc cggtccaggc tctggctgtg cgcatagctg ctgtggaaag 1020

gcacttcctc aaaggtgtag ctgaattcaa agttattgcc cgttctcagc atctgagaag 1080

gaaagtactc caggcagcag aaggaggaac gtcccacaga ctgactgccg ttgtttagag 1140

tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct 1200

ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg 1260

tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct 1320

ggatgttgaa caacttgaac cgcagctttc tgggccggaa tccccagttg ttgttgatga 1380

gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc 1440

agggggtgct gtagccgaag aagtggttgt cgttggtagc cccgctctga cttgatatct 1500

gcttgtagag gtggttgttg taggtgggca gggcccaggt gcgggtgctg gtggtgatga 1560

ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt 1620

cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc 1680

ccagacctga gggcgcggcg ggaggttctc cgagaggttg ggggtcgggc actgactctg 1740

agtcgccagt ctgcccaaag ttgagcttct ttttagcggg ctgctggcct ttcttgccga 1800

tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccggaagcc gtcttagcgc 1860

cttcctcaac cagaccgaga ggttcgagaa cccgcttctt ggcctggaag actgctcgcc 1920

cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt 1980

ggttgtactt gaggtacggg ttgtcccccc gctcgagctg cttgtcgtag gccttgtcgt 2040

gctcgagggc cgcggcgtct gcctcgttga ccggctctcc cttgtcgagt ccgttgaagg 2100

gtccgaggta cttgtagcca ggaagcacca gaccccggcc gtcgtcctgc ttttgctggt 2160

tggctttggg tttcggggct ccaggtttca agtcccacca ctcgcgaatg ccctcagaga 2220

ggttgtcctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt 2280

tattgctcag aaacacagtc atccaggtcc acgttgacca gatcgcaggc cgagcaagca 2340

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ctgacgaccg gttgagattc tgacacgccg gggaaacatt ctgaacagtc tctggtcccg 2460

tgcgtgaagc aaatgttgaa attctgattc attctctcgc atgtcttgca gggaaacagc 2520

atctgaagca tgcccgcgtg acgagaacat ttgttttggt acctgtcggc aaagtccacc 2580

ggagctcctt ccgcgtctga cgtcgatgga tccgcgactg aggggcaagc ccgcttgggc 2640

tcgcttttat ccgcgtcatc gggggcgggt ctcttgttgg ctccaccctt tctgacgtag 2700

aactcatgcg ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc 2760

tgctttgtca ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc 2820

cggtcttgta acggctgctg gtgctcgaag gtggtgctgt tcccgtcaat cacggcgcac 2880

atgttggtgt tggaagtgac gatcacgggg gtgggatcga tctgggcgga cgacttgcac 2940

ttttggtcca cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg 3000

gccgtcatct tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga 3060

aagttctcat tggtccagtt gacgcagccg aagggcgaat tc 3102

<210> 145
<211> 728

<212> PRT
<213> Adeno-associated virus

<400> 145

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160


Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175


Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190


Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
```

```
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415
```

```
His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
```

625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 146
<211> 728
<212> PRT
<213> Artificial Sequence

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

<400> 146

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Gly Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

```
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285
```

```
Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asp Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
```

```
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720
```

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 147
<211> 3106
<212> DNA
<213> Adeno-associated virus

<400> 147
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat cagccggttt 60

attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct 120

cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg 180

aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga 240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag 300

taaacacctc tggaggatta gcaggtaccg gggtgttttt gatgagaatt tgaggaggcg 360

ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag 420

gaattttggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccgg 480

gcagagcccc ctggctgttg acagtctgtg tctggggtcc ggccgtagac gattgcaggt 540

tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct 600

cgctggtcat tagcacgttt tccagcgttg tcttgttggc agcccccgtt ttgccaaaaa 660

ccagcactcc gttgatggga aagaactggt cctcgtcgtc cttgttggtg gccatggcta 720

cgcccgggtt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg 780

caaagttact gttgttgttg ctgtctatgt tttttgacag tctctgctgc cgataacagg 840

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gcacttcctc aaaggtgtag ctgaattcaa agttatcgcc cgttctcagc atctgagaag 1080

gaaagtactc caggcagtag aaggaggaac gtcccacaga ctgactgccg ttgtttagag 1140

tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct 1200

ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg 1260

tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct 1320

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gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc 1440

agggggtgct gtagccgaag aagtggttgt cgttggtagc cccgctctga cttgatatct 1500

gcttgtagag gtggttgttg taggtgggca gggcccaggt gcgggtgctg gtggtgatga 1560

ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt 1620

cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc 1680

ccagacctga gggcgcggcg ggaggttctc cgagaggttg ggggtcgggc actgactctg 1740

agtcgccagt ctgcccaaag ttgagcttct ttttagcggg cggctggccg ttcttgccga 1800

tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccaggagcc gtcttagcgc 1860

cttcctcaac cagaccgaga ggttcgagaa cccgcttctt ggcctggaag actgctcgcc 1920

cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt 1980

ggttgtactt gaggtacggg ttgtcccccc gctcgagctg cttgtcgtag gccttgtcgt 2040

gctcgagggc cgcggcgtct gcctcgttga ccggctctcc cttgtcgagt ccgttgaagg 2100

gtccgaggta cctgtagcca ggaagcacca gaccccggcc gtcgtcctgc ttttgctggt 2160

tggctttggg tttcggggct ccaggtttca agtcccacca ctcgcgaatg ccctcagaga 2220

ggttgccctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt 2280

tattgctcag aaacacagtc atccaggtcc acgttggcca gatcgcaggc cgagcaagca 2340

atctcgggag cccgccccag cagatgatga atggcacaga gtttccgata cgtcctcttt 2400

ctgacgaccg gttgagattc tgacacgccg gggaaacatt ctgaacagtc tctggtcccg 2460

tgcgtgaagc aaatgttgaa attctgattc attctctcgc atgtcttgca ggggaacagc 2520

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tcgcttttat ccgcgtcatc gggggcgggt ctcttgttgg ctccaccctt tctgacgtag 2700

aactcatacg ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc 2760

tgctttgtca ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc 2820

cggtcttgta acggctgctg gtgctcgaag gtggtgctgt tcccgtcaat cacggcgcac 2880

atgttggtgt tggaagtgac gatcacgggg gtgggatcga tctgggcgga cgacttgcac 2940

ttttggtcca cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg 3000

gccgtcatcc tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga 3060

aagttctcat tggtccagtt gacgcagccg tagaaagggc gaattc 3106

<210> 148
<211> 728
<212> PRT
<213> Artificial Sequence

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

<400> 148

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365
```

```
Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Met Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Gly Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575
```

```
Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Gly Val Phe Thr Pro
                645                 650                 655

Ala Leu Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 149
<211> 3098
<212> DNA
<213> Adeno-associated virus

<400> 149

```
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta       60

acaagtaatt acaggttacg ggtgaggtaa cgggtgccaa tggggcgagg ctcagtataa      120

acccccttcgt tgttgacagc aaattccaca ttattagact tggcataatt tgaggtgtac      180

tgaatctctg gattccagcg tttgctgttt tctttctgca gttcccactc gatctccacg      240
```

ctgacctggc cggtgctgta ctgcgtgata aatgaggcaa actaggcagg agtaaacacc 300

cctggaggat tagcaggtac cggggtgttt ttgatgagaa tttgaggagg cgggtgtttg 360

agtccaaatc cgcccatcag gggagacggg tgaaagttgc cgtccgtgtg aggaattttg 420

gcccagatgg gaccctgcag gtacacgtcc cggttctgcc agaccatgcc gggcagagcc 480

ccctggctgt tgacagtctg tgtctggggt ccggccgtag acgattgcag gttgctggag 540

accacaccgt attcttctgt agccacggga ttggtggttt tgatctcctc ctcgctggtc 600

attagcacgt tttccagcgt tgtcttgttg gcagcccccg ttttgccaaa aaccagcact 660

ccgttgatgg gaaagaactg gccctcgtcg tccttgttgg tggccatggc tacgcccggg 720

ttggttaatg aatttctacc attcagatgg tatttagtgg ccccggtcca ggcaaagtta 780

ctgttgttgt tgctgtctat gttttttgac agtctctgct gccgataaca gggtccgggc 840

agccagttct ttgattgctc ggccatggtg ttgggcccag cctgatggaa ctgcagctcc 900

cttgtggacc ccgtagtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgagg 960

ggattcatca gccggtccag gctctggctg tgcgcatagc tgctgtggaa aggcacttcc 1020

tcaaaggtgt agctgaattc aaagttattg cccgttctca gcatctgaga aggaaagtac 1080

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gagccgagga cgtacggcag ttggtactcc gagtccgaga agacctgaat cgtgctggta 1260

aggttattag cgatggtcgt aacgccgtcg ttcgtcgtga cctccttgac ctggatgttg 1320

aacaacttga accgcagctt tctgggccgg aatccccagt tgttgttgat gagtcgctgc 1380

cagtcacgtg gtgagaagtg gcagtggaat ctgttgaagt caaaatagcc ccaggggtg 1440

ctgtagccga agaagtggtt gtcgttggta gccccgctct gacttgatat ctgcttgtag 1500

aggtggttgt tgtaggtggg cagggcccag gtgcgggtgc tggtggtgat gactctgtcg 1560

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gagggcgcgg cgggaggttc tccgagaggt tgggggtcgg gcactgactc tgagtcgcca 1740

gtctgcccaa agttgagctt ctttttagcg ggctgctggc ctttcttgcc gatgcccgtg 1800

gaggagtcgg gggattctat gggtctcttc tttccaggag ccgtcttagc gccttcctca 1860

accagaccga gaggttcgag aacccgcttc ttggcctgga agactgctcg cccgaggttg 1920

cccccaaaag acgtatcttc ttgaagacgc tcctgaaact cagcgtcggc gtggttgtac 1980

ttgaggtacg ggttgtcccc ctgctcgagc tgcttgtcgt aggccttgtc gtgctcgagg 2040

gccgcggcgt ctgcctcgtt gaccggctct cccttgtcga gtccgttgaa gggtccgagg 2100

tacttgtagc caggaagcac cagaccccgg ccgtcgtcct gcttttgctg gttggctttg 2160

ggtttcgggg ctccaggttt caagtcccac cactcgcgaa tgccctcaga gaggttgtcc 2220

tcgagccaat ctggaagata accatcggca gccatacctg gtttaagtca tttattgctc 2280

agaaacacag tcatccaggt ccacgttgac cagatcgcag gccgagcaag caatctcggg 2340

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cggttgagat tctgacacgc cggggaaaca ttctgaacag tctctggtcc cgtgcgtgaa 2460

gcaaatgttg aaattctgat tcattctctc gcatgtcttg cagggaaaca gcatctgaag 2520

catgcccgcg tgacgagaac atttgttttg gtacctgtcg gcaaagtcca ccggagctcc 2580

ttccgcgtct gacgtcgatg gatccgcgac tgaggggcag gcccgcttgg gctcgctttt 2640

atccgcgtca tcgggggcgg gcctcttgtt ggctccaccc tttctgacgt agaactcatg 2700

cgccacctcg gtcacgtgat cctgcgccca gcggaagaac tctttgactt cctgctttgt 2760

caccttgcca aagtcctgct ccagacggcg ggtgagttca aatttgaaca tccggtcttg 2820

taacggctgc tggtgctcga aggtggtgct gttcccgtca atcacggcgc acatgttggt 2880

gttggaagtg acgatcacgg gggtgggatc gatctgggcg gacgacttgc acttttggtc 2940

cacgcgcacc ttgctgccgc cgagaatggc cttggcggac tccacgacct tggccgtcat 3000

cttgccctcc tcccaccaga tcaccatctt gtcgacgcaa tcgttgaagg gaaagttctc 3060

attggtccag ttgacgcagc cgtagaaagg gcgaattc 3098

<210> 150
<211> 2187
<212> DNA
<213> Adeno-associated virus

<400> 150
atggctgccg atggttatct tccagattgg ctcgagggca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaacggccag 480

ccgcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 540

ccccaacctc tcggagaacc tcccgccgcg ccctcaggtc tgggatctgg tacaatggct 600

gcaggcggtg gcgcaccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 660

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 720

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 780

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 840

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 900

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 960

acgaacgacg gcgttacgac catcgctaat aaccttacca gcacgattca ggtcttctcg 1020

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1080

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1140

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acgggcgata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1260

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1320

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1380

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1440

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1500

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1560

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1620

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1680

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1740

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tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2040

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2100

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2160

acccgttacc tcacccgtaa cctgtaa 2187

<210> 151
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 151

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Gly Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
```

```
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asp Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560
```

```
Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 152
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 152

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220
```

```
His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240


Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255


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


Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285


Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300


Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320


Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335


Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350


Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365


Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380


Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400


Thr Gly Asp Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415


His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430


Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445
```

```
Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655
```

```
Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 153
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 153

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

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

```
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540
```

```
Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 154
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 154

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205
```

```
Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430
```

```
Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640
```

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 155
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 155

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
```

```
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525
```

```
Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 156

<211> 2215
<212> DNA
<213> Artificial Sequence

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

<400> 156
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacgac aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca gcagcgagta tcaaagacat ctgcggataa caacaacagt 1500

gaatactcgt ggactggagc taccaagtac cacctcaatg gcagagactc tctggtgaat 1560

ccgggcccgg ccatggcaag ccacaaggac gatgaagaaa agttttttc ctcagagcgg 1620

ggttctcatc tttgggaagc aaggctcaga gaaaacaaat gtggacattg aaaaggtcat 1680

gattacagac gaagaggaaa tcaggacaac caatcccgtg gctacggagc agtatggttc 1740

tgtatctacc aacctccaga gaggcaacag acaagcagct accgcagatg tcaacacaca 1800

aggcgttctt ccaggcatgg tctggcagga cagagatgtg taccttcagg ggcccatctg 1860

ggcaaagatt ccacacacgg acggacattt tcacccctct cccctcatgg gtggattcgg 1920

acttaaacac cctccgcctc agatcctgat caagaacacg cctgtacctg cggatcctcc 1980

gaccaccttc aaccagtcaa agctgaactc tttcatcacc cagtattcta ctggccaagt 2040

cagcgtggag atcgagtggg agctgcagaa ggaaaacagc aagcgctgga accccgagat 2100

ccagtacacc tccaactact acaaatctac aagtgtggac tttgctgtta atacagaagg 2160

cgtgtactct gaaccccgcc ccattggcac ccgttacctc acccgtaatc tgtaa 2215

<210> 157
<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 157

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
```

```
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Lys Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp
                485                 490                 495
```

```
Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala
            580                 585                 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
```

705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 158
<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 158

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Lys Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp
                485                 490                 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
```

565 570 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Gln Gly Asn Thr Gln Ala
580 585 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
595 600 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 159
<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 159

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ala Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
```

```
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp
                485                 490                 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Gln Gly Asn Thr Gln Ala
            580                 585                 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640
```

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 160
<211> 729
<212> PRT
<213> Artificial Sequence

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

<400> 160

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
```

```
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495
```

```
Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Glu His Pro Pro Pro Gln Ile
625                 630                 635                 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
```

705 710 715 720

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 161
<211> 3075
<212> DNA
<213> Adeno-associated virus

<400> 161
tgagaacttt cctttcaacg attgcgtcgg acaagatggt gatctggtgg gaggagggga 60

agatgaccgc caaggtcgtg gagtcggcca aagccattct tggaggaagc aaggtgcgtg 120

tggaccagaa atgcaagtcc tcggcccaga tagacccgac tcccgtgatc gtcacctcca 180

acaccaacat gtgcgccgtg attgacggga actcaacgac cttcgagcac cagcagccgt 240

tgcaagaccg gatgttcaaa tttgaactta cccgccgtct ggatcatgac tttggaaagg 300

tcaccaagca ggaagtgaaa gacttttttcc ggtgggcaaa ggatcacgtg gttgaggtgg 360

agcatgaatt ctacgtcaaa aagggtggag ctaagaaaag acccgccccc agtgacgcag 420

atataagtga gcccaaacgg gcgcgcgagt cagttgcgca gccatcaacg tcagacgcgg 480

aagcttcgat caactacgcg gacaggtacc aaaaacaaat gttctcgtca cgtgggcatg 540

aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 600

ttcactcacg gacagaaaga ctgtttagag tgctttcccg tgtcagaatc tcaacccgtt 660

tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaggtg 720

ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctctgaa 780

caataaatga tttaaatcag gtatggctgc cgatggttat cctccagatt ggctcgagga 840

cactctctct gaagggataa gacagtggtg gaagctcaaa cctggcccac caccaccaaa 900

gcccgcagag cggcataagg acgacagcag gggtcttgtg cttcctgggt acaagtacct 960

cggacccttc aacggactcg acaaggggga gccggtcaac gaggcagacg ccgcggccct 1020

cgagcacgac aaggcctacg accggcagct cgacagcgga gacaacccgt acctcaagta 1080

caaccacgcc gacgcagagt ttcaggagcg ccttaaagaa gatacgtctt ttgggggcaa 1140

cctcggacga gcagtcttcc aggcgaaaaa gagggttctt gaacctctgg gcctggttga 1200

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caataacgag ggtgccgatg gagtgggtaa ttcctcagga aattggcatt gcgattccca 1500

atggctgggc gacagagtca tcaccaccag cacccgaacc tgggccctgc ccacatacaa 1560

caaccacctc tacaagcaaa tctccagcca atcaggagcc agcaacgaca accactactt 1620

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acgtgactgg caaagactca tcaacaacaa ctggggattc cggcccaaaa gactcaactt 1740

caagctcttt aatattcaag tcaaagaggt cacgcagaat gacggtacga cgacgattgc 1800

caataacctt accagcacgg ttcaggtgtt tactgactcg gagtaccagc tcccgtacgt 1860

cctgggctcg gcgcatcaag gatgcctccc gccgtttcca gcggacgtct tcatggtccc 1920

acagtatgga tacctcaccc tgaacaacgg gagtcaggcg gtaggacgct cttcctttta 1980

ctgcctggag tactttcctt ctcagatgct gcgtactgga aacaactttc agttcagcta 2040

cacttttgaa gacgtgcctt tccacagcag ctacgctcac agccagagtc tggatcggct 2100

gatgaatcct ctgatcgacc agtacctgta ttatctgaac aagacacaaa caaatagtgg 2160

aactcttcag cagtctcggc tactgtttag ccaagctgga ccaaccaaca tgtctcttca 2220

agctaaaaac tggctgcctg gaccttgcta cagacagcag cgtctgtcaa aacaggcaaa 2280

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ggactcgttg gttaatccag gaccagctat ggccagtcac aaggatgacg aagaaaagtt 2400

tttccccatg catggaaccc tgatatttgg taaacaagga acaaatgcca acgacgcgga 2460

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ggagcagtac gggactgtgt caaataattt gcaaaactca aacactggtc caactactgg 2580

aactgtcaat cgccaaggag cgttacctgg tatggtgtgg caggatcgag acgtgtacct 2640

gcagggaccc atttgggcca agattcctca caccgatgga cactttcatc cttctccact 2700

gatgggaggt tttggactca aacacccgcc tcctcagatc atgatcaaaa acactcccgt 2760

tccagccaat cctcccacaa acttcagttc tgccaagttt gcttctttca tcacacagta 2820

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ctggaatccc gaaattcagt acacttccaa ctacaacaag tctgttaatg tggactttac 2940

tgtggacact aatggtgtgt attcagagcc tcgccccatt ggcaccagat acctgactcg 3000

taatctgtaa ttgcttgtta atcaataaac cgtttaattc gtttcagttg aactttggtc 3060

tctgcgaagg gcgaa 3075

<210> 162
<211> 3142
<212> DNA
<213> Adeno-associated virus

<400> 162
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cgcgaattcg cctttcgcag agaccaaagt tcaactgaaa cgaattaaac ggtttattga 120

ttaacaagca attacagatt acgagtcagg tatctggtgc caatggggcg aggctctgaa 180

tacacaccat tagtgtccac agtaaagtcc acattaacag acttgttgta gttggaagtg 240

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acgctgacct gtcccgtgga atactgtgtg atgaaagaag caaacttggc agaactgaag 360

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ttgagtccaa aacctcccat cagtggagaa ggatgaaagt gtccatcggt gtgaggaatc 480

ttggcccaaa tgggtccctg caggtacacg tctcgatcct gccacaccat accaggtaac 540

gctccttggt gattgacagt tccagtagtt ggaccagtgt ttgagttttg caaattattt 600

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gtaatcatga cattttccaa atccgcgtcg ttggcatttg ttccttgttt accaaatatc 720

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accgtgctgg taaggttatt ggcaatcgtc gtcgtaccgt cattctgcgt gacctctttg 1380

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ccggttcccg aggaggagtc tggctccaca ggagagtgct ctaccggcct ctttttccc 1920

ggagccgtct taacaggctc ctcaaccagg cccagaggtt caagaaccct ctttttcgcc 1980

tggaagactg ctcgtccgag gttgccccca aaagacgtat cttctttaag gcgctcctga 2040

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tccttatgcc gctctgcggg ctttggtggt ggtgggccag gtttgagctt ccaccactgt 2280

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gtaaaaggaa agttctcatt gg 3142

<210> 163
<211> 735
<212> PRT
<213> Adeno-associated virus 2

<400> 163

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asp Lys Ala Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560
```

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

<210> 164
<211> 740
<212> PRT
<213> Adeno-associated virus 2

<400> 164

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
```

```
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
```

```
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
```

```
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu Leu
                725                 730                 735

Leu Ala Ala Ala
            740
```

<210> 165
<211> 734
<212> PRT
<213> Adeno-associated virus 2

<400> 165

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Met Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
```

```
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Ile Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730
```

<210> 166
<211> 734

<212> PRT
<213> Adeno-associated virus 2

<400> 166

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


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


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


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


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
```

```
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415
```

```
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
```

625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Glu Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730

<210> 167
<211> 739
<212> PRT
<213> Adeno-associated virus 2

<400> 167

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu Leu
                725                 730                 735
```

Leu Ala Ala

<210> 168
<211> 725
<212> PRT
<213> Adeno-associated virus 2

<400> 168

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
```

595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro
725

<210> 169
<211> 707
<212> PRT
<213> Adeno-associated virus 2

<400> 169

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
```

```
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480
```

```
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Cys Ile Tyr Gln Pro Pro Glu Arg Gln Gln Thr Ser Ser Tyr
            580                 585                 590

Arg Arg Cys Gln His Thr Arg Arg Ser Ser Arg His Gly Leu Ala Gly
        595                 600                 605

Gln Arg Cys Val Pro Ser Gly Ala His Leu Gly Lys Asp Ser Thr His
    610                 615                 620

Gly Arg Thr Phe Ser Pro Leu Ser Pro His Gly Trp Ile Arg Thr Thr
625                 630                 635                 640

Pro Ser Ser Thr Asp Ser His Gln Glu His Pro Gly Thr Cys Glu Ser
                645                 650                 655

Phe Asp His Leu Gln Cys Gly Lys Val Cys Phe Leu His His Thr Val
            660                 665                 670

Leu His Gly Thr Gly Gln Arg Gly Asp Arg Val Arg Ala Ala Glu Gly
        675                 680                 685

Lys Gln Gln Thr Leu Glu Ser Arg Asn Ser Val His Phe Gln Leu Gln
    690                 695                 700
```

Gln Val Cys
705

<210> 170
<211> 739
<212> PRT
<213> Adeno-associated virus 2

<400> 170

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
```

595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu Leu
725 730 735

Leu Ala Ala

<210> 171
<211> 737
<212> PRT
<213> Adeno-associated virus 2

<400> 171

Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser
    450                 455                 460
```

```
Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn
                485                 490                 495

Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala
            580                 585                 590

Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

Leu

<210> 172
<211> 741
<212> PRT
<213> Adeno-associated virus 2

<400> 172

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
```

```
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
```

```
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Leu Ala Asn His Asn
            580                 585                 590

Asn Thr Thr Asn Ala Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln
        595                 600                 605

Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln
    610                 615                 620

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro
625                 630                 635                 640

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
                645                 650                 655

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser
            660                 665                 670

Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
        675                 680                 685

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
    690                 695                 700

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Ile Asn Val
705                 710                 715                 720

Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile
                725                 730                 735

Gly Thr Arg Tyr Leu
            740


<210>  173
<211>  730
<212>  PRT
```

<213> Adeno-associated virus 2

<400> 173

```
Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


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


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Asn Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg
725 730

<210> 174
<211> 735
<212> PRT
<213> Adeno-associated virus 2

<220>
<221> MOD_RES
<222> (239)..(239)
<223> Xaa = any amino acid

<400> 174

Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Xaa Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
```

```
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Asn Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
```

705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

<210> 175
<211> 733
<212> PRT
<213> Adeno-associated virus 2

<400> 175

Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Leu Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Asn Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590
```

```
Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr
                725                 730
```

<210> 176
<211> 734
<212> PRT
<213> Adeno-associated virus 2

<400> 176

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Cys Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
```

```
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Asn Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Asn Gln Ser Gly Ser Ala Gln Asn Asn Asp Leu Leu Phe Ser Arg
    450                 455                 460

Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro Gly
465                 470                 475                 480
```

```
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn Gly
            500                 505                 510

Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly Lys
    530                 535                 540

Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg Phe
                565                 570                 575

Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala Thr
            580                 585                 590

Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
```

690 695 700

Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu Tyr
705 710 715 720

Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730

<210> 177
<211> 734
<212> PRT
<213> Adeno-associated virus 2

<400> 177

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Ser Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
```

```
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575
```

```
Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Ile Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730
```

<210> 178
<211> 738
<212> PRT
<213> Adeno-associated virus 2

<400> 178

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30
```

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Gly Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
```

675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu Leu
725 730 735

Arg Pro

<210> 179
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 179
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960

aaagaggtca cgcagaatgg cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tcctttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg gcaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga cgggaggttt tggactcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 180
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 180

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser

```
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Gly Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
```

```
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Gly Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Thr Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655
```

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 181
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 181
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc tcgcagagcg gcatcaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

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aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caaccttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag 1320

tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680

gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actacagaaa atgtcaatca ccagggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

tacagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg 2040

gagattgagt gggagctgcg gaaggagaac agcaaacgct ggaaccccga gatccagtat 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 182
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 182

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Leu Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Thr Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Leu Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
```

645 650 655

Pro Pro Thr Asn Tyr Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Arg Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 183
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 183
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatcaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

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tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcgtcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680

gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actacagaaa atgtcaatca ccagggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920

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ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg 2040

gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 184
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 184

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
```

```
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr Arg Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 185
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 185
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

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gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

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cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag 1320

tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tgggaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680

gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actacagaaa atgtcaatca ccagggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg 2040

gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

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<210> 186
<211> 735

<212> PRT
<213> Adeno-associated virus

<400> 186

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1               5                  10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


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


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
```

```
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Pro Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415
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```
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
```

625 630 635 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 187
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 187
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacttg ggccctgccc acctacaaca accatctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840

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cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

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tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

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tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

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ttcagtgcgg caaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

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<210> 188
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 188

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


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


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


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


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
```

```
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Gly Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

```
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
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<211>  3161
<212>  DNA
<213>  Adeno-associated virus

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aaggtcatgg agtcggccaa agccattctc ggaggaagca aggtgcgcgt ggaccagaaa      180

tgtaagtcct cggcccagat agacccgact cccgtgattg tcacctccaa caccaacatg      240

tgcgccgtga ttgacgggaa ctcaacgacc ttcgagcacc agcagccgtt gcaagaccgg      300

atgttcaaat ttgaactcac ccgccgtctg gatcatgact ttgggaaggt caccaagcag      360

gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc      420

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cccaaacggg cgcgcgggtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc      540

aactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg      600
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cagaaggact gtttagagtg ctttcccgtg tcagaatctc aacccgtttc tgtcgtcaaa 720

aaggcgtatc agaaactttg ctacattcat catatcatgg gaaaggtgcc agacgcttgc 780

actgcctgcg atctggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt 840

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gaattcgttt aaaccctgca ggactagtcc ctttagtgag g 3161

<210> 190
<211> 3162
<212> DNA
<213> Adeno-associated virus

<400> 190
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tggggcgagg ctctgaatac acgccattag tgtccacagt aaagtccaca ttaacagact 180

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<210> 191
<211> 3164
<212> DNA
<213> Adeno-associated virus

<400> 191
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<210> 192
<211> 3163
<212> DNA
<213> Adeno-associated virus

<400> 192
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tctctgcgaa gggcgaattc gcggccgcta aattcaattc gcc 3163

<210> 193
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 193

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Tyr Lys Gly Glu Pro
50 55 60

Val Asp Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
195 200 205

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Leu Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
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Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

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His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asp Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Pro Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 194
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 194

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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactctac      180

aagggagagc cggtcgacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

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caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gccaaaaaga gggttcttga acctctgggc ttggttgggg agcctgttaa aacggctccg      420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga      480

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tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct      600

actacaatgg ctacaggcag tggcgcacca gtggcagaca ataacgaggg tgccgatgga      660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc      720
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<210> 195
<211> 3161
<212> DNA

<213> Adeno-associated virus

<400> 195
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caagacccct gctgtcgtcc ttatgccgct ctgcgggctt tggtggtggt gggccaggtt 2220

tgagcttcca ccactgtctt attccttcag agagagtgtc ctcgagccaa tctggaagat 2280

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gcaactgact cgcgcgcccg tttgggctca cttatatctg cgtcactggg ggcgggtctt 2700

ttcttggctc cacccttttt gacgtagaat tcatgctcca cctcaaccac gtgatccttt 2760

gcccaccgga aaaagtcttt cacttcctgc ttggtgacct tcccaaagtc atgatccaga 2820

cggcgggtta gttcaaattt gaacatccgg tcttgcaacg gctgctggtg ttcgaaggtc 2880

gttgagttcc cgtcaatcac ggcgcacatg ttggtgttgg aggtggcgat cacgggagtc 2940

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atggcttcgg ccgattccac gaccttggcg gtcatctttc cctcctccca ccagatcacc 3060

atcttgtcga cacagtcgtt gaagggaaag ttctcattgg tccagttgac gcagcaaggg 3120

cgaattcgtt taaacctgca ggaactagtc ccttagtgag g 3161

<210> 196
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 196

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Tyr Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Gly Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro

```
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asp Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
```

```
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 197
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 197

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atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccgccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactctac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccgg cgcggagttt      300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gccaaaaaga gggttcttga acctctgggc ttggttgagg agcctgttaa aacggctccg      420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga      480

aaagcgggca accagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac      540
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tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca gtggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggctctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg accaaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

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cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaatca aatagtggaa cccttcagca gtctcggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

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gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740

aataatttgc aagactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactta tgggaggttt tggactcaaa 1920

cacccacctc ctcagatcat gattaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca agtcagcgta 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtac 2100

acttccaact ataacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 198
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 198

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Cys Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

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

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Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
```

```
385                 390                 395                 400

Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 199
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 199
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctgc aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagacag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctc cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

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ctgactctga acaacggcag tcaggccgtg ggccgttcct ccttctactg cctggagtac 1200

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gtgccttttc acagcagcta cgcgcatagc caaagcctgg accggctgat gaaccccctc 1320

atcgaccagt acctgtacta cctgtctcgg actcagtcca cgggaggtac cgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aataacatgt cggctcaggc caaaaactgg 1440

ctacccgggc cctgctaccg gcagcaacgc gtctccacga cactgtcgca aaataacaac 1500

agcaactttg cttggaccgg tgccaccaag tatcatctga atggcagaga ctctctggta 1560

aatcccggtg tcgctatggc aacgcacaag gacgacgaag agcgattttt tccatccagc 1620

ggagtcttga tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtt 1680

atgctaacca gtgaggaaga aatcaaaacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaacagt 1800

caaggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatc 1860

tgggccaaga ttcctcacac ggacggcaac tttcatcctt cgccgctgat gggaggcttt 1920

ggactgaaac acccgcctcc tcagatcctg attaagaata cacctgttcc cgcggatcct 1980

ccaactacct tcagtcaagc caagctggcg tcgttcatca cgcagtacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaagagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta taacaaatct gttaatgtgg actttactgt ggacactaat 2160

ggtgtgtatt cagagcctcg ccccattggc accagatacc tgactcgtaa tctgtaa 2217

<210> 200
<211> 3167
<212> DNA
<213> Adeno-associated virus

<400> 200
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taaacggttt attgattaac aagcaattac agattacgag tcaggtacct ggtgccaatg 120

gggcgaggct ctgaatacac accattagtg tccacagtaa agtccacatt aacagatttg 180

ttgtagttgg aagtgtactg aatctcggga ttccagcgtt tgctgttctc cttctgcagc 240

tcccactcga tctccacgct gacctgcccc gtggagtact gtgtaatgaa ggaagcaaac 300

tttgccgcac tgaaggtagt cgaaggattc gcaggtaccg gggtgttctt gatgagaatc 360

tgcgggggag ggtgtttaag tccgaatccg cccatgaggg gagaggggtg aaaatgtccg 420

tccgtgtgtg gaatctttgc ccagatgggc ccctgcaggt acacgtctct gtcctgccac 480

accatgcctg gaagaacgcc ttgtgtgttg acatctgagg tagctgcttg tgtgttgccg 540

ctctggaggt tggtagatac agaaccatac tgctccgtag ccacgggatt ggtggtcctg 600

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tgttttccaa agatgagaac cccgctctga ggaaaaaact tttcttcatc gtccttgtgg 720

ctggccatgg ccgggcccgg attcaccaga gagtctcttc cattaaggtg gtacttggta 780

gctccagtcc acgagtattc actgttgttg ttatccgcag atgtctttga tactcgctgc 840

tggcggtaac agggtccagg aagccagttc ctagactggt cccgaatgtc acttgctccg 900

gcctgagaaa actgaagcct tgactgcgtg gtggttccgc ttggagtgtt tgttctgctc 960

aagtaataca ggtactggtc gatgagagga ttcatgagac ggtccaaact ctggctgtgg 1020

gcgtagctgc tgtggaaagg aacgtcctca aaggtgtagc tgaaggtaaa gttgtttccg 1080

gtacgcagca tctgagaagg aaagtactcc aggcagtaaa atgaagagcg tcctactgcc 1140

tgactcccgt tgttcagggt gaggtatcca tactgtggca ccatgaagac gtctgctggg 1200

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tcagtaaaca cctgaaccgt gctggtaagg ttattggcaa tcgtcgtcgt accgtcattc 1320

tgcgtgacct ccttgacttg aatgttaaag agcttgaagt tgagtctttt gggccggaat 1380

ccccaattgt tgttgatgag tctttgccag tcacgtggcg aaaagtggca gtggaatctg 1440

ttgaagtcaa aataccccca aggggtgctg tagccaaagt agtggttgtc gtttgaggct 1500

cctgattggc tggaaatctg cttgtagagg tggttgttgt aggtgggcag agcccaggtg 1560

cgggtgctgg tggtgatgac tctgtcgccc atccatgtgg aatcgcaatg ccaatttccc 1620

gaggaattac ccactccgtc ggcgccctcg ttattgtctg ccattggtgc gccactgcct 1680

gtagccatcg tattagttcc cagaccagag ggggctgctg gtggctgtcc gagaggctgg 1740

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<210> 201
<211> 3161
<212> DNA
<213> Adeno-associated virus

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<212> PRT
<213> Adeno-associated virus

<400> 205

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35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Glu Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
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Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
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Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
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Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
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Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
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Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
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Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
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Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
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Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Ser Trp
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Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
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Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
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Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
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Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
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Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
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Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
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Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
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Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
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Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
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Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
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Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605
```

```
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ser Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Pro Thr Arg Asn Leu
                725                 730                 735
```

<210> 206
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 206

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atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420

ggagaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga      480
```

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gccagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggtattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctcg tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 207
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 207

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Glu Lys Arg
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

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

```
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp Tyr Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605
```

```
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Val Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 208
<211> 2209
<212> DNA
<213> Adeno-associated virus

<400> 208

```
atggctgccg atggttatcc tccagattgg ctcgaggaca ctctctctga agggataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt      300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420
```

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcggcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatcg ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaat 2209

<210> 209
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 209

Met Ala Ala Asp Gly Tyr Pro Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

```
Lys Ala Gly Gln Arg Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590
```

```
Gly Thr Val Asn Arg Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 210
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 210

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atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aggtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgtcga cgcggagttt      300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360
```

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa ggcggctccg 420

ggagaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

cattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccccca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg cgccagatac ctgactcgta atctgtaa 2208

<210> 211
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 211

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Val
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

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

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

```
Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly His Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
```

```
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590
```

```
Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Pro Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Ala Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 212
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 212

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atggctgccg atggttatct tccagattgg ctcgaggaca ccctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

cggcagctcg acagcggaga taacccgtac ctcaagtaca accacgccga cgcggagttt      300
```

caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccggcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 213
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 213

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Arg Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
```

```
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575
```

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
580 585 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 214
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 214
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcgg cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagacgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 215
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 215

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Gly Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
```

```
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Thr Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575
```

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
580 585 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 216
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 216
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctgcaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ttttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

acctacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc gggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 217
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 217

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Cys Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
```

```
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560
```

```
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Tyr Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Arg Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 218
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 218
atggctgccg atggttatct tccagattgg ctcgaggaca ccctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga taacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccggcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 219
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 219

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Arg Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
```

```
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560
```

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
580 585 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 220
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 220
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

ggcagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctca acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg 420

ggaaaaaaga gaccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accacaagca ctcgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactattttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

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aacaacggga gtcaggcggt aggacgctct ccctttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc caccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagat gtgtaccttc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcagattat gatcaaaaac actcccgttc cagccaatcc tcctacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacaataa tggcgtgtac 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 221
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 221

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Gly Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
```

```
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Pro Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540
```

```
Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590


Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Asn Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  222
<211>  2208
<212>  DNA
<213>  Adeno-associated virus

<400>  222
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atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

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catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 223
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 223

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540
```

```
Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590


Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  224
<211>  2208
<212>  DNA
<213>  Adeno-associated virus
```

<400> 224
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tatttcgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgccttccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacgg ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacgtt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

gtctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gcggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgt ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 225
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 225

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Gly Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Val Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
```

```
Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Val Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Ala Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Val Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 226
<211> 2208

<212> DNA
<213> Adeno-associated virus

<400> 226
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga aactcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttctgga acctctgagc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctccc gcagagccag attcctcctc cggaactgga 480

aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780

tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctagagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc gagtgacatt caggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gtcagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa agacgatgaa gaaaagtttt ttcctcagag cggggttctt 1620

atctttggga agcaaggctc agagaaaaca aatgtggata ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtcgggca agacagagac gtgtacctgc aggggcctac ttgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 227
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 227

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

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

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Gln Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
```

```
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Gly Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Thr Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 228
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 228
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttctgga acctctgggc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcagagccag attcctcctc cggaactgga 480

aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780

tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctagggta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gtcagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa agacgatgaa gaaaagtttt ttcctcagag cggggttctt 1620

atctttggga agcaaggccc agagaaaaca aatgtggata ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca agacagagac gtgtacctgc aggggcctat ttgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 229
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 229

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Gly Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 230
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 230

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

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

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro

```
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
```

610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 231
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 231

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 232
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 232
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgcgg cctggtttga ggaaacctgt taagacggct 420

ccgggaaaaa agaggccggt agagcactct cctgtggagc cagactcctc ctcgggaacc 480

ggaaaagcgg gccagcagcc tgcaagaaaa agattaaatt ttggtcagac tggagacgca 540

gactccgtac ctgaccccca gcctctcgga cagccaccag cagccccctc tggtctggga 600

tctactacaa tggctacagg cagtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctgga cgacagagtc 720

atcgccacca gcacccgaac ctgggccctg cccacataca acaaccacct ctacaagcaa 780

atctccagcc aatcaggagc ctgcaacgac aaccactact ttggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacagca actggggatt ccggcccaaa agactcaact tcaagctctt taatattcaa 960

gtcaaagagg tcacgcagaa tgacggtacg acgacgattg ccaataacct taccagcacg 1020

gttcaggtgt ttactgactc ggagtaccag ctcccgtacg tcccgggctc ggcgcatcaa 1080

ggatgcctcc cgccgtttcc agcggacgtc ttcatggtcc cacagtatgg atacctcacc 1140

ctgaacaacg ggagtcaggc ggtaggacgc tcttcctttt actgcctgga gtactttcct 1200

tctcagatgc tgcgtactgg aaacaacttt cagttcagct acacttttga agacgtgcct 1260

ttccacagca gctacgctca ctgccagagt ctggatcggc tgatgaatcc tctgatcgac 1320

cagtacctgt attatctgaa caagacacaa acaaatagtg gaactcttca gcagtctcgg 1380

ctactgttta gccaagctgg accaaccaac atgtctcttc aagctaaaaa ctggctgcct 1440

ggaccttgct acagacagca gcgtctgtca aaacaggcaa acgacaataa caactgcaac 1500

tttccctgga ctgcagctac aaagtatcat ctaaatggcc gggactcgtt ggttaatcca 1560

ggaccagcta tggccagtca caaggatgac gaagaaaagt ttttccccat gcatggaacc 1620

ctgatatttg gtaaacaagg aacaaatgcc aacgacgcgg atttggaaaa tgtcatgatt 1680

acagatgaag aagaaatcag gcccaccaat cccgtggcta cggagcagta cgggactgtg 1740

tcaaataatt tgcaaaactc aaacactggt ccaactacag gaactgtcaa tcaccaagga 1800

gcgttacctg gtatggtgtg gcaggatcga gacgtgtacc tgcagggacc catttgggcc 1860

aagattcctc acaccgatgg acactttcat ccttctccac tgatgggagg ttttggactc 1920

aaacacccgc ctcctcagat catgatcaaa agcactcccg ttccagccaa tcctcccaca 1980

aacttcagtt ctgccaagtt tgcttcttcc atcacacagt attccacggg acaggtcagc 2040

gtggagatcg agtgggagct gcagaaggag aacagcaaac gctggaatcc cgaaattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtggacac taatggtgtg 2160

tattcagagc ctcgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 233
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 233

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Arg Pro Gly Leu Arg Lys Pro Val Lys Thr Ala Pro Gly Lys Lys
    130                 135                 140

Arg Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr
145                 150                 155                 160

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

Thr Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Asp Asp Arg Val
225                 230                 235                 240

Ile Ala Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Cys Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Cys Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys
        435                 440                 445

Thr Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn
                485                 490                 495
```

```
Asn Asn Cys Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Ser Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Ser Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 234
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 234
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttctgga acctctgggc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcagagccag attcctcctc cggaactgga 480

aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780

tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctagagta ctttccttct 1200

cagatgctgc gtaccggaaa cagctttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gtcagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa agacgatgaa gaaaagttct ttcctcagag cggggttctt 1620

atctttggga agcaaggctc agagaaaaca aatgtggata ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca agacagagac gtgtacctgc aggggcctat ttgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 235
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 235

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
```

```
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Ser Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480
```

```
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
```

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 236
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 236
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 237
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 237

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Gly Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480
```

```
Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Ser Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 238
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 238
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtt cacagcccgc taaaaagaaa ctcaatttcg gtcagactgg cgacacagag 540

tcagtccccg accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atgggagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gcgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc taatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gctttcaata aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagattg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 239
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 239

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 240
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 240
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagcggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggtacttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cggcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

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aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 241
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 241

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

```
Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Gly Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 242
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 242
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagcggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtccttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggtacttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacgaga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 243
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 243

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Glu Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
```

```
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 244
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 244
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagcggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggtacttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtaccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

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caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 245
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 245

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

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Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
```

```
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655
```

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 246
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 246
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagcggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggtactcga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagc aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc cgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 247
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 247

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Ala Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655
```

```
Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 248
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 248

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
```

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320
```

```
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
```

```
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 249
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 249
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgttcggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccccg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 250
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 250

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
```

```
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
```

```
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Cys His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
```

725 730 735

Asn Leu

<210> 251
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 251

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Leu Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Ala Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Pro Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
```

```
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Arg Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590
```

```
Pro Thr Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Ala Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Ala Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 252
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 252

```
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240
```

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcggac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtt 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt atcttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcgcc 1020

agcaccatcc aggtgtttac ggactcggaa taccagccgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctcg ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ctgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatcg cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgcgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 253
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 253
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcgtc 900

aacaacaacc ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 254
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 254

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Val Asn Asn Asn Arg
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
```

675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 255
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 255

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350
```

```
Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Ser Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560
```

```
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 256
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 256

atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgagct ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattctgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 257
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 257

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Pro Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Pro Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320
```

```
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Val Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540
```

```
Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 258
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 258
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tacaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ccggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgccacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccgtcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgttg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 259
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 259

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Ser Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
```

```
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Leu
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735
```

Asn Leu

<210> 260
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 260
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aagcaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggactt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 261
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 261

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Pro Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

```
His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Leu His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Val Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495
```

```
Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700
```

```
Asn Tyr Ala Lys Ser Ala Ser Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720


Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735


Leu
```

<210> 262
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 262

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
```

```
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Leu His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575
```

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
580 585 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Ala Ser Val Asp Phe Thr Val Asp Asn Asn Gly
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 263
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 263
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ccgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgcctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccttg cccacctaca ataaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaaact cttcaacatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacaacca tcgctaataa ccttaccagc 1020

acggttcaag tcttctcgga ctcggagtac cagcttccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctctccaca gcagctacgc gcacagccag agcctggacc ggctgatgaa tcctctcatc 1320

gtccaatacc tgtattacct gaacagaact caaaatcagt ccggaagtgc ccaaaacaag 1380

gacttgctgt tcagccgtgg gtctccagct ggcatgtctg ttcagcccaa aaactggcta 1440

cctggaccct gttatcggca gcagcgcgtt tctaaaacaa aaacagacaa caacaacagc 1500

aattttacct ggactggtgc ttcaaaatat aacctcaatg ggcgtgaatc catcatcaac 1560

cctggcactg ctatggcctc acacaaagac gacgaagaca agttctttcc catgagcggt 1620

gtcatgattt ttggaaaaga gagcgccgga gcttcaaaca ctgcattgga caatgtcatg 1680

attacagacg aagaggaaat taaagccact aaccctgtgg ccaccgaaag atttgggacc 1740

gtggcagtca atttccagag cagcagcaca gaccctgcga ccggagatgt gcatgctatg 1800

ggagcattac ctggcatggt gtggcaagat agagacgtgt acctgcaggg tcccatttgg 1860

gccaaaattc ctcacacaga tggacacttt cacccgtctc ctcttatggg cggctttgga 1920

ctcaagaacc cgcctcctca gatcctcatc aaaaacacgc ctgttcctgc gaatcctccg 1980

gcggagtttt cagctacaaa gtttgcttca ttcatcaccc aatactccac aggacaagtg 2040

agtgtggaaa ttgaatggga gctgcagaaa gaaaacagca agcgctggaa tcccgaagtg 2100

cagtacacat ccaattatgc aaaatctgcc agcgttgatt ttactgtgga caacaatgga 2160

ctttatactg agcctcgccc cattggcacc cgttacctta cccgtcccct gtaa 2214

<210> 264
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 264

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Pro Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
```

```
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 265
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 265
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcagacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctga gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagggccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacccgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaaggtaga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 266
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 266

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
```

```
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Pro Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210>  267
<211>  736
<212>  PRT
<213>  Adeno-associated virus
```

<400> 267

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 268
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 268

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
```

```
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 269

<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 269
atggctgccg atggctatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatagggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata ccccaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccgtgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 270
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 270

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Pro Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Val Ala Ser His Lys Asp
```

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        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 271
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 271
atggctgccg acggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgggc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actccccctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcactgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggccgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctctt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ctccacagca gctgcgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacagggac 1380

ttgctgttca gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccgcagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 272
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 272

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Pro Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
```

```
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Arg Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Ser Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Leu His Ser Ser Cys Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Arg Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510
```

```
Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Ala Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
```

725 730 735

<210> 273
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 273

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

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

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Leu His Ser Ser Cys Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Arg Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

```
Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 274
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 274

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atggctgccg atggctatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatagggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgttaa gacggctccg      420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga      480
```

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacagt cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctc 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

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ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 275
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 275

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

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

```
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Ser His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605
```

```
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 276
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 276

```
Arg Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu
1               5                   10                  15

Ser Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys
            20                  25                  30

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

Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
```

```
    50                  55                  60

Pro Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
65                  70                  75                  80

Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His
                85                  90                  95

Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly
            100                 105                 110

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

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

Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

```
His Tyr Phe Gly Tyr Gly Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Glu Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
```

```
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700
```

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 277
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 277

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Gly Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Glu Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575
```

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 278
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 278
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gccagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtactt caacgggggc cagcaacgac aaccactact tcggctacgg caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcgaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaacacaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcaccgctg tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaagcactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 279
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 279

Arg Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu
1 5 10 15

Ser Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys
20 25 30

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

Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
50 55 60

Pro Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
65 70 75 80

Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His
85 90 95

Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly
100 105 110

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

```
Pro Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys
    130                 135                 140

Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Glu Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560
```

```
Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 280
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 280

```
Arg Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu
1               5                  10                  15

Ser Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys
            20                  25                  30

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

Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
    50                  55                  60

Pro Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
65                  70                  75                  80

Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His
                85                  90                  95

Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly
            100                 105                 110

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

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

Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
```

```
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

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

645 650 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 281
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 281

Arg Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu
1 5 10 15

Ser Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys
20 25 30

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

Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
50 55 60

Pro Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
65 70 75 80

```
Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His
                85                  90                  95

Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly
            100                 105                 110

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

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

Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510
```

```
Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Asn Ser Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735
```

Leu

<210> 282
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 282
atggctgccg atggttatct tccagattgg ctcaaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcgggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agtacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaacagga 480

aaagcgggcc agcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaag ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggctctgccc acctacaaca accatctgta caagcagatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc ccggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgagga tgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcaaag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcagaac caccaatccc gtggccacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctactgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgcacctgc aggggcctat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcaaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtatt ccacagggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 283
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 283

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Lys Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Gly Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu Tyr Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Ser Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
```

```
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val His Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
```

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 284
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 284
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcgcaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 285
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 285

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
```

```
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480
```

```
Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser Arg Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
```

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 286
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 286
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgtcaa gacggctcca 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcggct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtacgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 287
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 287

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Gly Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480
```

```
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685
```

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 288
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 288
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa tcggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta cagacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

agcaacggga gtcaggcagt aggacgctct tcattttact gcccggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacctaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atttgtaa 2208

<210> 289
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 289

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Arg His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Arg Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Ser Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Pro Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Pro Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685
```

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 290
<211> 2205
<212> DNA
<213> Adeno-associated virus

<400> 290
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ctgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcagacag ccaccagcag cccccacaag tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accaccttta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tcctttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtttg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctaaacag aacacaaaca gctagtggaa ctcagcagtc tcggctactg 1380

tttagccaag ctggacccac aagcatgtct cttcaagcta aaaactggct gcctggaccg 1440

tgttatcgcc agcagcgttt gtcaaagcag gcaaacgaca acaacaacag caactttccc 1500

tggactggag ctaccaagta ctacctcaat ggcagagact ctttggtgaa cccgggcccg 1560

gccatggcca gccacaagga cgatgaagaa aagtttttcc ccatgcatgg aaccctaata 1620

tttggtaaag aaggaacaaa tgctaccaac gcggaattgg aaaatgtcat gattacagat 1680

gaagaggaaa tcaggaccac caatcccgtg gctacagagc agtacggata tgtgtcaaat 1740

aatttgcaaa actcaaatac tgctgcaagt actgaaactg tgaatcacca aggagcatta 1800

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cctcacaccg atggacactt tcatccttct ccactgatgg gaggttttgg actcaaacac 1920

ccgcctcctc agattatgat caaaaacact cccgttccag ccaatcctcc cacaaacttc 1980

agttctgcca agtttgcttc cttcatcaca cagtattcca cgggacaggt cagcgtggag 2040

atcgagtggg agctgcagaa ggagaacagc aaacgctgga atcccgaaat tcagtacact 2100

tccaactaca acaaatctgt taatgtggac tttactgtgg acactaatgg tgtgtattca 2160

gagcctcgcc ccattggcac cagatacctg actcgtaatc tgtaa 2205

<210> 291
<211> 734
<212> PRT
<213> Adeno-associated virus

<400> 291

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Arg Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
    450                 455                 460
```

```
Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
                485                 490                 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr Tyr Leu Asn Gly Arg
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540

Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575

Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
            580                 585                 590

Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
            660                 665                 670
```

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
690 695 700

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 292
<211> 3160
<212> DNA
<213> Adeno-associated virus

<400> 292
acccttcact aaagggacta gtcctgcagg tttaaacgaa ttcgcccttg ctgcgtcaac 60

tggaccaatg agaactttcc cttcaacgac tgtgtcgaca agatggtgat ttggtgggag 120

gaggggaaga tgaccgccaa ggtcgtggag tcggccaaag ccattctcgg aggaagcaag 180

gtgcgcgtgg accagaaatg caagtcctcg gcccagatag atccgactcc cgtgatcgtc 240

acctccaaca ccaacatgtg cgccgtgatt gacgggaact caacgacctt cgaacaccag 300

cagccgttgc aagaccggat gttcaaattt gaactcaccc gccgtctgga tcatgacttt 360

gggaaggtca ccaagcggga agtcaaagac tttttccggt gggcaaagga tcacgtggtt 420

gaggtggagc atgaattcta cgtcaaaaag ggtggagcca agaaaagacc cgcccctagt 480

gacgcagata taagtgagcc caaacgggtg cgcgagtcag ttgcgcagcc atcgacgtca 540

gacgcggaag cttcgatcaa ctacgcggac aggtaccaaa acaaatgttc tcgtcacgtg 600

ggcatgaatc tgatgctgtt tccctgcaga caatgcgaga gaatgaatca aaattcaaat 660

atctgcttca ctcacggaca gaaagactgt ttagagtgct ttcccgtgtc agaatctcaa 720

cctgtttctg tcgtcaaaaa ggcgtatcag aaactgtgct acattcatca tatcatggga 780

aaggtgccag acgcttgcac tgcctgcgat ctggtcaatg tggatttgga tgactgcatc 840

tctgaacaat aaatgattta aatcaggtat ggctgccgat ggttatcttc cagattggct 900

cgaggacact ctctctgaag gaataagaca gtggtggaag ctcaaacctg gcccaccacc 960

accaaagccc gcagagcggc ataaggacga cagcaggggt cttgtgcttc ctgggtacaa 1020

gtacctcgga cccttcaacg gactcgacaa gggagagccg gtcaacgagg cagacgccgc 1080

ggccctcgag cacgacaagg cctacgaccg gcagctcgac agcggagaca acccgtacct 1140

caagtacaac cacgccgacg cggagtttca ggagcgtctt aaagaagata cgtcttttgg 1200

gggcaacctc ggacgagcag tcttccaggc gaaaaagagg gttcttgaac ctctgggcct 1260

ggttgaggaa cctgttaaga cggctccggg aaaaaagagg ccggtagagc actctcctgc 1320

ggagccagac tcctcctcgg gaaccggaaa agcgggccag cagcctgcaa gaaaaagact 1380

gaatttcggt cagactggag acgcagactc cgtacctgac ccccagcctc tcagacagcc 1440

accagcagcc cccacaagtt tgggatctac tacaatggct acaggcagtg gcgcaccaat 1500

ggcagacaat aacgagggtg ccgatggagt gggtaattcc tcaggaaatt ggcattgcga 1560

ttcccaatgg ctgggcgaca gagtcatcac caccagcacc cgaacctggg ccctgcccac 1620

ctacaacaac cacctttaca agcaaatctc cagccaatca ggagcctcaa acgacaacca 1680

ctactttggc tacagcaccc cctgggggta ttttgacttc aacagattcc actgccactt 1740

ttcaccacgt gactggcaaa gactcatcaa caacaactgg ggattccgac ccaagagact 1800

caacttcaag ctctttaaca ttcaagtcaa agaggtcacg cagaatgacg gtacgacgac 1860

gattgccaat aaccttacca gcacggttca ggtgtttact gactcggagt accagctccc 1920

gtacgtcctc ggctcggcgc atcaaggatg cctcccgccg tttccagcgg acgtcttcat 1980

ggtcccacag tatggatacc tcaccctgaa caacgggagt caggcggtag gacgctcttc 2040

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cagctacact tttgaagacg tgcctttcca cagcagctac gctcacagcc agagtttgga 2160

tcggctgatg aatcctctga tcgaccagta cctgtattat ctaaacagaa cacaaacagc 2220

tagtggaact cagcagtctc ggctactgtt tagccaagct ggacccacaa gcatgtctct 2280

tcaagctaaa aactggctgc ctggaccgtg ttatcgccag cagcgtttgt caaagcaggc 2340

aaacgacaac aacaacagca actttccctg gactggagct accaagtact acctcaatgg 2400

cagagactct ttggtgaacc cgggcccggc catggccagc cacaaggacg atgaagaaaa 2460

gtttttcccc atgcatggaa ccctaatatt tggtaaagaa ggaacaaatg ctaccaacgc 2520

ggaattggaa aatgtcatga ttacagatga agaggaaatc aggaccacca atcccgtggc 2580

tacagagcag tacggatatg tgtcaaataa tttgcaaaac tcaaatactg ctgcaagtac 2640

tgaaactgtg aatcaccaag gagcattacc tggtatggtg tggcaggatc gagacgtgta 2700

cctgcaggga cccatttggg ccaagattcc tcacaccgat ggacactttc atccttctcc 2760

actgatggga ggttttggac tcaaacaccc gcctcctcag attatgatca aaaacactcc 2820

cgttccagcc aatcctccca caaacttcag ttctgccaag tttgcttcct tcatcacaca 2880

gtattccacg ggacaggtca gcgtggagat cgagtgggag ctgcagaagg agaacagcaa 2940

acgctggaat cccgaaattc agtacacttc caactacaac aaatctgtta atgtggactt 3000

tactgtggac actaatggtg tgtattcaga gcctcgcccc attggcacca gatacctgac 3060

tcgtaatctg taattgcttg ttaatcaata aaccgtttaa ttcgtttcag ttgaactttg 3120

gtctctgcga agggcgaatt cgcggccgct aaatcaatcg 3160

<210> 293
<211> 734
<212> PRT
<213> Adeno-associated virus

<400> 293

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys Arg Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Gly Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
    450                 455                 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
                485                 490                 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Gly
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540
```

```
Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575

Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
            580                 585                 590

Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Arg Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
        675                 680                 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
    690                 695                 700

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705                 710                 715                 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730
```

<210> 294
<211> 3157
<212> DNA
<213> Adeno-associated virus

<400> 294
ctcactaagg gactagtcct gcaggtttaa acgaattcgc ccttgctgcg tcaactggac 60

caatgagaac tttcccttca acgactgtgt cgacaagatg gtgatttggt gggaggaggg 120

gaagatgacc gccaaggtcg tggagtcggc caaagccact ctcggaggaa gcaaggtgcg 180

cgtggaccag aaacgcaagt cctcggccca gatagatccg actcccgtga tcgtcacctc 240

caacaccaac atgtgcgccg tgattgacgg gaactcaacg accttcgaac accagcagcc 300

gttgcaagac cgaatgttca aatttgaact cacccgccgt ctggatcatg acttcgggaa 360

ggtcaccaag caggaagtca aagacttttt ccggtgggca aaggatcacg tggttgaggt 420

ggagcatgaa ttctacgtca aaaagggtgg agccaagaaa agacccgccc ctagtgacgc 480

agatataagt gagcccaaac gggtgcgcga gtcagttgcg cagccatcga cgtcagacgc 540

ggaagcttcg atcaactacg cggacaggta ccaaaacaaa tgttctcgtc acgtgggcat 600

gaatctgatg ctgtttccct gcagacaatg cgagagaatg aatcaaaatt caaatatctg 660

cttcactcac ggacagaaag actgtttaga gtgctttccc gtgtcagaat ctcaacctgt 720

ttctgtcgtc aaaaaggcgt atcagaaact gtgctacatt catcatatca tgggaaaggt 780

gccagacgct tgcactgcct gcgatctggt caatgtggat ttggatgact gcatctctga 840

acaataaatg atttaaatca ggtatggctg ccgatggtta tcttccagat tggctcgagg 900

acactctctc tgaaggaata agacagtggt ggaagctcaa acctggccca ccaccaccaa 960

agcccgcaga gcggcataag gacgacagca ggggtcttgt gcttcctggg tacaagtacc 1020

tcggaccctt caacggactc gacaagggag agccggtcaa cgaggcagac gccgcggctc 1080

tcgagcacga caaggcctac gaccggcagc tcgacagcgg agacaacccg tacctcaagt 1140

acaaccacgc cgacgcggag tttcaggagc gtcttaaaga agatacgtct tttgggggca 1200

acctcggacg agcagtcttc caggcgaaaa agagggttct tgaacctctg ggcctggttg 1260

aggaacctgt taagacggct ccgggaaaaa agaggccggt agagcactct cctgcggagc 1320

cagactcctc ctcgggaacc ggaaaagcgg gccagcagcc tgcaagaaaa agactgaatt 1380

tcggtcagac tggagacgca gactccgtac ctgaccccca gcctctcgga cagccaccag 1440

cagcccccac aagtttggga tctactacaa tggctacagg cagtggcgca ccaatggcag 1500

acaataacga gggtgccgat ggagtgggta attcctcagg aaattggcat tgcgattccc 1560

aatggctggg cgacagagtc atcaccacca gcacccgaac ctgggccctg cccacctaca 1620

acaaccacct ttacaagcaa atctccagcc aatcaggagc ctcaaacgac aaccactact 1680

ttggctacag cacccctgg gggtattttg acttcaacag attccactgc cgcttttcac 1740

cacgtgactg gcaaagactc atcaacaaca actggggatt ccgacccaag agactcaact 1800

tcaagctctt taacattcaa gtcaaagagg tcacgcagaa tgacggtacg acgacgattg 1860

ccaataacct taccagcacg gttcaggtgt ttactgactc ggagtaccag ctcccgtacg 1920

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tgatgaatcc tctgatcgac cagtacctgt attatctaaa cagaacacaa acagctagtg 2220

gaactcagca gtctcggcta ctgtttagcc aagctggacc cacaagcatg tctcttcaag 2280

ctaaaaactg gctgcctgga ccgtgttatc gccagcagcg tttgtcaaag caggcaaacg 2340

acaacaacaa cagcaacttt ccctggactg gagctaccaa gtaccacctc aatggcggag 2400

actctttggt gaacccgggc ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt 2460

tccccatgca tggaacccta atatttggta aagaaggaac aaatgctacc aacgcggaat 2520

tggaaaatgt catgattaca gatgaagagg aaatcaggac caccaatccc gtggctacag 2580

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ctgtgaatca ccaaggagca ttacctggta tggtgtggca ggatcgagac gtgtacctgc 2700

ggggacccat ttgggccaag attcctcacg ccgatggaca ctttcatcct tctccactga 2760

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cagccaatcc tcccacaaac ttcagttctg ccaagtttgc ttccttcatc acacagtatt 2880

ccacgggaca ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct 2940

ggaatcccga aattcagtac acttccaact acaacaaatc tgttaatgtg gactttactg 3000

tggacactaa tggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta 3060

atctgtaatt gcttgttaat caataaaccg tttaattcgt ttcagttgaa ctttggtctc 3120

tgcgaagggc gaattcgcgg ccgctaaatt caattcg 3157

<210> 295
<211> 734
<212> PRT
<213> Adeno-associated virus

<400> 295

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

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Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Cys Phe Pro Ser
385                 390                 395                 400
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```
Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
    450                 455                 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
                485                 490                 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540

Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575

Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
            580                 585                 590

Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620
```

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
645 650 655

Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
690 695 700

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 296
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 296
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctggatac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggca accagcctgc aagaaaaaga ttgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcat ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcgtc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta caagcagatt 780

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cacagcagct acgctcacag tcaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccactacgca gtccaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcaaag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaaa 1860

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caccctcctc cacagattct cattaagaat accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagcgcgg caaagtttgc ttccttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggggtgtat 2160

tcagagcctc gccctattgg caccagatac ctgactcgta atctgtaa 2208

<210> 297
<211> 3159
<212> DNA
<213> Adeno-associated virus

<400> 297
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ccttcaacga ttgcgtcgac aagatggtga tctggtggga ggagggaaag atgaccgcca 120

aggtcgtgga gtcggccaaa gccattctcg gaggaagcaa ggtgcgtgtg gaccaaaagt 180

gcaagtcttc ggcccagatc gacccgactc ccgtgatcgt cacctccaac accaacatgt 240

gcgccgtgat tgatggaaac tcaacgacct tcgagcacca gcagccgttg caagaccgga 300

tgttcaaatt tgaacttacc cgccgtctgg atcatgactt tggaaaggtc accaagcagg 360

aagtgaaaga ctttttccgg tgggcaaagg atcacgtggt tgaggtggag catgagttct 420

acgtcaaaaa gggtggagcc aaaaaaagac ccgcccccag tgacgcagat ataagtgagc 480

ccaaacgggc gcgcgagtca gttgcgcagc catcgacgtc agacgcggaa gcttcgatca 540

actacgcgga caggtaccaa aacaaatgtt ctcgtcacgt gggcatgaat ctgatgctgt 600

ttccctgcag acaatgcgag agaatgaatc agaattcaaa tatctgcttc actcacggac 660

agaaagactg tccatagtgc tttcccgtgt cagaatctca acccgtttct gtcgtcaaaa 720

aggcgtatca gaaactgtgc tacattcatc acatcatggg aaaggtgcca gacgcttgca 780

ctgcttgcga cctggtcaat gtggatttgg atgactgcat ctctgaacaa taaatgattt 840

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cataaggacg acagcagggg tcttgtgctt cctggataca agtacctcgg acccttcaac 1020

ggactcgaca agggagagcc ggtcaacgag gcagacgccg cggccctcga gcacgacaag 1080

gcctacgacc ggcagctcga cagcggagac aacccgtacc tcaagtacaa ccacgccgac 1140

gcggagtttc aggagcgcct taaagaagat acgtcttttg ggggcaacct cggacgagca 1200

gtcttccagg cgaaaaagag ggttcttgaa cctctgggcc tggttgagga acctgttaag 1260

acggctccgg gaaaaaagag gccggtagag cactctcctg tggagccaga ctcctcctcg 1320

ggaaccggaa aagcgggcaa ccagcctgca agaaaaagat tgaatttcgg tcagactgga 1380

gacgcagact ccgtacctga cccccagcct ctcggacagc caccagcatc cccctctggt 1440

ctgggaacta atacgatggc tacaggcagt ggcgcaccaa tggcagacaa taacgagggc 1500

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agagtcgtca ccaccagcac ccgcacctgg gccctgccca cctacaacaa ccacctctac 1620

aagcagattt ccagccaatc aggagccagc aacgacaacc actactttgg ctacagcacc 1680

ccttgggggt attttgactt caacagattc cactgccact tttcgccacg cgactggcag 1740

agactcatca acaacaactg gggattccgg cccaaaagac tcaacttcaa gctgtttaac 1800

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attcagtaca cttccaacta caacaaatct gttaatgtgg actttactgt ggacactaat 3000

ggggtgtatt cagagcctcg ccctattggc accagatacc tgactcgtaa tctgtaattg 3060

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aattcgttta aacctgcagg actagtccct ttagtgagg 3159

<210> 298
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 298

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

```
Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ser Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Val
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
```

```
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590
```

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 299
<211> 2205
<212> DNA
<213> Adeno-associated virus

<400> 299
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agcaggggtc ttgtgcttcc tggatacaag tacctcggac ccttcaacgg actcgacaag 180

ggagagccgg tcaacgaggc agacgccgcg gccctcgagc acgacaaggc ctacgaccgg 240

cagctcgaca gcggagacaa cccgtacctc aagtacaacc acgccgacgc ggagtttcag 300

gagcgcctta aagaagatac gtcttttggg ggcaacctcg gacgagcagt cttccaggcg 360

aaaaagaggg ttcttgaacc tctgggcctg gttgaggaac ctgttaagac ggctccggga 420

aaaaagaggc ccgtagagca ctctcctgtg gagccagact cctcctcggg aaccggaaaa 480

gcgggcaacc agcctgcaag aaaaagattg aatttcggtc agactggaga cgcagactcc 540

gtacctgacc cccagcctct cggacagcca ccagcagccc cctctggtct gggaactaat 600

acgatggcta caggcagtgg cgcaccaatg gcagacaata acgagggcgc cgacggagtg 660

ggtaattcct cgggagattg gcattgcgat tccacatgga tgggcgacag agtcatcacc 720

accagcaccc gcacctgggc cctgcccacc tacaacaacc acctctacaa gcagatttcc 780

agccaatcag gagccagcaa tgacaaccac tactttggct acagcacccc ttgggggtat 840

tttgacttca acagattcca ctgccacttt tcgccacgcg actggcagag actcatcaac 900

aacaactggg gattccggcc caaaagactc aacctcaagc tgtttaacat tcaagtcaag 960

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agcgcggcaa agtttgcttc cttcatcaca cagtattcca cggggcaggt cagcgtggag 2040

atcgagtggg agctgcagaa ggagaacagc aaacgctgga atcccgaaat tcagtacact 2100

tccaactaca acaaatctgt taatgtggac tttactgtgg acactaatgg ggtgtattca 2160

gagcctcgcc ctattggcac cagatacctg actcgtaatc tgtaa 2205

<210> 300
<211> 3156
<212> DNA
<213> Adeno-associated virus

<400> 300
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cccttcaacg attgcgtcga caagatggtg atctggtggg aggagggaaa gatgaccgcc 120

aaggtcgtgg agtcggccaa agccattctc ggaggaagca aggtgcgtgt ggaccaaaag 180

tgcaagtctt cggcccagat cgacccgact cccgtgatcg tcacctccaa caccaacatg 240

tgcgccgtga ttgatggaaa ctcaacgacc ttcgagcacc agcagccgtt gcaagaccgg 300

atgttcaaat ttgaacttac ccgccgtctg gatcatgact ttggaaaggt caccaagcag 360

gaagtgaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgagttc 420

tacgtcaaaa agggtggagc caaaaaaaga cccgccccca gtgacgcaga tataagtgag 480

cccaaacggg cgcgcgagtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc 540

aactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg 600

tttccctgca gacaatgcga gcgaatgaat cagaattcaa atatctgctt cactcacgga 660

cagaaagact gtttagagtg ctttcccgtg tcagaatctc aacccgtttc tgtcgtcaaa 720

aaggcgtatc agaaactgtg ctacattcat cacatcatgg gaaaggtgcc agacgcttgc 780

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ttcgtttaaa cctgcaggac tagtcccttt agtgag 3156

<210> 301
<211> 734
<212> PRT
<213> Adeno-associated virus

<400> 301

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Lys
20 25 30

Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Arg
65 70 75 80

Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
115 120 125

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Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly Lys
145                 150                 155                 160

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

Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro Ala
            180                 185                 190

Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly Ala
        195                 200                 205

Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser
    210                 215                 220

Gly Asp Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255

Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr Phe
            260                 265                 270

Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
        275                 280                 285

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
    290                 295                 300

Phe Arg Pro Lys Arg Leu Asn Leu Lys Leu Phe Asn Ile Gln Val Lys
305                 310                 315                 320

Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu Thr
                325                 330                 335

Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu Pro Tyr Val
            340                 345                 350
```

```
Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
        355                 360                 365

Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln
    370                 375                 380

Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
385                 390                 395                 400

Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp
                405                 410                 415

Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
            420                 425                 430

Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Asn
        435                 440                 445

Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln Ala
    450                 455                 460

Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn Asn
                485                 490                 495

Gly Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys Gln
    530                 535                 540

Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr Asp
545                 550                 555                 560
```

```
Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575

Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Arg Ala Ala Thr Ser
            580                 585                 590

Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
        675                 680                 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
    690                 695                 700

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705                 710                 715                 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730
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<210> 302
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 302

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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtacg accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa gacggctccg 420

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aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgatgg cgccgacgga 660

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tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggatcagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg acaacaacaa cagtgaatac 1500

tcgtggattg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggcaatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggaa aacaaggatc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcagaac caccaatccc gtggccacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca tctactgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcctat ctgggcaaag 1860

attccgcaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacagattct catcaaaaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtatt ccacggggcg ggtcagcgtg 2040

gagatcgagt gggagctaca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 303
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 303

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Asp Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
```

```
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Ile Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560
```

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ser Thr
580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Arg Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 304
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 304
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagacag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattccg catggctggg cgacagagtc 720

atcaccacca gcacccgacc ctgggccctc cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtcct cggctctgcg 1080

caccagggct gcccgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaacggcag tcaggccgtg ggccgttcct ccttctactg cctggagtac 1200

tttccttctc aaatgcggag aacgggcaac aactttgagt tcagctacca gtttgaggac 1260

gtgccttttc acagcagcta cgcgcatagc caaagcctgg accggctgat gaacccccctc 1320

atcgaccagt acctgtacta cctgtctcgg actcagtcca cgggaggtac cgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aataacatgt cggctcaggc caaaaactgg 1440

ctacccgggc cctgctaccg gcagcaacgc gtctccacga cactgtcgca aaataacaac 1500

agcaactttg cttggaccgg tgccaccaag tatcatctga atggcagaga ctctctggta 1560

aatcccggtg tcgctatggc aacgcacaag gacgacgaag agcgattttt tccatccagc 1620

ggagtcttga tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtt 1680

atgctaacca gtgaggaaga aatcaaaacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaacagt 1800

caaggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatc 1860

tgggccaaga ttcctcacac ggacggcaac tttcatcctt cgccgctgat gggaggcttt 1920

ggactgaaac acccgcctcc tcagatcctg attaagaata cacctgttcc cgcggatcct 1980

ccaactacct tcagtcaagc caagctggcg tcgttcatca cgcagtacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaagagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt cagagcctcg ccccattggc acccgttacc tcacccgtaa cctgtaa 2217

<210> 305
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 305

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Ala Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Pro Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540
```

```
Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 306
<211> 735

<212> PRT
<213> Adeno-associated virus

<400> 306

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly

```
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415
```

```
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
```

625 630 635 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 307
<211> 3158
<212> DNA
<213> Adeno-associated virus

<400> 307
gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt 60

cctttcaatg attgcgtcga caagatggtg atctggtggg aggagggaaa gatgaccgcc 120

aaggtcgtgg agtcggccaa agccattctc ggaggaagca aggtgcgcgc ggaccagaaa 180

tgcaagtcct cggcccagat agacccgact cccgtgattg tcacctccaa caccaacatg 240

tgcgccgtga ttgacgggaa ctcaacgacc ttcgaacacc agcagccgtt gcaagaccgg 300

atgttcaaat ttgaactcac ccgccgtctg gatcatgact ttgggaaggt caccaagcag 360

gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc 420

tacgtcaaaa agggtggagc taagaaaaga cccgccccca gtgacgcaga tataagtgag 480

cccaaacggg cgcgcgagtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc 540

aactacgcgg gcaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg 600

tttccctgca gacaatgcga gagaatgaat cagaattcaa atatctgctt cactcacgga 660

cagaaagact gtttagagtg ctttcccgtg tcagaatctc aacccgtttc tgtcgtcaaa 720

aaggcgtatc agaaactttg ctacattcat catatcatgg gaaaggtgcc agacgcttgc 780

actgcctgcg atctggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt 840

taaatcaggt atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga 900

aggaataaga cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg 960

gcataaggac gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa 1020

cggactcgac aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa 1080

ggcctacgac cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga 1140

cgcggagttt caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc 1200

agtcttccag gcaaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa 1260

aacggctccg ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc 1320

gggaaccgga aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg 1380

agacgcagac tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg 1440

tctgggatct actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg 1500

tgccgatgga gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggcga 1560

cagagtcatc accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta 1620

caagcaaatc tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac 1680

cccctggggg tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca 1740

aagactcatc aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa 1800

cattcaagtc aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac 1860

cagcacggtt caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc 1920

gcatcaagga tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata 1980

cctcaccctg aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta 2040

ctttccttct cagatgctgc gtaccggaaa caactttcaa ttcagctaca cttttgaaga 2100

cgtgcctttc cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct 2160

ggtcgaccag tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca 2220

gtctcggcta ctgtttagcc aagctggacc caccaacatg tctcttcaag ctaaaaactg 2280

gctgcctgga ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa 2340

cagcaacttt ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt 2400

taatccagga ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca 2460

tggaaccctt atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt 2520

catgattaca gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg 2580

aactgtatca aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca 2640

ccaaggagcg ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat 2700

ttgggccaag attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt 2760

tggactcaaa cacccacctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc 2820

tcccacaaac ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca 2880

ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga 2940

aattcagtac acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa 3000

tggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaatt 3060

gcttgttaat caataaaccg tttaattcgt ttcagttgaa ctttggtctc tgcgaagggc 3120

gaattcgttt aaacctgcag gactagtccc tttagtga 3158

<210> 308
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 308

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

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Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Pro Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
```

```
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Arg Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Val Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
```

705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 309
<211> 3159
<212> DNA
<213> Adeno-associated virus

<400> 309
gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt 60

cctttcaatg attgcgtcga caagatggtg atctggtggg aggagggaaa gatgaccgcc 120

aaggtcgtgg agtcggccaa agccattctc ggaggaagca aggtgcgcgt ggaccagaaa 180

tgcaagtcct cggcccagat agacccgact cccgtgattg tcacctccaa caccgacatg 240

tgcgccgtga ttgacgggaa ctcaacgacc ttcgaacacc agcagccgtt gcaagaccgg 300

atgttcaaat ttgaactcac ccgccgtctg gatcatgact ttgggaaggt caccaagcag 360

gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc 420

tacgtcaaaa agggtggagc taagaaaaga cccgccccca gtgacgcaga tataagtgag 480

cccaaacggg cgcgcgagtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc 540

aactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg 600

tttccctgca gacaatgcga gagaatgaat cagaattcaa atatctgctt cactcacgga 660

cagaaagact gtttagagtg ctttcccgtg tcagaatctc aacccgtttc tgtcgtcaaa 720

aaggcgtatc agaaactttg ctacattcat catatcatgg gaaaggtgcc agacgcttgc 780

actgcctgcg atctggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt 840

taaatcaggt atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga 900

aggaataaga cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg 960

gcataaggac gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa 1020

cggactcgac aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa 1080

ggcctacgac cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga 1140

cgcggagttt caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc 1200

agtcttccag gcaaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa 1260

aacggctccg ggaaaaaaga ggccggtaga gcaccctcct gtggagccag actcctcctc 1320

gggaaccgga aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg 1380

agacgcagac tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg 1440

tctgggatct actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg 1500

tgccgatgga gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggcga 1560

cagagtcatc accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta 1620

caagcaaatc tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac 1680

cccctggggg tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca 1740

aagactcatc aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa 1800

cattcaagtc aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac 1860

cagcacggtt caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc 1920

gcatcaagga tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata 1980

cctcaccctg aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta 2040

ctttccttct cagatgctgc gtaccggaaa caactttcag ttcagctaca cttttgaaga 2100

cgtgcctttc cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct 2160

gatcgaccag tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca 2220

gtctcggcta ctgtttagcc aagctggacc caccaacatg tctcttcaag ctaaaaaccg 2280

gctgcctgga ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa 2340

cagcaacttt ccctggaccg cagctacaaa gtatcatcta aatggccggg actcgttggt 2400

taatccagga ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca 2460

tggaaccctt atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt 2520

catgattaca gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg 2580

aactgtatca aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca 2640

ccaaggagcg ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat 2700

ttgggccaag attcctcaca ccgatggaca ctttcatcct tctccactgg tgggaggttt 2760

tggactcaaa cacccacctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc 2820

tcccacaaac ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca 2880

ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga 2940

aattcagtac acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa 3000

tggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaatt 3060

gcttgttaat caataaaccg tttaattcgt ttcagttgaa ctttggtctc tgcgaagggc 3120

gaattcgttt aaacctgcag gactagtccc tttagtgag 3159

<210> 310
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 310
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtaccttg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac cccaagtaca accacgccga cgcggagttc 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggctctgccc acctacaaca accacctcta caagcagatt 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcgccac gtgactggca aagactcatc 900

aacaacaatt ggggattccg gcccaaaaga ctcaacttca agctctttaa cattcaagtc 960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgcccacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctt aatggaagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

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caccctcccc cgcagattct catcaagaac accccggtac ctgcgaatcc ttcgactacc 1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccaggtac ctgactcgta atctgtaa 2208

<210> 311
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 311

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685
```

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 312
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 312
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtaccttg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acggcggaga caacccgtac ctcaagtaca accacgccga cgcggagttc 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctctt gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaggaga ttgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggctctgccc acctacaaca accacctcta caggcagatt 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcgccac gtgactggca aagactcatc 900

aacaacaatt ggggatcccg gcccaaaaga ctcaacttca agctctttaa cattcaagtc 960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

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aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgcccacag ccagagtttg gaccgtctca tgaatcctct cgtcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctt aatggaagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtgtggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

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caccctcccc cgcagattct catcaagaac accccggtac ctgcgaatcc ttcgactacc 1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 313
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 313

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Gly Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Leu Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
```

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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Arg Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Ser Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

```
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  314
<211>  738
<212>  PRT
<213>  Adeno-associated virus

<400>  314

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Ala Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Glu Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
```

```
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Cys Ala His Ser Gln Ser
            420                 425                 430

Ser Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Arg Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560
```

```
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 315
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 315
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcttggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaatgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcggcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacgacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 316
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 316

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Leu
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320
```

```
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Gly Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
```

```
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 317
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 317

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Pro Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

```
Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

```
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  318
<211>  735
<212>  PRT
<213>  Adeno-associated virus

<400>  318

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
```

```
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gly Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
```

```
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 319
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 319
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

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tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 320
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 320
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<210> 321
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 321
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

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<210> 322
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 322
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ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

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<210> 323
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 323

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Glu Gly Thr Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

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

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Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
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Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605
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Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 324
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 324

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aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

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gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420
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<210> 325
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 325

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Gln Asp Asn Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Ser Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

```
Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Cys Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Pro Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590
```

```
Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Cys Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 326
<211> 2214
<212> DNA
<213> Artificial Sequence

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

<400> 326
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gtttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 327
<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 327

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

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

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350
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```
Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560
```

```
Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 328
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 328
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 329
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 329

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510
```

```
Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 330
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 330
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcga 60

gagtggtggg cgctgcaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccggcaa cggactcgac 180

aaggggggaac ccgtcaacgc agcggacgcg gcagccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 331
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 331

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
```

```
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 332
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 332
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcaccagaac ctgggccctg cccacttaca acaaccatct ctacaagcaa 780

atctccagcc aatcaggagc ttcaaacgac aaccactact ttggctacag cacccttgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacttgag cagaacaaac actccaagtg gaaccaccac gcagtcaagg 1380

cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct 1440

ggaccctgtt accgccagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 333
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 333

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240
```

```
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445
```

```
Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 334
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 334
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcaccagaac ctgggccctg cccacttaca acaaccatct ctacaagcaa 780

atctccagcc aatcaggagc ttcaaacgac aaccactact ttggctacag cacccttgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct 1260

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cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct 1440

ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

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gccttacctg gaatggtgtg gcaagacaga gacgtgtacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 335
<211> 736
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 335

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


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


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205
```

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
               645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 336
<211> 2214
<212> DNA
<213> Artificial Sequence

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

<400> 336

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atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag      360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct      420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc      480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag      540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct      600
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aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat gactgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gtttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 337
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 337

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


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

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Leu Gly Asp Arg Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255

Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

```
Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 338
<211> 2214
<212> DNA
<213> Artificial Sequence

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

<400> 338
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaatacccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

ccttttcaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 339
<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 339

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

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

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575
```

```
Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
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<210> 340
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 340
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcaccagaac ctgggccctg cccacttaca acaaccatct ctacaagcaa 780

atctccagcc aatcaggagc ttcaaacgac aaccactact ttggctacag cacccttgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacttgag cagaacaaac actccaagtg gaaccaccac gcagtcaagg 1380

cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct 1440

ggaccctgtt accgccagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 341
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 341

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
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<210> 342
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 342
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctccc 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctctac gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaatttcg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aacacctact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 343
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 343

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

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Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn Thr
            260                 265                 270
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Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
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Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 344
<211> 2205
<212> DNA
<213> Artificial Sequence

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

<400> 344
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctcttcaa catccaggtc 960

aaagaggtta cggacaacaa tggagtcaag accatcgcca ataaccttac cagcacggtc 1020

caggtcttca cggactcaga ctatcagctc ccgtacgtgc tcgggtcggc tcacgagggc 1080

tgcctcccgc cgttcccagc ggacgttttc atgattcctc agtacgggta tctgacgctt 1140

aatgatggaa gccaggccgt gggtcgttcg tccttttact gcctggaata tttcccgtcg 1200

caaatgctaa gaacgggtaa caacttccag ttcagctacg agtttgagaa cgtacctttc 1260

catagcagct acgctcacag ccaaagcctg gaccgactaa tgaatccact catcgaccaa 1320

tacttgtact atctctcaaa gactattaac ggttctggac agaatcaaca aacgctaaaa 1380

ttcagtgtgg ccggacccag caacatggct gtccagggaa gaaactacat acctggaccc 1440

agctaccgac aacaacgtgt ctcaaccact gtgactcaaa acaacaacag cgaatttgct 1500

tggcctggag cttcttcttg ggctctcaat ggacgtaata gcttgatgaa tcctggacct 1560

gctatggcca gccacaaaga aggagaggac cgtttctttc ctttgtctgg atctttaatt 1620

tttggcaaac aaggaactgg aagagacaac gtggatgcgg acaaagtcat gataaccaac 1680

gaagaagaaa ttaaaactac taacccggta gcaacggagt cctatggaca agtggccaca 1740

aaccaccaga gtgcccaagc acaggcgcag accggctggg ttcaaaacca aggaatactt 1800

ccgggtatgg tttggcagga cagagatgtg tacctgcaag gacccatctg ggccaagatt 1860

cctcacacgg acggcaactt ccacccgtct ccgctgatgg gcggctttgg cctgaaacat 1920

cctccgcctc agatcctgat caagaacacg cctgtacctg cggatcctcc gaccaccttc 1980

aaccagtcaa agctgaactc tttcatcacg caatacagca ccggacaggt cagcgtggaa 2040

attgaatggg agctgcagaa ggaaaacagc aagcgctgga atcccgaagt gcagtataca 2100

tctaactatg caaaatctgc caacgttgat ttcactgtgg acaacaatgg actttatact 2160

gagcctcgcc ccattggcac ccgttacctc acccgtcccc tgtaa 2205

<210> 345
<211> 734
<212> PRT
<213> Artificial Sequence

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

<400> 345

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

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Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe Glu
                405                 410                 415

Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala
    450                 455                 460
```

```
Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro
465                 470                 475                 480

Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn
                485                 490                 495

Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg
            500                 505                 510

Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly
        515                 520                 525

Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln
    530                 535                 540

Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn
545                 550                 555                 560

Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly
                565                 570                 575

Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly
            580                 585                 590

Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro
                645                 650                 655

Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670
```

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr Ala
690 695 700

Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu Tyr Thr
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 346
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 346
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagt gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

accgacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 347
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 347

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Trp Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

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Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
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```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
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Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 348
<211> 2214
<212> DNA
<213> Artificial Sequence

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

<400> 348
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctcggcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtcttcatgg tgccacagta tggatacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggacttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 349
<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 349

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145 150 155 160

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

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Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

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

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
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Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Asp Leu Pro Gly Met Val Trp
        595                 600                 605
```

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 350
<211> 2205
<212> DNA
<213> Artificial Sequence

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

<400> 350
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aactgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

accaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctcttcaa catccaggtc 960

aaagaggtta cggacaacaa tggagtcaag accatcgcca ataaccttac cagcacggtc 1020

caggtcttca cggactcaga ctatcagctc ccgtacgtgc tcgggtcggc tcacgagggc 1080

tgcctcccgc cgttcccagc ggacgttttc atgattcctc agtacgggta tctgacgctt 1140

aatgatggaa gccaggccgt gggtcgttcg tccttttact gcctggaata tttcccgtcg 1200

caaatgctaa gaacgggtaa caacttccag ttcagctacg agtttgagaa cgtacctttc 1260

catagcagct acgctcacag ccaaagcctg gaccgactaa tgaatccact catcgaccaa 1320

tacttgtact atctctcaaa gactattaac ggttctggac agaatcaaca aacgctaaaa 1380

ttcagtgtgg ccggacccag caacatggct gtccagggaa gaaactacat acctggaccc 1440

agctaccgac aacaacgtgt ctcaaccact gtgactcaaa acaacaacag cgaatttgct 1500

tggcctggag cttcttcttg ggctctcaat ggacgtaata gcttgatgaa tcctggacct 1560

gctatggcca gccacaaaga aggagaggac cgtttctttc ctttgtctgg atctttaatt 1620

tttggcaaac aaggaactgg aagagacaac gtggatgcgg acaaagtcat gataaccaac 1680

gaagaagaaa ttaaaactac taacccggta gcaacggagt cctatggaca agtggccaca 1740

aaccaccaga gtgcccaagc acaggcgcag accggctggg ttcaaaacca aggaatactt 1800

ccgggtatgg tttggcagga cagagatgtg tacctgcaag gacccatctg ggccaagatt 1860

cctcacacgg acggcaactt ccacccgtct ccgctgatgg gcggctttgg cctgaaacat 1920

cctccgcctc agatcctgat caagaacacg cctgttcctg cgaatcctcc ggcggagttt 1980

tcagctacaa agtttgcttc attcatcacc cagtactcca caggacaagt gagtgtggaa 2040

attgaatggg agctgcagaa agaaaacagc aagcgctgga atcccgaagt gcagtacaca 2100

tccaattatg caaaatctgc caacgttgat tttactgtgg acaacaatgg actttatact 2160

gagcctcgcc ccattggcac ccgttacctt accaaacctc tgtaa 2205

<210> 351
<211> 734
<212> PRT
<213> Artificial Sequence

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

<400> 351

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Cys Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

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

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Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr
            340                 345                 350
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Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe Glu
                405                 410                 415

Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala
    450                 455                 460

Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro
465                 470                 475                 480

Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn
                485                 490                 495

Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg
            500                 505                 510

Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly
        515                 520                 525

Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln
    530                 535                 540

Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn
545                 550                 555                 560
```

```
Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly
                565                 570                 575

Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly
            580                 585                 590

Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
        675                 680                 685

Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr Ala
    690                 695                 700

Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu Tyr Thr
705                 710                 715                 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Lys Pro Leu
                725                 730
```

<210> 352
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 352
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcaccagaac ctgggccctg cccacttaca acaaccatct ctacaagcaa 780

atctccagcc aatcaggagc ttcaaacgac aaccactact ttggctacag cacccttgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacttgag cagaacaaac actccaagtg gaaccaccac gcagtcaagg 1380

cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct 1440

ggaccctgtt accgccagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 353
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 353

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

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Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
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Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 354
<211> 2214

<212> DNA
<213> Artificial Sequence

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

<400> 354
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 355
<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 355

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

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

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
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Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495
```

```
Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720
```

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 356
<211> 2205
<212> DNA
<213> Artificial Sequence

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

<400> 356
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctcttcaa catccaggtc 960

aaagaggtta cggacaacaa tggagtcaag accatcgcca ataaccttac cagcacggtc 1020

caggtcttca cggactcaga ctatcagctc ccgtacgtgc tcgggtcggc tcacgagggc 1080

tgcctcccgc cgttcccagc ggacgttttc atgattcctc agtacgggta tctgacgctt 1140

aatgatggaa gccaggccgt gggtcgttcg tccttttact gcctggaata tttcccgtcg 1200

caaatgctaa gaacgggtaa caacttccag ttcagctacg agtttgagaa cgtacctttc 1260

catagcagct acgctcacag ccaaagcctg gaccgactaa tgaatccact catcgaccaa 1320

tacttgtact atctctcaaa gactattaac ggttctggac agaatcaaca aacgctaaaa 1380

ttcagtgtgg ccggacccag caacatggct gtccagggaa gaaactacat acctggaccc 1440

agctaccgac aacaacgtgt ctcaaccact gtgactcaaa acaacaacag cgaatttgct 1500

tggcctggag cttcttcttg ggctctcaat ggacgtaata gcttgatgaa tcctggacct 1560

gctatggcca gccacaaaga aggagaggac cgtttctttc ctttgtctgg atctttaatt 1620

tttggcaaac aaggaactgg aagagacaac gtggatgcgg acaaagtcat gataaccaac 1680

gaagaagaaa ttaaaactac taacccggta gcaacggagt cctatggaca agtggccaca 1740

aaccaccaga gtgcccaagc acaggcgcag accggctggg ttcaaaacca aggaatactt 1800

ccgggtatgg tttggcagga cagagatgtg tacctgcaag gacccatttg ggccaaaatt 1860

cctcacacgg acggcaactt tcacccttct ccgctgatgg gagggtttgg aatgaaacac 1920

ccgcctcctc agatcctcat caaaaacaca cctgtacctg cggatcctcc aacggccttc 1980

aacaaggaca agctgaactc tttcatcacc cagtattcta ctggccaagt cagcgtggag 2040

atcgagtggg agctgcagaa ggaaaacagc aagcgctgga accccgagat ccagtacacc 2100

tccaactact acaaatctac aagtgtggac tttgctgtta atacagaagg cgtgtactct 2160

gaaccccgcc ccattggcac ccgttacctc acccgtaatc tgtaa 2205

<210> 357
<211> 734
<212> PRT
<213> Artificial Sequence

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

<400> 357

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe Glu
                405                 410                 415

Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445
```

```
Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala
    450                 455                 460

Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro
465                 470                 475                 480

Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn
                485                 490                 495

Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg
            500                 505                 510

Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly
        515                 520                 525

Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln
    530                 535                 540

Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn
545                 550                 555                 560

Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly
                565                 570                 575

Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly
            580                 585                 590

Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro
                645                 650                 655

Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670
```

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr
690 695 700

Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr Ser
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 358
<211> 2217
<212> DNA
<213> Artificial Sequence

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

<400> 358
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccccct ctcccctcat gggtggattc 1920

ggacttaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 359
<211> 738
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 359

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


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


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205
```

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415
```

```
Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
```

```
Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 360
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 360

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atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcga       60

gagtggtggg cgctgcaacc tggagcccct aaacccaagg caaatcaaca acatcaggac      120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccggcaa cggactcgac      180

aaggggggaac ccgtcaacgc agcggacgcg gcagccctcg agcacgacaa ggcctacgac      240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgccgagttc      300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc      480
```

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caggtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tcctttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 361
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 361

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145 150 155 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
```

```
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590
```

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 362
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 362
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcga 60

gagtggtggg cgctgcaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccggcaa cggactcgac 180

aaggggggaac ccgtcaacgc agcggacgcg gcagccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tcctttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 363
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 363

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
```

```
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560
```

```
Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 364
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 364
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 365
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 365

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 366
<211> 2217
<212> DNA
<213> Artificial Sequence

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

<400> 366
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca acggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaaccaccag cagcccccac aagtttggga 600

tctaatacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccttg cccacctaca ataaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa ccgcttccac tgccacttct cgccaagaga ctggcaaaga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaaact cttcaacatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacgacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta tggatacctc 1140

accctgaaca acggaagtca agcggtggga cgctcatcct tttactgcct ggagtacttc 1200

ccttcgcaga tgctaaggac tggaaataac ttccaattca gctatacctt cgaggatgta 1260

ccttttcaca gcagctacgc tcacagccag agtttggatc gcttgatgaa tcctcttatt 1320

gatcagtatc tgtactacct gaacagaacg caaggaacaa cctctggaac aaccaaccaa 1380

tcacggctgc tttttagcca ggctgggcct cagtctatgt ctttgcaggc cagaaattgg 1440

ctacctgggc cctgctaccg gcaacagaga ctttcaaaga ctgctaacga caacaacaac 1500

agtaactttc cttggacagc agccagcaaa tatcatctca atggccgcga ctcgctggtg 1560

aatccaggac cagctatggc cagtcacaag gacgatgaag aaaaattttt ccctatgcac 1620

ggcaatctaa tatttggcaa agaagggaca acggcaagta acgcagaatt agataatgta 1680

atgattacgg atgaagaaga gattcgtacc accaatcctg tggcaacaga gcagtatgga 1740

actgtggcaa ataacttgca gagctcaaat acagctccca cgactagaac tgtcaatgat 1800

caggggggcct tacctggcat ggtgtggcaa gatcgtgacg tgtaccttca ggggcccatc 1860

tgggcaaaga ttccacacac ggacggacat tttcacccct ctcccctcat gggtggattc 1920

ggacttaaac accctcctcc gcagattctc atcaagaaca ccccggtacc tgcgaatcct 1980

tcgaccacct tcagtgcggc aaagtttgct tccttcatca cacagtactc cacgggacag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggaaaaca gcaagcgctg gaacccggag 2100

atccagtaca cttccaacta ttacaagtct aataatgttg aatttgctgt taatactgaa 2160

ggtgtatata gtgaaccccg ccccattggc accagatacc tgactcgtaa tctgtaa 2217

<210> 367
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 367

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Thr Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270
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His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn
                485                 490                 495
```

```
Asp Asn Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser
        515                 520                 525

His Lys Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile
    530                 535                 540

Phe Gly Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val
545                 550                 555                 560

Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala
            580                 585                 590

Pro Thr Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 368
<211> 2208
<212> DNA
<213> Artificial Sequence

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

<400> 368
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgatt tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaatt ggggattccg gcccaagaga ctcagcttca agctcttcaa catccaggtc 960

aaggaggtca cgcagaatga aggcaccaag accatcgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct gattgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggactatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccg tctccgctga tgggcggctt tggcctgaaa 1920

catcctccgc ctcagatcct gatcaagaac acgcctgtac ctgcggatcc tccgaccacc 1980

ttcaaccagt caaagctgaa ctctttcatc actcagtatt ctactggcca agtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaagcgct ggaaccccga gatccagtac 2100

acctccaact actacaaatc tacaagtgtg gactttgctg ttaatacaga aggcgtgtac 2160

tctgaacccc gccccattgg cacccgttac ctcacccgta atctgtaa 2208

<210> 369
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 369

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
```

```
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Tyr Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
                645                 650                 655
```

```
Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 370
<211> 2214
<212> DNA
<213> Artificial Sequence

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

<400> 370
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccatttct caccacgtga ctggcagcga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacgac aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca gcagcgagta tcaaagacat ttgcggataa caacaacagt 1500

gaatactcgt ggactggagc taccaagtac cacctcaatg gcagagactc tctggtgaat 1560

ccgggcccgg ccatggcaag ccacaaggac gatgaagaaa agtttttttcc tcagagcggg 1620

gttctcatct ttgggaagca aggctcagag aaaacaaatg tggacattga aaaggtcatg 1680

attacagacg aagaggaaat caggacaacc aatcccgtgg ctacggagca gtatggttct 1740

gtatctacca acctccagag aggcaacaga caagcagcta ccgcagatgt caacacacaa 1800

ggcgttcttc caggcatggt ctggcaggac agagatgtgt accttcaggg gcccatctgg 1860

gcaaagattc cacacacgga cggacatttt cacccctctc ccctcatggg tggattcgga 1920

cttaaacacc ctccgcctca gatcctgatc aagaacacgc ctgtacccgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcaccc agtattctac tggccaagtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccgccc cattggcacc cgttacctca cccgtaatct gtaa 2214

<210> 371
<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 371

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


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


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415
```

```
Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Phe Ala Asp
                485                 490                 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala
            580                 585                 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620
```

```
His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 372
<211> 2217
<212> DNA
<213> Artificial Sequence

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

<400> 372

```
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420
```

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaaccaccag cagcccccac aagtttggga 600

tctaatacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccttg cccacctaca ataaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa ccgcttccac tgccacttct cgccaagaga ctggcaaaga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaaact cttcaacatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacgacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta tggatacctc 1140

accctgaaca acggaagtca agcggtggga cgctcatcct tttactgcct ggagtacttc 1200

ccttcgcaga tgctaaggac tggaaataac ttccaattca gctatacctt cgaggatgta 1260

ccttttcaca gcagctacgc tcacagccag agtttggatc gcttgatgaa tcctcttatt 1320

gatcagtatc tgtactacct gaacagaacg caaggaacaa cctctggaac aaccaaccaa 1380

tcacggctgc tttttagcca ggctgggcct cagtctatgt ctttgcaggc cagaaattgg 1440

ctacctgggc cctgctaccg gcaacagaga ctttcaaaga ctgctaacga caacaacaac 1500

agtaactttc cttggacagc agccagcaaa tatcatctca atggccgcga ctcgctggtg 1560

aatccaggac cagctatggc cagtcacaag gacgatgaag aaaaattttt ccctatgcac 1620

ggcaatctaa tatttggcaa agaagggaca acggcaagta acgcagaatt agataatgta 1680

atgattacgg atgaagaaga gattcgtacc accaatcctg tggcaacaga gcagtatgga 1740

actgtggcaa ataacttgca gagctcaaat acagctccca cgactagaac tgtcaatgat 1800

caggggggcct tacctggcat ggtgtggcaa gatcgtgacg tgtaccttca ggggcccatc 1860

tgggcaaaga ttccacacac ggacggacat tttcacccct ctcccctcat gggtggattc 1920

ggacttaaac accctcctcc gcagattctc atcaagaaca ccccggtacc tgcgaatcct 1980

tcgaccacct tcagtgcggc aaagtttgct tccttcatca cacagtactc cacgggacag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggaaaaca gcaagcgctg gaacccggag 2100

atccagtaca cttccaacta ttacaagtct aataatgttg aatttgctgt taatactgaa 2160

ggtgtatata gtgaaccccg ccccattggc accagatacc tgactcgtaa tctgtaa 2217

<210> 373
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 373

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn
                485                 490                 495

Asp Asn Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser
        515                 520                 525

His Lys Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile
    530                 535                 540

Phe Gly Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val
545                 550                 555                 560

Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575
```

Glu Gln Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala
580 585 590

Pro Thr Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 374
<211> 2208
<212> DNA
<213> Artificial Sequence

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

<400> 374
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 375
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 375

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
```

```
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 376
<211> 2208

<212> DNA
<213> Artificial Sequence

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

<400> 376
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgcc gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc caaaaagaga ctcaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacagca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac gactactttg gctacagcac cccttggggg 840

tattttgatt tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgagg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 377
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 377

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Ser Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn Asp Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Glu Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 378
<211> 2208
<212> DNA
<213> Artificial Sequence

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

<400> 378
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttc 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcaacttca agctctttaa catccaggtc 960

aaggaggtca cgcagaatga aggcaccaag accatcgcca ataacctcac cagcaccatc 1020

caggtgttta cggactcgga gtaccagctg ccgtacgttc tcggctctgc ccaccagggc 1080

tgcctgcctc cgttcccggc ggacgtgttc atgattcccc agtacggcta cctaacactc 1140

aacaacggta gtcaggccgt gggacgctcc tccttctact gcctggaata ctttccttcg 1200

cagatgctga gaaccggcaa caacttccag tttacttaca ccttcgagga cgtgcctttc 1260

cacagcagct acgcccacag ccagagcttg gaccggctga tgaatcctct gattgaccag 1320

tacctgtatt acttgtctcg gactcaaaca acaggaggca cgacaaatac gcagactctg 1380

ggcttcagcc aaggtgggcc taatacaatg gccaatcagg caaagaactg gctgcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acagggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc agggtcccat ttgggccaaa 1860

attcctcaca cagatggaca ctttcacccg tcccctctta tgggcggctt tggactcaag 1920

aacccgcctc ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcagag 1980

ttttcagcta caaagtttgc ttcattcatc acccaatact ccacaggaca agtgagtgtg 2040

gaaattgaat gggagctgca gaaagaaaac agcaagcgct ggaatcccga agtgcagtac 2100

acatccaatt atgcaaaatc tgccaacgtt gattttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctcacccgta atctgtaa 2208

<210> 379
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 379

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

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Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe Ser Gln
    450                 455                 460
```

```
Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495


Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685
```

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
690 695 700

Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 380
<211> 2214
<212> DNA
<213> Artificial Sequence

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

<400> 380
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccatttct caccacgtga ctggcagcga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

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gaatactcgt ggactggagc taccaagtac cacctcaatg gcagagactc tctggtgaat 1560

ccgggcccgg ccatggcaag ccacaaggac gatgaagaaa agtttttttcc tcagagcggg 1620

gttctcatct ttgggaagca aggctcagag aaaacaaatg tggacattga aaaggtcatg 1680

attacagacg aagaggaaat caggacaacc aatcccgtgg ctacggagca gtatggttct 1740

gtatctacca acctccagag aggcaacaga caagcagcta ccgcagatgt caacacacaa 1800

ggcgttcttc caggcatggt ctggcaggac agagatgtgt accttcaggg gcccatctgg 1860

gcaaagattc cacacacgga cggacatttt cacccctctc ccctcatggg tggattcgga 1920

cttaaacacc ctccgcctca gatcctgatc aagaacacgc ctgtacccgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcaccc agtattctac tggccaagtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccgccc cattggcacc cgttacctca cccgtaatct gtaa 2214

<210> 381
<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 381

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Phe Ala Asp
                485                 490                 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala
            580                 585                 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655
```

```
Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 382
<211> 2196
<212> DNA
<213> Adeno-associated virus

<400> 382

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atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt      300

caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag      360

gccaaaaaga gggtactcga gcctctgggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccagcag      480

cccgcgaaaa agagactgaa ttttgggcag actggcgact cagagtcagt gcctgacccc      540

caacctctct cagaaccacc cgcaggtccc tctggtctgg gatctggtac aatggctgct      600

ggcggtggcg ctccaatggc agacaataac gaaggcgccg acggagtggg taatgtctca      660
```

ggaaattggc attgcgattc cacatggctg ggcgaccgag tcatcaccac cagcactcgg 720

acctgggccc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg 780

ggaggcagca gcaacgacaa cacctacttt ggctacagca ccccctgggg gtattttgac 840

tttaacagat tccactgcca cttttcacca cgtgactggc agcgactcat caacaacaac 900

tgggggttcc ggcccaagaa gctcaacttc aagctcttca acatccaggt caaggaggtc 960

acccagaatg aaggcaccaa gaccatcgcc aataacctca ccagcacggt gcaggtcttt 1020

acggactcgg agtaccagct cccgtacgtg ctcggctctg cccaccaggg ctgcctgcct 1080

ccgttcccgg cggacgtgtt catgattccg cagtacgggt acctgacgct gaacaacggg 1140

agccaggccg tggggcgatc ctccttctac tgcctggagt actttccctc gcagatgctg 1200

agaacgggca acaactttac cttcagctac accttcgagg acgtgccctt ccacagcagc 1260

tacgcgcaca gccagagcct ggaccggctg atgaacccgc tgattgacca gtacctgtac 1320

tacctgtctc ggactcagac caacgggacc aatgccacgc agactctgtt gtttgctcag 1380

gccgggcctc agaacatgtc ggctcaggcc aagaactggc tgcctggtcc ttgctatcgg 1440

cagcagcgcg tctctacgac agtgtcgcaa aacaacaaca gcaactttac ctggaccggg 1500

gcgaccaagt accacctgaa cggccgagac tccctggtga gccccggtgt cgccatggca 1560

acgcacaagg acgacgagga gcgcttcttc ccgagcagcg gggtcctgat gtttggcaag 1620

cagggcgctg gaaaggacaa tgtcgagtac accaacgtga tgctcaccag cgaggaggag 1680

atcaagacca ccaaccctgt ggccacggag cagtacggcg tggtggctga caatctgcag 1740

cagaccaact cagctcccat tgtgggggca gtcaacagcc agggggcctt acccggtatg 1800

gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg 1860

gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc 1920

cagatcctga tcaaaaacac gccggtacct gcggatcccc cggtgaactt tacggacgct 1980

aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg 2040

gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat 2100

tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag tgaaccccgc 2160

cccattggca ctcgttacct cacccgtaat ctgtaa 2196

<210> 383

<211> 731
<212> PRT
<213> Adeno-associated virus

<400> 383

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Gln Gln
145                 150                 155                 160


Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser
                165                 170                 175


Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly
            180                 185                 190
```

```
Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp
        195                 200                 205

Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Val Ser Gly Asn Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
                245                 250                 255

Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro
                405                 410                 415
```

```
Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn
        435                 440                 445

Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Ser Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540

Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575

Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620
```

```
His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640


Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn
                645                 650                 655


Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            660                 665                 670


Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        675                 680                 685


Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala
    690                 695                 700


Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg
705                 710                 715                 720


Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730
```

<210> 384
<211> 2196
<212> DNA
<213> Adeno-associated virus

<400> 384

```
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt      300

caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag      360

gccaaaaaga gggtactcga gcctctgggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccggcag      480

cccgcgaaaa agagactgaa ttttgggcag actggcgact cagagtcagt gcctgacccc      540

caacctctct cagaaccacc cgcaggtccc tctggtctgg gatctggtac aatggctgca      600
```

ggcggtggcg ctccaatggc agacaataac gaaggcgccg acggagtggg taatgcctca 660

ggaaattggc attgcgattc cacatggctg ggcgaccgag tcatcaccac cagcactcgg 720

acctgggccc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg 780

ggaggcagca gcaacgacaa cacctacttt ggctacagca ccccctgggg gtattttgac 840

tttaacagat tccactgcca cttttcacca cgtgactggc agcgactcat caacaacaac 900

tggggattcc ggcccaagag gctcaacttc aagctcttca acatccaggt caaggaggtc 960

acccagaatg aaggcaccaa gaccatcgcc aataacctca ccagcacggt gcaggtcttt 1020

acggactcga agtaccagct cccgtacgtg ctcggctctg cccaccaggg ctgcctgcct 1080

ccgttcccgg cggacgtgtt catgattccg cagtacgggt acctgacgct gaacaacggg 1140

agccaggccg tggggcgatc ctccttctac tgcctggagt actttccctc gcagatgctg 1200

agaacgggca acaactttac cttcagctac accttcgagg acgtgccctt ccacagcagc 1260

tacgcgcaca gccagagcct ggaccggctg atgaacccgc tgattgacca gtacctgtac 1320

tacctgtctc ggactcagac caacgggacc aatgccacgc agactctgtt gtttgctcag 1380

gccgggcctc agaacatgtc ggctcaggcc aagaactggc tgcctggtcc ttgctatcgg 1440

cagcagcgcg tctctacgac agtgtcgcaa aacaacaaca gcaactttac ctggaccggg 1500

gcgaccaagt accacctgaa cggccgagac tccctggtga accccggtgt cgccatggca 1560

acgcacaagg acgacgagga gcgcttcttc ccgagcagcg gggtcctgat gtttggcaag 1620

cagggcgctg gaaaggacaa tgtcgagtac accaacgtga tgctcaccag cgaggaggag 1680

atcaagacca ccaaccctgt ggccacggag cagtacggtg tggtggctga caatctgcag 1740

cagaccaact cggctcccat tgtgggggca gtcaacagcc agggggcctt acccggtatg 1800

gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg 1860

gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc 1920

cagatcctga tcaaaaacac gccggtacct gcggatcccc cggtgaactt tacggacgct 1980

aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg 2040

gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat 2100

tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag tgaaccccgc 2160

cccattggca ctcgttacct cacccgtaat ctgtaa 2196

<210> 385
<211> 731
<212> PRT
<213> Adeno-associated virus

<400> 385

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Arg Gln
145                 150                 155                 160


Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser
                165                 170                 175


Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly
            180                 185                 190
```

```
Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp
        195                 200                 205

Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
                245                 250                 255

Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Thr Asp Ser Lys Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400
```

```
Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn
        435                 440                 445

Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540

Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575

Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620
```

```
His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640


Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn
                645                 650                 655


Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            660                 665                 670


Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        675                 680                 685


Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala
    690                 695                 700


Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg
705                 710                 715                 720


Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730
```

<210> 386
<211> 2196
<212> DNA
<213> Adeno-associated virus

<400> 386

```
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt      300

caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag      360

gccaaaaaga gggtactcga gcctctgggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccagcag      480

cccgcgaaaa agagactgaa ttttgggccg actggcgact cagagtcagt gcctgacccc      540
```

caacctctct cagaaccacc tgcaggtccc tctggtctgg gatctggtac aatggctgca 600

ggcggtggcg ctccaatggc agacaataac gaaggcgccg acggagtggg taatgtctca 660

ggaaattggc attgcgattc cacatggctg ggcgaccgag tcatcaccac cagcactcgg 720

acctgggccc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg 780

ggaggcagca gcaacgacaa cacctacttt ggctacagca ccccctgggg gtattttgac 840

tttaacagat tccactgcca cttttcacca cgcgactggc agcgactcat caacaacaac 900

tggggattcc ggcccaagaa gctcaacttc aagctcttca acatccaggt caaggaggtc 960

acccagaatg aaggcaccaa gaccaccgcc aataacctca ccagcacggt gcaggtcttt 1020

acggactcgg agtaccagct cccgtacgtg ctcggctctg cccaccaggg ctgcctgcct 1080

ccgttcccgg cggacgtgtt catgattccg cagtacgggt acctgacgct gaacaacggg 1140

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tacgcgcaca gccagagcct ggaccggctg atgaacccgc tgattgacca gtacctgtac 1320

tacctgtctc ggactcagac caacgggacc aatgccacgc agactctgtt gtttgctcag 1380

gccgggcctc agaacatgtc ggctcaggcc aagaactggc tgcctggtcc ttgctatcgg 1440

cagcagcgcg tctctacggc agtgtcgcaa aacaacaaca gcaactttac ctggaccggg 1500

gcgaccaagt accacctgaa cggccgagac tccctggtga accccggtgt cgccatggca 1560

acgcacaagg acgacgagga gcgcttcttc ccgagcagcg gggtcctgat gtttggcaag 1620

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gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg 1860

gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc 1920

cagatcctga tcaaaaacac gccggtacct gcggatcccc cggtgaactt tacggacgct 1980

aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg 2040

gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat 2100

tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag cgaaccccgc 2160

cccattggca ctcgttacct cacccgtaat ctgtaa 2196

<210> 387
<211> 731
<212> PRT
<213> Adeno-associated virus

<400> 387

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Gln Gln
145 150 155 160

Pro Ala Lys Lys Arg Leu Asn Phe Gly Pro Thr Gly Asp Ser Glu Ser
165 170 175

```
Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly
            180                 185                 190

Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp
        195                 200                 205

Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Val Ser Gly Asn Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
                245                 250                 255

Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Gln Asn Glu Gly Thr Lys Thr Thr Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400
```

```
Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn
        435                 440                 445

Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Thr Ala Val Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540

Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575

Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605
```

```
Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn
                645                 650                 655

Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            660                 665                 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        675                 680                 685

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala
    690                 695                 700

Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg
705                 710                 715                 720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730
```

<210> 388
<211> 4404
<212> DNA
<213> Adeno-associated virus

<400> 388

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atggctgccg atggttatct tccagattgg ctcgagggca acctctctga gggcattcgc       60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt      300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaacggccag      480
```

ccgcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 540

ccccaacctc tcggagaacc tcccgccgcg ccctcaggtc tgggatctgg tacaatggct 600

gcaggcggtg gcgcaccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 660

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 720

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 780

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 840

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 900

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 960

acgaacgacg gcgttacgac catcgctaat aaccttacca gcacgattca ggtcttctcg 1020

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1080

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1140

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1200

acgggcgata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1260

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1320

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1380

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1440

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1500

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1560

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1620

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1680

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1740

gccggacccc agacacagac tgtcaacagc cagggggctc tgcccggcat ggtctggcag 1800

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 1860

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 1920

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 1980

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2040

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2100

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2160

acccgttacc tcacccgtaa cctgtaaatg gctgccgatg gttatcttcc agattggctc 2220

gaggacaacc tctctgaggg cattcgcgag tggtgggact tgaaacctgg agccccgaaa 2280

cccaaagcca accagcaaaa gcaggacgac ggccggggtc tggtgcttcc tggctacaag 2340

tacctcggac ccttcaacgg actcgacaag ggggagcccg tcaacgcggc ggacgcagcg 2400

gccctcgagc acgacaaggc ctacgaccag cagctcaaag cgggtgacaa tccgtacctg 2460

cggtataacc acgccgacgc cgagtttcag gagcgtctgc aagaagatac gtcttttggg 2520

ggcaacctcg ggcgagcagt cttccaggcc aagaagcggg ttctcgaacc tctcggtctg 2580

gttgaggaag gcgctaagac ggctcctgga aagaagagac cggtagagcc atcaccccag 2640

cgttctccag actcctctac gggcatcggc aagaaaggcc agcagcccgc gaaaaagaga 2700

ctcaactttg ggcagactgg cgactcagag tcagtgcccg accctcaacc aatcggagaa 2760

ccccccgcag gcccctctgg tctgggatct ggtacaatgg ctgcaggcgg tggcgctcca 2820

atggcagaca ataacgaagg cgccgacgga gtgggtagtt cctcaggaaa ttggcattgc 2880

gattccacat ggctgggcga cagagtcatc accaccagca cccgaacctg ggccctcccc 2940

acctacaaca accacctcta caagcaaatc tccaacggga cttcgggagg aagcaccaac 3000

gacaacacct acttcggcta cagcaccccc tgggggtatt ttgactttaa cagattccac 3060

tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg attccggccc 3120

aagagactca acttcaagct cttcaacatc caggtcaagg aggtcacgca gaatgaaggc 3180

accaagacca tcgccaataa ccttaccagc acgattcagg tctttacgga ctcggaatac 3240

cagctcccgt acgtcctcgg ctctgcgcac cagggctgcc tgcctccgtt cccggcggac 3300

gtcttcatga ttcctcagta cgggtacctg actctgaaca atggcagtca ggccgtgggc 3360

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aacatgtcgg ctcaggccaa aaactggcta cccgggccct gctaccggca gcaacgcgtc 3660

tccacgacac tgtcgcaaaa taacaacagc aactttgcct ggaccggtgc caccaagtat 3720

catctgaatg gcagagactc tctggtaaat cccggtgtcg ctatggcaac ccacaaggac 3780

gacgaagagc gatttttttcc gtccagcgga gtcttaatgt ttgggaaaca gggagctgga 3840

aaagacaacg tggactatag cagcgttatg ctaaccagtg aggaagaaat taaaaccacc 3900

aacccagtgg ccacagaaca gtacggcgtg gtggccgata acctgcaaca gcaaaacgcc 3960

gctcctattg taggggccgt caacagtcaa ggagccttac ctggcatggt ctggcagaac 4020

cgggacgtgt acctgcaggg tcctatctgg gccaagattc ctcacacgga cggaaacttt 4080

catccctcgc cgctgatggg aggctttgga ctgaaacacc cgcctcctca gatcctgatt 4140

aagaatacac ctgttcccgc ggatcctcca actaccttca gtcaagctaa gctggcgtcg 4200

ttcatcacgc agtacagcac cggacaggtc agcgtggaaa ttgaatggga gctgcagaaa 4260

gaaaacagca aacgctggaa cccagagatt caatacactt ccaactacta caaatctaca 4320

aatgtggact ttgctgttaa cacagatggc acttattctg agcctcgccc catcggcacc 4380

cgttacctca cccgtaatct gtaa 4404

<210> 389
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 389

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735
```

Asn Leu

<210> 390
<211> 3129
<212> DNA
<213> Adeno-associated virus

<400> 390
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagtttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcagagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaaa aagacgtatc 720

ggaaactctg tgcgattcat catctgctgg gggcgggcac ccgagattgc ttgctcggcc 780

tgcgatctgg tcaacgtgga cctagatgac tgtgtttctg agcaataaat gacttaaacc 840

aggtatggct gccgatggtt atcttccaga ttggctcgag gacaacctct ctgagggcat 900

tcgcgagtgg tgggacttga aacctggagc cccgaaaccc aaagccaacc agcaaaagca 960

ggacgacggc cggggtctgg tgcttcctgg ctacaagtac ctcggaccct tcaacggact 1020

cgacaagggg gagcccgtca acgcggcgga cgcagcggcc ctcgagcacg acaaggccta 1080

cgaccagcag ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga 1140

gtttcaggag cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt 1200

ccaggccaag aagcgggttc tcgaacctct cggtctggtt gaggaaggcg ctaagacggc 1260

tcctggaaag aagagaccgg tagagccatc accccagcgt tctccagact cctctacggg 1320

catcggcaag aaaggccagc agcccgcgaa aaagagactc aactttgggc agactggcga 1380

ctcagagtca gtgcccgacc ctcaaccaat cggagaaccc cccgcaggcc cctctggtct 1440

gggatctggt acaatggctg caggcggtgg cgctccaatg gcagacaata acgaaggcgc 1500

cgacggagtg ggtagttcct caggaaattg gcattgcgat tccacatggc tgggcgacag 1560

agtcatcacc accagcaccc gaacctgggc cctccccacc tacaacaacc acctctacaa 1620

gcaaatctcc aacgggactt cgggaggaag caccaacgac aacacctact tcggctacag 1680

cacccctgg gggtattttg actttaacag attccactgc cacttctcac cacgtgactg 1740

gcagcgactc atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt 1800

caacatccag gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct 1860

taccagcacg attcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc 1920

tgcgcaccag ggctgcctgc ctccgttccc ggcggacgtc ttcatgattc ctcagtacgg 1980

gtacctgact ctgaacaatg gcagtcaggc cgtgggccgt tcctccttct actgcctgga 2040

gtactttcct tctcaaatgc tgagaacggg caacaacttt gagttcagct accagtttga 2100

ggacgtgcct tttcacagca gctacgcgca cagccaaagc ctggaccggc tgatgaaccc 2160

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aactcagcag ttgctatttt ctcaggccgg gcctaataac atgtcggctc aggccaaaaa 2280

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cagcggagtc ttaatgtttg ggaaacaggg agctggaaaa gacaacgtgg actatagcag 2520

cgttatgcta accagtgagg aagaaattaa aaccaccaac ccagtggcca cagaacagta 2580

cggcgtggtg gccgataacc tgcaacagca aaacgccgct cctattgtag gggccgtcaa 2640

cagtcaagga gccttacctg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc 2700

tatctgggcc aagattcctc acacggacgg aaactttcat ccctcgccgc tgatgggagg 2760

ctttggactg aaacacccgc ctcctcagat cctgattaag aatacacctg ttcccgcgga 2820

tcctccaact accttcagtc aagctaagct ggcgtcgttc atcacgcagt acagcaccgg 2880

acaggtcagc gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc 2940

agagattcaa tacacttcca actactacaa atctacaaat gtggactttg ctgttaacac 3000

agatggcact tattctgagc ctcgccccat cggcacccgt tacctcaccc gtaatctgta 3060

attgcttgtt aatcaataaa ccggttgatt cgtttcagtt gaactttggt ctctgcgaag 3120

ggcgaattc 3129

<210> 391
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 391

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
```

```
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575
```

```
Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 392
<211> 733
<212> PRT
<213> Artificial Sequence

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

<400> 392

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Arg Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
```

```
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
            260                 265                 270

Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
        275                 280                 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe
    290                 295                 300

Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305                 310                 315                 320

Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
                325                 330                 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
            340                 345                 350

Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
        355                 360                 365

Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
    370                 375                 380

Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385                 390                 395                 400

Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
                405                 410                 415

Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
            420                 425                 430
```

```
Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
        435                 440                 445

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480

Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser
                485                 490                 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Gly Asp Glu
        515                 520                 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
    530                 535                 540

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
                565                 570                 575

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
            580                 585                 590

Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
    610                 615                 620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
```

645 650 655

Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
690 695 700

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705 710 715 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 393
<211> 2501
<212> DNA
<213> Adeno-associated virus

<400> 393
gaattcgccc ttggctgcgt caactggacc aatgagaact ttcccttcaa cgattgcgtc 60

gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc 120

aaggccattc atcatctgct ggggcgggct cccgagattg cttgctcggc ctgcgatctg 180

gtcaacgtgg acctggatga ctgtgtttct gagcaataaa tgacttaaac caggtatggc 240

tgccgatggt tatcttccag attggctcga ggacaacctc tctgagggca ttcgcgagtg 300

gtgggacttg agacctggag ccccgaaacc caaagccaac cagcaaaagc aggacgacgg 360

ccggggtctg gtgcttcctg gctacaagta cctcggaccc ttcaacggac tcgacaaggg 420

agagccggtc aacgaggcag acgccgcggc cctcgagcac gacaaggcct acgacaagca 480

gctcgagcag ggggacaacc cgtacctcaa gtacaaccac gccgacgccg agtttcagga 540

gcgtcttcaa gaagatacgt cttttggggg caacctcggg cgagcagtct tccaggccaa 600

gaagcgggtt ctcgaacctc tcggtctggt tgaggaaggc gctaagacgg ctcctggaaa 660

gaagagaccc atagaatccc ccgactcctc cacgggcatc ggcaagaaag gccagcagcc 720

cgctaaaaag agactcaact ttgggcagac tggcgactca gagtcagtgc ccgaccctca 780

accaatcgga gaacccccg caggcccctc tggtctggga tctggcacaa tggctgcagg 840

cggtggcgct ccaatggcag acaataacga aggcgccgac ggagtgggta gttcctcagg 900

aaattggcat tgcgattcca catggctggg cgacagagtc atcaccacca gcacccgaac 960

ctgggccctc cccacctaca acaaccacct ctacaagcaa atctccaacg ggacatcggg 1020

aggaagcacc aacgacaaca cctacttcgg ctacagcacc ccctgggggt attttgactt 1080

taacagattc cactgccact tctcaccacg tgactggcag cgactcatca acaacaactg 1140

gggattccgg cccaagagac tcaacttcaa gctcttcaac atccaggtca aggaggtcac 1200

gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc agcacgattc aggtctttac 1260

ggactcggaa taccagctcc cgtacgtcct cggctctgcg caccagggct gcctgcctcc 1320

gttcccggcg gacgtcttca tgattcctca gtacgggtac ctgactctga acaacggcag 1380

tcaggccgtg ggccgttcct ccttctactg cctggagtac tttccttctc aaatgctgag 1440

aacgggcaac aactttgagt tcagctacca gtttgaggac gtgccttttc acagcagcta 1500

tgcgcacagc caaagcctgg accggctgat gaaccccctc atcgaccagt acctgtacta 1560

cctgtctcgg actcagtcca cgggaggtac cgcaggaact cagcagttgc tattttctca 1620

ggccgggcct aataacatgt cggctcaggc caaaaactgg ctacccgggc cctgctaccg 1680

gcagcaacgc gtctccacga cagtgtcgca aaataacaac agcaactttg cttggaccgg 1740

tgccaccaag tatcatctga atggcagaga ctctctggta aatcccggtg tcgctatggc 1800

aacgcacaag ggcgacgaag agcgattttt tccatccagc ggagtcttga tgtttgggaa 1860

acagggagct ggaaaagaca acgtagacta tagcagcgtt atgctaacca gtgaggaaga 1920

aatcaaaacc accaacccag tggccacaga acagtacggc gtggtggccg ataacctgca 1980

acagcaaaac gccgctccta ttgtaggggc cgtcaacagt caaggagcct tacctggcat 2040

ggtctggcag aaccgggacg tgtacctgca gggtcctatc tgggccaaga ttcctcacac 2100

ggacggcaac tttcatcctt cgccgctgat gggaggcttt ggactgaaac acccgcctcc 2160

tcagatcctg attaagaata cacctgttcc cgcggatcct ccaactacct tcagtcaagc 2220

caagctggcg tcgttcatca cgcagtacag caccggacag gtcagcgtgg aaattgaatg 2280

ggagctgcag aaagagaaca gcaagcgctg gaacccagag attcagtata cttccaacta 2340

ctacaaatct acaaatgtgg actttgctgt caatactgag ggtacttatt cagagcctcg 2400

ccccattggc acccgttacc tcacccgtaa cctgtaattg cctgttaatc aataaaccgg 2460

ttgattcgtt tcagttgaac tttggtctca agggcgaatt c 2501

<210> 394
<211> 2187
<212> DNA
<213> Adeno-associated virus

<400> 394
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaaaggccag 480

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 540

ccccaacctc tcggagaacc tcccgccgcg ccctcaggtc tgggatctgg tacaatggct 600

gcaggcggtg gcgcaccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 660

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 720

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 780

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 840

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 900

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 960

acgaacgacg gcgttacgac catcgctaat aaccttacca gcacgattca ggtcttctcg 1020

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1080

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1140

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1200

acgggcaata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1260

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1320

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1380

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1440

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1500

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1560

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg cgaaacgggg 1620

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1680

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1740

gccggacccc agacacagac tgtcaacagc caggggctc tgcccggcat ggtctggcag 1800

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 1860

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 1920

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 1980

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2040

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2100

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2160

acccgttacc tcacccgtaa cctgtaa 2187

<210> 395
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 395

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270
```

```
Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495
```

```
Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Glu Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700
```

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 396
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 396

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

```
Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
```

```
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590
```

```
Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605


Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620


Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655


Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670


Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685


Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700


Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210>  397
<211>  728
<212>  PRT
<213>  Adeno-associated virus

<400>  397

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255
```

```
Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480
```

```
Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685
```

```
Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 398
<211> 733
<212> PRT
<213> Artificial Sequence

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

<400> 398

```
Met Ala Ala Asp Gly His Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
            260                 265                 270

Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
        275                 280                 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Ser Trp Gly Phe
    290                 295                 300

Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305                 310                 315                 320

Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
                325                 330                 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
            340                 345                 350
```

```
Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
        355                 360                 365

Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
    370                 375                 380

Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385                 390                 395                 400

Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
                405                 410                 415

Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
            420                 425                 430

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
        435                 440                 445

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480

Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser
                485                 490                 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu
        515                 520                 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
    530                 535                 540

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545                 550                 555                 560
```

```
Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
                565                 570                 575

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
            580                 585                 590

Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
    610                 615                 620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
                645                 650                 655

Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
    690                 695                 700

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705                 710                 715                 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730
```

<210> 399
<211> 3113
<212> DNA
<213> Adeno-associated virus

<400> 399

```
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt       60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt      120
```

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg cttccctgca 600

agacatgcga gagaatgaat cagaatttca gcatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtca tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

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cctggaaaga agagacccat agaatccccc gactcctcca cgggcatcgg caagaaaggc 1320

cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgccc 1380

gaccctcaac caatcggaga acccccccgca ggcccctctg gtctgggatc tggtacaatg 1440

gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtagt 1500

tcctcaggaa attggcattg cgattccaca tagctgggcg acagagtcat caccaccagc 1560

acccgaacct gggccctccc cacctacaac aaccacctct acaagcaaat ctccaacggg 1620

acatcgggag gaagcaccaa cgacaacacc tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac 1740

aacagctggg gattccggcc caagagactc aacttcaagc tcttcaacat ccaggtcaag 1800

gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag cacgattcag 1860

gtctttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca ccagggctgc 1920

ctgcctccgt tcccggcgga cgtcttcatg attcctcagt acgggtacct gactctgaac 1980

aacggcagtc aggccgtggg ccgttcctcc ttctactgcc tggagtactt tccttctcaa 2040

atgctgagaa cgggcaacaa ctttgagttc agctaccagt ttgaggacgt gccttttcac 2100

agcagctacg cgcacagcca aagcctggac cggctgatga acccccctcat cgaccagtac 2160

ctgtactacc tgtctcggac tcagtccacg ggaggtaccg caggaactca gcagttgcta 2220

ttttctcagg ccgggcctaa taacatgtcg gctcaggcca aaaactggct acccgggccc 2280

tgctaccggc agcaacgcgt ctccacgaca ctgtcgcaaa ataacaacag caactttgct 2340

tggaccggtg ccaccaagta tcatctgaat ggcagagact ctctggtaaa tcccggtgtc 2400

gctatggcaa cgcacaagga cgacgaagag cgatttttc catccagcgg agtcttgatg 2460

tttgggaaac agggagctgg aaaagacaac gtggactata gcagcgttat gctaaccagt 2520

gaggaagaaa tcaaaaccac caacccagtg gccacagaac agtacggcgt ggtggccgat 2580

aacctgcaac agcaaaacgc cgctcctatt gtaggggccg tcaacagtca aggagcctta 2640

cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcctatctg ggccaagatt 2700

cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg actgaaacac 2760

ccgcctcctc agatcctgat taagaataca cctgttcccg cggatcctcc aactaccttc 2820

agtcaagcca agctggcgtc gttcatcacg cagtacagca ccggacaggt cagcgtggaa 2880

attgaatggg agctgcagaa agagaacagc aagcgctgga acccagagat tcagtatact 2940

tccaactact acaaatctac aaatgtggac tttgctgtca atactgaggg tacttattca 3000

gagcctcgcc ccattggcac ccgttacctc acccgtaacc tgtaattgcc tgttaatcaa 3060

taaaccggtt aattcgtttc agttgaactt tggtctctgc gaagggcgaa ttc 3113

<210> 400
<211> 731
<212> PRT
<213> Artificial Sequence

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

<400> 400

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Arg Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205
```

```
Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Arg Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
```

```
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser Thr Gly
        435                 440                 445

Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly Pro Asn
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540

Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575

Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590

Ser Gln Gly Ala Leu Pro Gly Met Ala Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640
```

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Thr
645 650 655

Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
660 665 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
675 680 685

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr
690 695 700

Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu Pro Arg
705 710 715 720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 401
<211> 3106
<212> DNA
<213> Adeno-associated virus

<400> 401
gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgattg 60

cgtcgacaag atggtgatct ggtgggagga gggcaagatg acggccaagg tcgtggagtc 120

cgccaaggcc attctcggcg gcagcaaggt gcgcgtggac caaaagtgca agtcgtccgc 180

ccagatcgac cccacccccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga 240

cgggaacagc accaccttcg agcaccagca gccgttgcag gaccggatgt tcaaatttga 300

actcacccgc cgtctggagc atgactttgg caaggcgaca aagcaggaag tcaaagagtt 360

cttccgctgg gcgcaggatc acgtgaccga ggtggcgcat gagttctacg tcagaaaggg 420

tggagccaac aagagacccg cccccgatga cgcggataaa agcgagccca agcgggcccg 480

cccctcagtc gcggatccat cgacgtcaga cgcggaagga gctccggtgg actttgccga 540

caggtaccaa aacaaatgtt ctcgtcacgc gggcatgctt cagatgctgt ttccctgcaa 600

aacatgcgag agaatgaatc agaatttcaa catttgcttc acgcacggga ccagagactg 660

ttcagaatgt ttccccggcg tgtcagaatc tcaaccggtc gtcagaaaga ggacgtatcg 720

gaaactctgt gccattcatc atctgctggg gcgggctccc gagattgctt gctcggcctg 780

cgatctggtc aacgtggacc tggatgactg tgtttctgag caataaatga cttaaaccag 840

gtatggctgc cgatggttat cttccagatt ggctcgagga caacctctct gagggcattc 900

gcgagtggtg ggacttgaaa cctggagccc cgaaacccaa agccaaccag caaaagcagg 960

acgacggccg gggtctggtg cttcctggct acaagtacct cggacccttc aacggactcg 1020

acaagggaga gccggtcaac gaggcagacg ccgcggccct cgagcacgac aaggcctacg 1080

acaagcagct cgagcagggg gacaacccgt acctcaagta caaccacgcc gacgccgagt 1140

ttcaggagcg tcttcaagaa gatacgtctt ttgggggcaa cctcgggcga gcagtcttcc 1200

gggccaagaa gcgggttctc gaacctctcg gtctggttga ggaaggcgct aagacggctc 1260

ctggaaagaa gagacccata gaatcccccg actcctccac gggcatcggc aagaaaggcc 1320

agcagcccgc taaaaagaag ctcaactttg ggcagactgg cgactcagag tcagtgcccg 1380

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gcggggctac caacgacaac cacttcttcg gctacagcac cccctggggc tattttgact 1680

tcaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatc aacaacaacc 1740

ggggattccg gcccagaaag ctgcggttca agttgttcaa catccaggtc aaggaggtca 1800

cgacgaacga cggcgttacg accatcgcta ataaccttac cagcacgatt caggtcttct 1860

cggactcgga gtaccaactg ccgtacgtcc tcggctctgc gcaccagggc tgcctccctc 1920

cgttccctgc ggacgtgttc atgattcctc agtacggata tctgactcta aacaacggca 1980

gtcagtctgt gggacgttcc tccttctact gcctggagta ctttccttct cagatgctga 2040

gaacgggcaa taactttgaa ttcagctacc agtttgagga cgtgcccttt cacagcagct 2100

acgcgcacag ccaaagcctg gaccggctga tgaacccccc catcgaccag tacctgtact 2160

acctgtctcg gactcagtcc acgggaggta ccgcaggaac tcagcagttg ctattttctc 2220

aggccgggcc taataacatg tcggctcagg ccaaaaactg gctacccggg ccctgctacc 2280

ggcagcaacg cgtctccacg acactgtcgc aaaataacaa cagcaacttt gcttggaccg 2340

gtgccaccaa gtatcatctg aatggcagag actctctggt aaatcccggt gtcgctatgg 2400

caacgcacaa ggacgacgaa gagcgatttt ttccatccag cggagtcttg atgtttggga 2460

aacagggagc tggaaaagac aacgtggact atagcagcgt tatgctaacc agtgaggaag 2520

aaatcaaaac caccaaccca gtggccacag aacagtacgg cgtggtggcc gataacctgc 2580

aacagcaaaa cgccgctcct attgtagggg ccgtcaacag tcaaggagcc ttacctggca 2640

tggcctggca gaaccgggac gtgtacctgc agggtcctat ctgggccaag attcctcaca 2700

cggacggcaa ctttcatcct tcgccgctga tgggaggctt tggactgaaa cacccgcctc 2760

ctcagatcct gattaagaat acacctgttc ccgcggatcc tccaactacc ttcagtcaag 2820

ccaagctggc gtcgttcatc acgcagtaca gcaccggaca ggtcagcgtg gaaattgaat 2880

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gccccattgg cacccgttac ctcacccgta acctgtaatt gcctgttaat caataaaccg 3060

gttaattcgt ttcagttgaa ctttggtctc tgcgaagggc gaattc 3106

<210> 402
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 402

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
```

```
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495
```

```
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720
```

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 403
<211> 3197
<212> DNA
<213> Adeno-associated virus

<400> 403
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaagggag agccggtcaa cgaggcagac gccgcggccc tcgagcacga caaggcctac 1080

gacaagcagc tcgagcaggg ggacaacccg tacctcaagt acaaccacgc cgacgccgag 1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460

agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

ttgcctgtta atcaataaac cggttaattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattcgt ttaaacctgc aggactagtc cctttagtga gggttaattc tgagcttggc 3180

gtaatcatgg gtcatag 3197

<210> 404
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 404

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Arg Lys Leu Arg Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Thr Asp Asp Gly Val Thr Thr Ile Ala
```

```
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ala Arg Thr Gln Ser Thr Thr Gly Ser Thr Arg Glu Leu Gln Phe His
    450                 455                 460

Gln Ala Gly Pro Asn Thr Met Ala Glu Gln Ser Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Asn Ile Asp Ser Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Thr Asn Pro Gly Val Ala Met Ala Thr Asn Lys
        515                 520                 525

Asp Asp Glu Asp Gln Phe Phe Pro Ile Asn Gly Val Leu Val Phe Gly
    530                 535                 540
```

```
Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met Thr
545                 550                 555                 560


Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
                565                 570                 575


Gly Val Val Ser Ser Asn Leu Gln Ser Ser Thr Ala Gly Pro Gln Thr
            580                 585                 590


Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly Asn Phe His Pro Ser Pro Leu Met Asp Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Ala Lys Ser Asn Asn Val Glu Phe Ala Val Asn Asn Glu Gly Val Tyr
705                 710                 715                 720


Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  405
<211>  3276
<212>  DNA
<213>  Adeno-associated virus
```

<400> 405
gaattcgccc ttcgcagaga ccaaagttca actgaaacga attaaccggt ttattgatta 60

acaggcaatt acaggttacg ggtgaggtaa cgggtgccaa tggggcgagg ctcagtataa 120

acccccttcgt tgttgacagc aaattccaca ttattagact tggcataatt tgaggtgtac 180

tgaatctctg gattccagcg tttgctgttt tctttctgca gttcccactc gatctccacg 240

ctgacctggc cggtgctgta ctgcgtgata aatgaggcaa acttggcagg agtaaacacc 300

tctggaggat tagcaggtac cggggtgttt ttgatgagaa tttgaggagg cgggtgtttg 360

agtccaaatc cgtccatcag gggagacggg tgaaagttgc cgtccgtgtg aggaattttg 420

gcccagatgg gaccctgcag gtacacgtcc cggttctgcc agaccatgcc gggcagagcc 480

ccctggctgt tgacagtctg tgtctggggt ccggccgtag acgattgcag gttgctggag 540

accacaccgt attcttctgt agccacggga ttggtggttt tgatctcctc ctcgctggtc 600

attagcacgt tttccagcgt tgtcttgttg gcagcccccg ttttgccaaa aaccagcact 660

ccgttgatgg gaaagaactg gtcctcgtcg tccttgttgg tggccatggc tacgcccggg 720

ttggttaatg aatttctacc attcagatgg tatttagtgg ccccggtcca ggcaaagtta 780

ctgttgttgt tgctgtctat gttttttgac agtctctgct gccgataaca gggtccgggc 840

agccagttct ttgattgctc ggccatggtg ttgggcccag cctgatggaa ctgcagctcc 900

cttgtggacc ccgtagtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgagg 960

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gagccgagga cgtacggcag ttggtactcc gagtccgaga agacctgaat cgtgctggta 1260

aggttattag cgatggtcgt aacgccgtcg tccgtcgtga cctccttgac ctggatgttg 1320

aacaacttga accgcagctt tctgggccgg aatccccagt tgttgttgat gagtcgctgc 1380

cagtcacgtg gtgagaagtg gcagtggaat ctgttaaagt caaaataccc ccaggggtg 1440

ctgtagccga agtaggtgtt gtcgttggtg cttcctcccg atgtcccgtt ggagatttgc 1500

ttgtagaggt ggttgttgta ggtggggagg gcccaggttc gggtgctggt ggtgatgact 1560

ctgtcgccca gccatgtgga atcgcaatgc caatttcctg aggaactacc cactccgtcg 1620

gcgccttcgt tattgtctgc cattggagcg ccaccgcctg cagccattgt accagatccc 1680

agaccagagg ggcctgcggg gggttctccg attggttgag ggtcgggcac tgactctgag 1740

tcgccagtct gcccaaagtt gagtctcttt ttcgcgggct gctggcctgt cttgccgatg 1800

cccgtagagg agtctggaga acgctggggt gatggctcta ccggtctctt ctttccagga 1860

gccgtcttag cgccttcctc aaccagaccg agaggttcga gaacccgctt cttggcctgg 1920

aagactgctc gcccgaggtt gcccccaaaa gacgtatctt cttgaagacg ctcctgaaac 1980

tcggcgtcgg cgtggttgta cttgaggtac gggttgtccc cctgctcgag ctgcttgtcg 2040

taggccttgt cgtgctcgag ggccgcggcg tctgcctcgt tgaccggctc tcccttgtcg 2100

agtccgttga agggtccgag gtacttgtag ccaggaagca ccagaccccg gccgtcgtcc 2160

tgcttttgct ggttggcttt gggtttcggg gctccaggtt tcaagtccca ccactcgcga 2220

atgccctcag agaggttgtc ctcgagccaa tctggaagat aaccatcggc agccatacct 2280

ggtttaagtc atttattgct cagaaacaca gtcatccagg tccacgttga ccagatcgca 2340

ggccgagcaa gcaatctcgg gagcccgccc cagcagatga tgaatggcac agagtttccg 2400

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ggcaaagtcc accggagctc cttccgcgtc tgacgtcgat ggatgcaaaa tgtcgcaaaa 2640

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ccgcgtctga cgtcgatgga tccgcgactg aggggcaggc ccgcttgggc tcgcttttat 2820

ccgcgtcatc gggggcgggt ctcttgttgg ctccaccctt tctgacgtag aactcatgcg 2880

ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc tgctttgtca 2940

ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc cggtcctgca 3000

acggctgctg gtgctcgaag gtggtgctgt tcccgtcaat cacggcgcac atgttggtgt 3060

tggaagtgac gatcacgggg gtgggatcga tctgggcgga agacttgcac ttttggtcca 3120

cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg gccgtcatct 3180

tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga aagttctcat 3240

tggtccagtt gacgcagccg tagaaagggc gaattc 3276

<210> 406
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 406

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

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

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
```

385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
530 535 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
580 585 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

```
Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 407
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 407

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480
```

```
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
               485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
               565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
               645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685
```

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 408
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 408

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
```

```
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560
```

```
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 409
<211> 728
<212> PRT
<213> Artificial Sequence

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

<400> 409

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Arg Lys Gly Gln
145   150   155   160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165   170   175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180   185   190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala

```
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415
```

```
His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
```

625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 410
<211> 2489
<212> DNA
<213> Adeno-associated virus

<400> 410
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtgaagt 120

ccgccaaggc cattcatcat ctgctggggc gggctcccga gattgcttgc tcggcctgcg 180

atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt 240

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 300

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 360

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 420

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 480

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 540

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 600

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 660

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcag gaaaggccag 720

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 780

cctcaaccaa tcggagaacc ccccgcaggc ccctctggtc tgggatctgg tacaatggct 840

gcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 900

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 960

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 1020

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 1080

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 1140

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 1200

acgaacgacg gcgttacgac catcgccaat aaccttacca gcacgattca ggtcttctcg 1260

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1320

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1380

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1440

acgggcaata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1500

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1560

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1620

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1680

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1740

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1800

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1860

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1920

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1980

gccggacccc agacacagac tgtcaacagc caggggggctc tgcccggcat ggtctggcag 2040

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 2100

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 2160

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 2220

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2280

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2340

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2400

acccgttacc tcacccgtaa cctgtaattg cctgttaatc aataaaccgg ttaattcgtt 2460

tcagttgaac tttggtcaag ggcgaattc 2489

<210> 411
<211> 728
<212> PRT
<213> Artificial Sequence

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

<400> 411

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

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

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350
```

```
Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Arg Gln
465                 470                 475                 480

Arg Leu Ser Lys Asp Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575
```

```
Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 412
<211> 3098
<212> DNA
<213> Adeno-associated virus

<400> 412

```
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt       60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt      120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcttccg      180
```

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accggagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaagggag agccggtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

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caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagacccat agaatccccc gactcctcca cgggcatcgg caagaaaggc 1320

cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgccc 1380

gaccctcaac caatcggaga acccccccgca ggcccctctg gtctgggatc tggtacaatg 1440

gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtaat 1500

gcctccggaa attggcattg cgattccaca tggctgggcg acagagtcat caccaccagc 1560

acccgcacct gggccctgcc cacctacaac aaccacctct acaagcagat atcaagtcag 1620

agcggggcta ccaacgacaa ccacttcttc ggctacagca ccccctgggg ctattttgac 1680

ttcaacagat tccactgcca cttctcacca cgtgactggc agcgactcat caacaacaac 1740

tggggattcc ggcccagaaa gctgcggttc aagttgttca acatccaggt caaggaggtc 1800

acgacgaacg acggcgttac gaccatcgct aataacctta ccagcacgat tcaggtcttc 1860

tcggactcgg agtaccaact gccgtacgtc ctcggctctg cgcaccaggg ctgcctccct 1920

ccgttccctg cggacgtgtt catgattcct cagtacggat atctgactct aaacaacggc 1980

agtcagtctg tgggacgttc ctccttctac tgcctggagt actttccttc tcagatgctg 2040

agaacgggca ataactttga attcagctac acctttgagg aagtgccttt ccacagcagc 2100

tatgcgcaca gccagagcct ggaccggctg atgaatcccc tcatcgacca gtacctgtac 2160

tacctggccc ggacccagag cactacgggg tccacaaggg agctgcagtt ccatcaggct 2220

gggcccaaca ccatggccga gcaatcaaag aactggctgc ccggaccctg ttatcggcgg 2280

cagagactgt caaaagacat agacagcaac aacaacagta actttgcctg gaccggggcc 2340

actaaatacc atctgaatgg tagaaattca ttaaccaacc cgggcgtagc catggccacc 2400

aacaaggacg acgaggacca gttctttccc atcaacggag tgctggtttt tggcaaaacg 2460

ggggctgcca acaagacaac gctggaaaac gtgctaatga ccagcgagga ggagatcaaa 2520

accaccaatc ccgtggctac agaagaatac ggtgtggtct ccagcaacct gcaatcgtct 2580

acggccggac cccagacaca gactgtcaac agccaggggg ctctgcccgg catggtctgg 2640

cagaaccggg acgtgtacct gcagggtccc atctgggcca aaattcctca cacggacggc 2700

aactttcacc cgtctcccct gatgggcgga tttggactca aacacccgcc tcctcaaatt 2760

ctcatcaaaa acaccccggt acctgctaat cctccagagg tgtttactcc tgccaagttt 2820

gcctcattta tcacgcagta cagcaccggc caggtcagcg tggagatcga gtgggaactg 2880

cagaaagaga acagcaaacg ctggaatcca gagattcagt acacctcaaa ttatgccaag 2940

tctaataatg tggaatttgc tgtcaacaac gaaggggttt atactgagcc tcgccccatt 3000

ggcacccgtt acctcacccg taacctgtaa ttacttgtta atcaataaac cggttgattc 3060

gtttcagttg aactttggtc tctgcgaagg gcgaattc 3098

<210> 413
<211> 685
<212> PRT
<213> Artificial Sequence

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

<400> 413

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
```

```
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430
```

```
Leu Asp Arg Leu Thr Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ala Arg Thr Gln Ser Thr Thr Gly Ser Thr Arg Gly Leu Gln Phe His
    450                 455                 460

Gln Ala Gly Pro Asn Thr Met Ala Glu Gln Ser Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Asn Ile Asp Ser Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Thr Asn Pro Gly Val Ala Met Ala Thr Asn Lys
        515                 520                 525

Asp Asp Glu Asp Gln Phe Phe Pro Ile Asn Gly Val Leu Val Phe Gly
    530                 535                 540

Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met Thr
545                 550                 555                 560

Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
                565                 570                 575

Gly Val Val Ser Ser Asn Leu Gln Ser Ser Thr Ala Gly Pro Gln Thr
            580                 585                 590

Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Tyr Thr Ser Asn Tyr Tyr Lys
```

645 650 655

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
660 665 670

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
675 680 685

<210> 414
<211> 2969
<212> DNA
<213> Adeno-associated virus

<400> 414
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatc 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaagggag agccggtcaa cgaggcagac gccgcggccc tcgagcacga caaggcctac 1080

gacaagcagc tcgagcaggg ggacaacccg tacctcaagt acaaccacgc cgacgccgag 1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gacgaacccc 2160

ctcatcgacc agtacctgta ctacctggcc cggacccaga gcactacggg gtccacaagg 2220

gggctgcagt tccatcaggc tgggcccaac accatggccg agcaatcaaa gaactggctg 2280

cccggaccct gttatcggca gcagagactg tcaaaaaaca tagacagcaa caacaacagt 2340

aactttgcct ggaccggggc cactaaatac catctgaatg gtagaaattc attaaccaac 2400

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gtgctggttt ttggcaaaac gggggctgcc aacaagacaa cgctggaaaa cgtgctaatg 2520

accagcgagg aggagatcaa aaccaccaat cccgtggcta cagaagaata cggtgtggtc 2580

tccagcaacc tgcaatcgtc tacggccgga ccccagacac agactgtcaa cagccagggg 2640

gctctgcccg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 2700

aaaattcctc acacggacgg caactttcac ccgtctcccc tgatgggcgg atttggactc 2760

aaacacccgc ctcctcaaat tctcatcaag tatacttcca actactacaa atctacaaat 2820

gtggactttg ctgtcaatac tgagggtact tattcagagc ctcgccccat tggcacccgt 2880

tacctcaccc gtaacctgta attgcctgtt aatcaataaa ccggttaatt cgtttcagtt 2940

gaactttggt ctctgcgaag ggcgaattc 2969

<210> 415
<211> 733
<212> PRT
<213> Artificial Sequence

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

<400> 415

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
            260                 265                 270

Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
        275                 280                 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe
    290                 295                 300

Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305                 310                 315                 320

Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
                325                 330                 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
            340                 345                 350
```

```
Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
        355                 360                 365

Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
    370                 375                 380

Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385                 390                 395                 400

Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
                405                 410                 415

Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
            420                 425                 430

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
        435                 440                 445

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480

Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser
                485                 490                 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Gly Asp Glu
        515                 520                 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
    530                 535                 540

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
                565                 570                 575
```

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
580 585 590

Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
595 600 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
610 615 620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625 630 635 640

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
645 650 655

Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
690 695 700

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705 710 715 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Ser Leu
725 730

<210> 416
<211> 3113
<212> DNA
<213> Adeno-associated virus

<400> 416
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

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cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgccc 1380

gaccctcaac caatcggaga acccccccgca ggcccctctg gtctgggatc tggtacaatg 1440

gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtagt 1500

tcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat caccaccagc 1560

acccgaacct gggccctccc cacctacaac aaccacctct acaagcaaat ctccaacggg 1620

acatcgggag gaagcaccaa cgacaacacc tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac 1740

aacaactggg gattccggcc caagagactc aacttcaagc tcttcaacat ccaggtcaag 1800

gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag cacgattcag 1860

gtctttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca ccagggctgc 1920

ctgcctccgt tcccggcgga cgtcttcatg attcctcagt acgggtacct gactctgaac 1980

aacggcagtc aggccgtggg ccgttcctcc ttctactgcc tggagtactt tccttctcaa 2040

atgctgagaa cgggcaacaa ctttgagttc agctaccagt ttgaggacgt gccttttcac 2100

agcagctatg cgcacagcca aagcctggac cggctgatga acccccctcat cgaccagtac 2160

ctgtactacc tgtctcggac tcagtccacg ggaggtaccg caggaactca gcagttgcta 2220

ttttctcagg ccgggcctaa taacatgtcg gctcaggcca aaaactggct acccgggccc 2280

tgctaccggc agcaacgcgt ctccacgaca gtgtcgcaaa ataacaacag caactttgct 2340

tggaccggtg ccaccaagta tcatctgaat ggcagagact ctctggtaaa tcccggtgtc 2400

gctatggcaa cgcacaaggg cgacgaagag cgatttttc catccagcgg agtcttgatg 2460

tttgggaaac agggagctgg aaaagacaac gtggactata gcagcgttat gctaaccagt 2520

gaggaagaaa tcaaaaccac caacccagtg gccacagaac agtacggcgt ggtggccgat 2580

aacctgcaac agcaaaacgc cgctcctatt gtaggggccg tcaacagtca aggagcctta 2640

cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcctatctg ggccaagatt 2700

cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg actgaaacac 2760

ccgcctcctc agatcctgat taagaataca cctgttcccg cggatcctcc aactaccttc 2820

agtcaagcca agctggcgtc gttcatcacg cagtacagca ccggacaggt cagcgtggaa 2880

attgaatggg agctgcagaa agagaacagc aagcgctgga acccagagat tcagtatact 2940

tccaactact acaaatctac aaatgtggac tttgctgtca atactgaggg tacttattca 3000

gagcctcgcc ccattggcac ccgttacctc acccgtagcc tgtaattgcc tgttaatcaa 3060

taaaccggtt gattcgtttc agttgaactt tggtctctgc gaagggcgaa ttc 3113

<210> 417
<211> 738
<212> PRT
<213> Artificial Sequence

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

<400> 417

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
```

```
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430
```

```
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

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

645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 418
<211> 3128
<212> DNA
<213> Adeno-associated virus

<400> 418
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcgcggg accagagact 660

gttcagaatg tttcccgggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

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caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

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tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgcg gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcat agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

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aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460

agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

ttgcctgtta atcaataaac cggttaattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> 419
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 419

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
```

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        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495
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Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
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705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 420
<211> 1933
<212> DNA
<213> Adeno-associated virus

<220>
<221> misc_feature
<222> (1302)..(1302)
<223> n is a, c, t, or g

<400> 420
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggtgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat gnaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

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gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 421
<211> 733
<212> PRT
<213> Artificial Sequence

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

<400> 421

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255
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Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Ser Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Gly Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala Tyr Ser Gln Ser Pro Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460
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Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480


Arg Leu Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495


Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510


Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525


Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540


Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560


Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575


Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590


Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605


Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620


His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640


Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655


Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670


Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685
```

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
690 695 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 422
<211> 3105
<212> DNA
<213> Adeno-associated virus

<400> 422
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acaagatggt gatctggtgg gaggagggca agatgaccgc caaggtcgtg gagtccgcca 120

aggccattct gggcggaagc aaggtgcgcg tggaccaaaa gtgcaagtca tcggcccaga 180

tcgaccccac gcccgtgatc gtcacctcca acaccaacat gtgcgccgtg atcgacggga 240

acagcaccac cttcgagcac cagcagccgc tgcaggaccg catgttcaag ttcgagctca 300

cccgccgtct ggagcacgac tttggcaagg tgaccaagca ggaagtcaaa gagttcttcc 360

gctgggctca ggatcacgtg actgaggtgg cgcatgagtt ctacgtcaga aagggcggag 420

ccaccaaaag acccgccccc agtgacgcgg atataagcga gcccaagcgg gcctgcccct 480

cagttgcgga gccatcgacg tcagacgcgg aagcaccggt ggactttgcg gacaggtacc 540

aaaacaaatg ttctcgtcac gcgggcatgc ttcagatgct gtttccctgc aagacatgcg 600

agagaatgaa tcagaatttc aacgtctgct tcacgcacgg ggtcagagac tgctcagagt 660

gcttccccgg cgcgtcagaa tctcaacccg tcgtcagaaa aaagacgtat cagaaactgt 720

gcgcgattca tcatctgctg gggcgggcac ccgagattgc gtgttcggcc cgcgatctcg 780

tcaacgtgga cttggatgac tgtgtttctg agcaataaat gacttaaacc aggtatggct 840

gctgacggtt atcttccaga ttggctcgag gacaacctct ctgagggcat tcgcgagtgg 900

tgggacctga aacctggagc ccccaagccc aaggccaacc agcagaagca ggacgacggc 960

cggggtctgg tgcttcctgg ctacaagtac ctcggaccct tcaacggact cgacaagggg 1020

gagcccgtca acgcggcgga cgcagcggcc ctcgagcacg acaaggccta cgaccagcag 1080

ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga gtttcaggag 1140

cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt ccaggccaag 1200

aagagggtac tcgaacctct gggcctggtt gaagaaggtg ctaagacggc tcctggaaag 1260

aagagaccgt tagagtcacc acaagagccc gactcctcct caggaatcgg caaaaaaggc 1320

aaacaaccag ccaaaaagag actcaacttt gaagaggaca ctggagccgg agacggaccc 1380

cctgaaggat cagataccag cgccatgtct tcagacattg aaatgcgtgc agcaccgggc 1440

ggaaatgctg tcgatgcggg acaaggttcc gatggagtgg gtaatgcctc gggtgattgg 1500

cattgcgatt ccacctggtc tgagggcaag gtcacaacaa cctcgaccag aacctgggtc 1560

ttgcccacct acaacaacca cttgtacctg cggctcggaa caacatcaaa cagcaacacc 1620

tacaacggat tctccacccc ctggggatac tttgacttta acagattcca ctgtcacttc 1680

tcaccacgtg actggcaaag actcatcaac aacaactggg gactacgacc aaaagccatg 1740

cgcgttaaaa tcttcaatat ccaagttaag gaggtcacaa cgtcgaacgg cgagactacg 1800

gtcgctaata accttaccag cacggttcag atatttgcgg actcgtcgta tgagctcccg 1860

tacgtgatgg acgctggaca agagggaagt ctgtctcctt tccccaatga cgtcttcatg 1920

gtgcctcaat atggctactg tggcattgtg actggcgaaa atcagaacca gacggacaga 1980

aatgctttct actgcctgga gtattttcct tcacaaatgc tgagaactgg caataacttt 2040

gaaatggctt acaactttgg gaaggtgccg ttccactcaa tgtatgctta cagccagagc 2100

ccggacagac tgatgaatcc cctcctggac cagtacctgt ggcacttaca gtcgaccacc 2160

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gcaacagctg gaccttcaga tggggacttc agcaacgccc agctcatctt ccctggacca 2460

tcagtcaccg gaaacacaac aacctcagca aacaatctgt tgtttacatc agaagaagaa 2520

attgctgcca ccaacccaag agacacggac atgtttggtc agattgctga caataatcag 2580

aatgctacaa ctgctcccat aaccggcaac gtgactgcta tgggagtgct tcctggcatg 2640

gtgtggcaaa acagagacat ttactaccaa gggccaattt gggccaagat cccacacgcg 2700

gacggacatt ttcatccttc accgctaatt ggcggttttg gactgaaaca tccgcctccc 2760

cagatattta tcaaaaacac ccccgtacct gccaatcctg cgacaacctt cactgcagcc 2820

agagtggact ctttcatcac acaatacagc accggccagg tcgctgttca gattgaatgg 2880

gaaatcgaaa aggaacgctc caaacgctgg aatcctgaag tgcagtttac ttcaaactat 2940

gggaaccagt cttctatgtt gtgggctccc gatacaactg ggaagtatac agagccgcgg 3000

gttattggct ctcgttattt gactaatcat ttgtaactgc ctagttaatc aataaaccgt 3060

gtgattcgtt tcagttgaac tttggtctct gcgaagggcg aattc 3105

<210> 423
<211> 733
<212> PRT
<213> Adeno-associated virus

<400> 423

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335
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Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560
```

```
Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
    690                 695                 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705                 710                 715                 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730
```

<210> 424
<211> 3105
<212> DNA
<213> Adeno-associated virus

<400> 424
gaattcgccc ttgctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg 60

acaagatggt gatctggtgg gaggagggca agatgaccgc caaggtcgtg gagtccgcca 120

aggccattct gggcggaagc aaggtgcgcg tggaccaaaa gtgcaagtca tcggcccaga 180

tcgaccccac gcccgtgatc gtcacctcca acaccaacat gtgcgccgtg atcgacggga 240

acagcaccac cttcgagcac cagcagccgc tgcaggaccg catgttcaag ttcgagctca 300

cccgccgtct ggagcacgac tttggcaagg tgaccaagca ggaagtcaaa gagttcttcc 360

gctgggctca ggatcacgtg actgaggtgg cgcatgagtt ctacgtcaga aagggcggag 420

ccaccaaaag acccgccccc agtgacgcgg atataagcga gcccaagcgg gcctgcccct 480

cagttgcgga gccatcgacg tcagacgcgg aagcaccggt ggactttgcg gacaggtacc 540

aaaacaaatg ttctcgtcac gcgggcatgc ttcagatgct gtttccctgc aagacatgcg 600

agagaatgaa tcagaatttc aacgtctgct tcacgcacgg ggtcagagac tgctcagagt 660

gcttccccgg cgcgtcagaa tctcaacccg tcgtcagaaa aaagacgtat cagaaactgt 720

gcgcgattca tcatctgctg gggcgggcac ccgagattgc gtgttcggcc tgcgatctcg 780

tcaacgtgga cttggatgac tgtgtttctg agcaataaat gacttaaacc aggtatggct 840

gctgacggtt atcttccaga ttggctcgag gacaacctct ctgagggcat tcgcgagtgg 900

tgggacctga aacctggagc ccccaagctc aaggccaacc agcagaagca ggacgacggc 960

cggggtctgg tgcttcctgg ctacaagtac ctcggaccct tccacggact cgacaagggg 1020

gagcccgtca acgcggcgga cgcagcggcc ctcgagcacg acaaggccta cgaccagcag 1080

ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga gtttcaggag 1140

cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt ccaggccaag 1200

aagagggtac tcgaaccact gggcctggtt gaagaaggtg ctaagacggc tcctggaaag 1260

aagagaccgt tagagtcacc acaagagccc gactcctcct caggaatcgg caaaaaaggc 1320

aaacaaccag ccaaaaagag actcaacttt gaagaggaca ctggagccgg agacggaccc 1380

cctgaaggat cagataccag cgccatgtct tcagacattg aaatgcgtgc agcaccgggc 1440

ggaaatgctg tcgatgcggg acaaggttcc gatggagtgg gtaatgcctc gggtgattgg 1500

cattgcgatt ccacctggtc tgagggcaag gtcacaacaa cctcgaccag aacctgggtc 1560

ttgcccacct acaacaacca cttgtacctg cggctcggaa caacatcaaa cagcaacacc 1620

tacaacggat tctccacccc ctggggatac tttgacttta acagattcca ctgtcacttc 1680

tcaccacgtg actggcaaag actcatcaac aacaactggg gactacgacc aaaagccatg 1740

cgcgttaaaa tcttcaatat ccaagttaag gaggtcacaa cgtcgaacgg cgagactacg 1800

gtcgctaata accttaccag cacggttcag atatttgcgg actcgtcgta tgagctcccg 1860

tacgtgatgg acgctggaca agagggaagt ctgcctcctt tccccaatga cgtcttcatg 1920

gtgcctcaat atggctactg tggcattgtg actggcgaaa atcagaacca gacggacaga 1980

aatgctttct actgcctgga gtattttcct tcacaaatgc tgagaactgg caataacttt 2040

gaaatggctt acaactttga gaaggtgccg ttccactcaa tgtatgctca cagccagagc 2100

ctggacagac tgatgaatcc cctcctggac cagtacctgt ggcacttaca gtcgaccacc 2160

tctggagaga ctctgaatca aggcaatgca gcaaccacat ttggaaaaat caggagtgga 2220

gactttgcct tttacagaaa gaactggctg cctgggcctt gtgttaaaca gcagagattc 2280

tcaaaaactg ccagtcaaaa ttacaagatt cctgccagcg ggggcaacgc tctgttaaag 2340

tatgacaccc actatacctt aaacaaccgc tggagcaaca tagcgcctgg acctccaatg 2400

gcaacagctg gaccttcaga tggggacttc agcaacgccc agctcatctt ccctggacca 2460

tcagtcaccg gaaacacaac aacctcagca aacaatctgt tgtttacatc agaaggagaa 2520

attgctgcca ccaacccaag agacacggac atgtttggtc agattgctga caataatcag 2580

aatgctacaa ctgctcccat aaccggcaac gtgactgcta tgggagtgct tcctggcatg 2640

gtgtggcaaa acagagacat ttactaccaa gggccaattt gggccaagat cccacacgcg 2700

gacggacatt ttcatccttc accgctaatt ggcggttttg gactgaaaca tccgcctccc 2760

cagatattta tcaaaaacac ccccgtacct gccaatcctg cgacaacctt cactgcagcc 2820

agagtggact ctttcatcac acaatacagc accggccagg tcgctgttca gattgaatgg 2880

gaaatcgaaa aggaacgctc caaacgccgg aatcctgaag tgcagtttac ttcaaactat 2940

gggaaccagt cttctatgtt gtgggctccc gatacaactg ggaagtatac agagccgcgg 3000

gttattggct ctcgttattt gactaatcat ttgtaactgc ctagttaatc aataaaccgt 3060

gtgattcgtt tcagttgaac tttggtctct gcgaagggcg aattc 3105

<210> 425
<211> 733
<212> PRT
<213> Artificial Sequence

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

<400> 425

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

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

Gly Tyr Glu Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145   150   155   160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165   170   175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180   185   190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala

```
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

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

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
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625 630 635 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Tyr Pro Ala
645 650 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
675 680 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Cys Gly Asn
690 695 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 426
<211> 3105
<212> DNA
<213> Adeno-associated virus

<400> 426
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcacacggt ttattgatta 60

actaggcagt tacaaatgat tagtcaaata acgagagcca ataacccgcg gctctgtata 120

cttcccagtt gtatcgggag cccacaacat agaagactgg ttcccacagt ttgaagtaaa 180

ctgcacttca ggattccagc gtttggagcg ttccttttcg atttcccatt caatctgaac 240

agcgacctgg ccggtgctgt attgtgtgat gaaagagtcc actctggctg cagtgaaggt 300

tgtcgcagga taggcaggta cgggggtgtt tttgataaat atctggggag gcggatgttt 360

cagtccaaaa ccgccaatta gcggtgaagg atgaaaatgt ccgtccgcgt gtgggatctt 420

ggcccaaatt ggcccttggt agtaaatgtc tctgttttgc cacaccatgc caggaagcac 480

tcccatagca gtcacgttgc cggttatggg agcagttgta gcattctgat tattgtcagc 540

aatctgacca aacatgtccg tgtctcttgg gttggtggca gcaatttctt cttctgatgt 600

aaacaacaga ttgtttgctg aggttgttgt gtttccggtg actgatggtc cagggaagat 660

gagctgggcg ttgctgaagt ccccatctga aggtccagct gttgccattg gaggtccagg 720

cgctatgttg ctccagcggt tgtttaaggt atagtgggtg tcatacttta acagagcgtt 780

gcccccgctg gcaggaatct tgtaattttg actggcagtt tttgagaatc tctgctgttt 840

aacacaaggc ccaggcagcc agttctttct gtaaaaggca aagtctccac tcctgatttt 900

tccaaatgtg gttgctgcat tgccttgatt cagagtctct ccagaggtgg tcgactgtaa 960

gtgccacagg tactggtcca ggaggggatt catcagtccg tccaggctct ggctgtgagc 1020

atacattgag tggaacggca ccttctcaaa gttgtaagcc gtttcaaagt tattgccagt 1080

tctcagcatt tgtgaaggaa aatactccag gcagtagaaa gcatttctgt ccgtctggtt 1140

ctgattttcg ccagtcacaa tgccacagta gccatattga ggcaccatga agacgtcatt 1200

ggggaaagga ggcagacttc cctcttgtcc agcgtccatc acgtacggga gctcatacga 1260

cgagtccgca aatatctgaa ccgtgctggt aaggttatta gcgaccgtag tctcgccgtt 1320

cgacgttgtg acctccttaa cttggatatt gaagatttta acgcgcatgg cttttggtcg 1380

tagtccccag ttgttgttga tgagtctttg ccagtcacgt ggtgagaagt gacagtggaa 1440

tctgttaaag tcaaagtatc cccagggggt ggagaatccg ttgtaggtgt tgctgtttga 1500

tgttgttccg agccgcaggt acaagtggtt gttgtaggtg ggcaagaccc aggttctggt 1560

cgaggttgtt gtgaccttgc cctcagacca ggtggaatcg caatgccaat cacccgaggc 1620

attacccact ccatcggaac cttgtcccgc atcgacagca tttccgcccg gtgctgcacg 1680

catttcaatg tctgaagaca tggcgctggt atctgatcct tcaggggggtc cgtctccggc 1740

tccagtgtcc tcttcaaagt tgagtctctt tttggctggt tgtttgcctt ttttgccgat 1800

tcctgaggag gagtcgggct cttgtggtga ctctaacggt ctcttctttc caggagccgt 1860

cttagcacct tcttcaacca ggcccagagg ttcgagtacc ctcttcttgg cctggaagac 1920

tgctcgcccg aggttgcccc caaaagacgt atcttcttgc agacgctcct gaaactcggc 1980

gtcggcgtgg ttataccgca ggtacggatt gtcacccgct ttgagctgct ggtcgtaggc 2040

cttgtcgtgc tcgagggccg ctgcgtccgc cgcgttgacg ggctcccccct tgtcgagtcc 2100

gttgaagggt ccgaggtact cgtagccagg aagcaccaga ccccggccgt cgtcctgctt 2160

ctgctggttg gccttgggct tgggggctcc aggtttcagg tcccaccact cgcgaatgcc 2220

ctcagagagg ttgtcctcga gccaatctgg aagataaccg tcagcagcca tacctggttt 2280

aagtcattta ttgctcagaa acacagtcat ccaagtccac gttgacgaga tcgcaggccg 2340

aacacgcaat ctcgggtgcc cgccccagca gatgatgaat cgcgcacagt ttctgatacg 2400

tctttttct gacgacgggt tgagattctg acgcgccggg gaagcactct gagcagtctc 2460

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gaaacagcat ctgaagcatg cccgcgtgac gagaacattt gttttggtac ctgtccgcaa 2580

ggtccaccgg tgcttccgcg tctgacgtcg atggctccgc aactgagggg caggcccgct 2640

tgggctcgct tatatccgcg tcactggggg cgggtctttt ggtggctccg ccctttctga 2700

cgtagaactc atgcgccacc tcagtcacgt gatcctgagc ccagcggaag aactctttga 2760

cttcctgctt ggtcaccttg ccaaagtcgt gctccagacg gcgggtgagc tcgaacttga 2820

acatgcggtc ctgcagcggc tgctggtgct cgaaggtggt gctgttcccg tcgatcacgg 2880

cgcacatgtt ggtgttggag gtgacgatca cgggcgtggg gtcgatctgg gccgatgact 2940

tgcacttttg gtccacgcgc accttgcttc cgcccagaat ggccttggcg gactccacga 3000

ccttggcggt catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcgttga 3060

agggaaagtt ctcattggtc cagttgacgc agcaagggcg aattc 3105

<210> 427
<211> 729
<212> PRT
<213> Artificial Sequence

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

<400> 427

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

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Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270
```

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Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Gly Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495
```

```
Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Pro Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625                 630                 635                 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700
```

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705 710 715 720

Gly Thr Arg Tyr Leu Pro Arg Asn Leu
725

<210> 428
<211> 3094
<212> DNA
<213> Adeno-associated virus

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agccattctg ggcggaagca aggtgcgcgt cgaccaaaag tgcaagtcct cggcccagat 180

cgatcccacc cccgtgatcg tcacctccaa caccaacatg tgcgccgtga tcgacgggaa 240

cagcaccacc ttcgagcacc agcagccgtt gcaggaccgg atgttcaaat ttgaactcac 300

ccgccgtctg gaacacgact ttggcaaggt gaccaagcag gaagtcaaag agttcttccg 360

ctgggctagt gatcacgtga ctgaggtgac gcatgagttc tacgtcagaa agggcggagc 420

cagcaaaaga cccgcccccg atgacgcgga tataagcgag cccaagcggg cctgtccctc 480

agtcacggac ccatcgacgt cagacgcgga aggagctccg gtggactttg ccgacaggta 540

ccaaaacaaa tgttctcgtc acgcgggcat gcttcagatg ctgtttccct gcaaaacgtg 600

cgagagaatg aatcagaatt tcaacatttg cttcacgcac ggggtcagag actgtttaga 660

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<210> 429
<211> 1458
<212> PRT
<213> Artificial Sequence

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

<400> 429

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350
```

```
Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
```

```
               565                 570                 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Glu His Pro Pro Pro Gln Ile
625                 630                 635                 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720

Gly Thr Arg Tyr Leu Thr Arg Asn Leu Met Ala Ala Asp Gly Tyr Leu
                725                 730                 735

Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu Gly Ile Arg Glu Trp Trp
            740                 745                 750

Asp Leu Lys Pro Gly Ala Pro Lys Pro Lys Ala Asn Gln Gln Lys Gln
        755                 760                 765

Asp Asp Gly Arg Gly Leu Val Leu Pro Gly Tyr Lys Tyr Leu Gly Pro
    770                 775                 780
```

```
Phe Asn Gly Leu Asp Lys Gly Glu Pro Val Asn Ala Ala Asp Ala Ala
785                 790                 795                 800


Ala Leu Glu His Asp Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp
                805                 810                 815


Asn Pro Tyr Leu Arg Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg
            820                 825                 830


Leu Gln Glu Asp Thr Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe
        835                 840                 845


Gln Ala Lys Lys Arg Val Leu Glu Pro Leu Gly Leu Val Glu Glu Gly
    850                 855                 860


Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro Ile Gly Ser Pro Asp Ser
865                 870                 875                 880


Ser Thr Gly Ile Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Lys Leu
                885                 890                 895


Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro
            900                 905                 910


Leu Gly Glu Pro Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met
        915                 920                 925


Ala Ala Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp
    930                 935                 940


Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu
945                 950                 955                 960


Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr
                965                 970                 975


Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ser Ser Ser Gly Ala
            980                 985                 990


Thr Asn Asp Asn His Tyr Phe Gly  Tyr Ser Thr Pro Trp  Gly Tyr Phe
```

```
        995                 1000                1005

Asp Phe  Asn Arg Phe His Cys  His Phe Ser Pro Arg  Asp Trp Gln
    1010                1015                1020

Arg Leu  Ile Asn Asn Asn Trp  Gly Phe Arg Pro Lys  Lys Leu Arg
    1025                1030                1035

Phe Lys  Leu Leu Asn Ile Gln  Val Lys Glu Val Thr  Thr Asn Asp
    1040                1045                1050

Gly Val  Thr Thr Ile Ala Asn  Asn Leu Thr Ser Thr  Val Gln Val
    1055                1060                1065

Phe Ser  Asp Ser Glu Tyr Gln  Leu Pro Tyr Val Leu  Gly Ser Ala
    1070                1075                1080

His Gln  Gly Cys Leu Pro Pro  Phe Pro Ala Asp Val  Phe Met Ile
    1085                1090                1095

Pro Gln  Tyr Gly Tyr Leu Thr  Leu Asp Asn Gly Ser  Gln Ser Val
    1100                1105                1110

Gly Arg  Ser Ser Phe Tyr Cys  Leu Glu Tyr Phe Pro  Ser Gln Met
    1115                1120                1125

Leu Arg  Thr Gly Asn Asn Phe  Glu Phe Ser Tyr Ser  Phe Glu Asp
    1130                1135                1140

Val Pro  Phe His Ser Ser Tyr  Ala His Ser Gln Ser  Leu Asp Arg
    1145                1150                1155

Leu Met  Asn Pro Leu Ile Asp  Gln Tyr Leu Tyr Tyr  Leu Ala Arg
    1160                1165                1170

Thr Gln  Ser Thr Thr Gly Ser  Thr Arg Glu Leu Gln  Phe His Gln
    1175                1180                1185

Ala Gly  Pro Asn Thr Met Ala  Glu Gln Ser Lys Asn  Trp Leu Pro
    1190                1195                1200
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Gly Pro  Cys Tyr Arg Gln Gln  Arg Leu Ser Lys Asn  Leu Asp Phe
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Asn Asn  Asn Ser Asn Phe Ala  Trp Thr Ala Ala Thr  Lys Tyr His
    1220                1225                1230

Leu Asn  Gly Arg Asn Ser Leu  Thr Asn Pro Gly Ile  Pro Met Ala
    1235                1240                1245

Thr Asn  Lys Asp Asp Glu Asp  Gln Phe Phe Pro Ile  Asn Gly Val
    1250                1255                1260

Leu Val  Phe Gly Lys Thr Gly  Ala Ala Asn Lys Thr  Thr Leu Glu
    1265                1270                1275

Asn Val  Leu Met Thr Ser Glu  Glu Glu Ile Lys Thr  Thr Asn Pro
    1280                1285                1290

Val Ala  Thr Glu Glu Tyr Gly  Val Val Ser Ser Asn  Leu Gln Ser
    1295                1300                1305

Ser Thr  Ala Gly Pro Gln Ser  Gln Thr Ile Asn Ser  Gln Gly Ala
    1310                1315                1320

Leu Pro  Gly Met Val Trp Gln  Asn Arg Asp Val Tyr  Leu Gln Gly
    1325                1330                1335

Pro Ile  Trp Ala Lys Ile Pro  His Thr Asp Gly Asn  Phe His Pro
    1340                1345                1350

Ser Pro  Leu Met Gly Gly Phe  Gly Leu Lys His Pro  Pro Pro Gln
    1355                1360                1365

Ile Leu  Ile Lys Asn Thr Pro  Val Pro Ala Asn Pro  Pro Glu Val
    1370                1375                1380

Phe Thr  Pro Ala Lys Phe Ala  Ser Phe Ile Thr Gln  Tyr Ser Thr
    1385                1390                1395

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

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Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala
1415 1420 1425

Lys Ser Asn Asn Val Glu Phe Ala Val Asn Pro Asp Gly Val Tyr
1430 1435 1440

Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
1445 1450 1455

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<211> 3095
<212> DNA
<213> Adeno-associated virus

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tgaatttctg ggttccagcg cttgctgttt tctttctgca gctcccactc gatttccacg 240

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taccgcaggt acggattgtc acccgctttg agctgctggt cgtaggcctt gtcgtgctcg 2040

agggccgctg cgtccgccgc gttgacgggc tccccccttgt cgagtccgtt gaagggtccg 2100

aggtacttgt agccaggaag caccagaccc cggccgtcgt cctgcttttg ctggttggct 2160

ttgggtttcg gggctccagg tttcaggtcc caccactcgc gaatgccctc agagaggttg 2220

tcctcgagcc aatctggaag ataaccatcg gcagccatac ctggtttaag ccatttattg 2280

ctcagaaaca cagtcgtcca ggtccacgtt gaccaggtcg caggccgagc aggcaatctc 2340

gggtgcccgc cccagcagat gatgaatcgc acacagcttc cgatacgtct tttttctgac 2400

gaccggttga gattctgaca cgccggggaa acattctaaa cagtctctga ccccgtgcgt 2460

gaagcaaatg ttgaaattct gattcattct ctcgcacgtt ttgcagggaa acagcatctg 2520

aagcatgccc gcgtggcgag aacatttgtt ttggtacctg tcggcaaagt ccaccggagc 2580

tccttccgcg tctgacgtcg atgggtccgt gactgaggga caggcccgct tgggctcgct 2640

tatatccgcg tcatcggggg cgggtctttt gctggctccg ccctttctga cgtagaactc 2700

atgcgtcacc tcagtcacgt gatcactagc ccagcggaag aactctttga cttcctgctt 2760

tgtcaccttg ccaaagtcgt gttccagacg gcgggtgagt tcaaatttga acatccggtc 2820

ctgcaacggc tgctggtgct cgaaggtggt gctgttcccg tcgatcacgg cgcgcatgtt 2880

ggtgttggag gtgacgatca cgggggtggg atcgatctgg gcggacgact tgcacttttg 2940

gtccacgcgc accttgctgc cgccgagaat ggccttggcg gactccacga ccttggccgt 3000

catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcgttga agggaaagtt 3060

ctcattggtc cagttgacgc agcaagggcg aattc 3095

<210> 432
<211> 729
<212> PRT
<213> Adeno-associated virus

<400> 432

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320
```

```
Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540
```

```
Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Glu His Pro Pro Pro Gln Ile
625                 630                 635                 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 433
<211> 729
<212> PRT
<213> Adeno-associated virus

<400> 433

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
        195                 200                 205
```

```
Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
```

```
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625                 630                 635                 640
```

```
Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 434
<211> 729
<212> PRT
<213> Adeno-associated virus

<400> 434

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300
```

```
Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525
```

```
Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625                 630                 635                 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 435
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 435
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tacaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcggcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gcccttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgcacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgctacc tcacccgtaa tctgtaa 2217

<210> 436
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 436

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Pro Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
```

```
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735
```

Asn Leu

<210> 437
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 437
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg ataacttgca gcaaaccaat acggggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 438
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 438

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270
```

```
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495
```

```
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

```
Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 439
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 439

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asp Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
```

```
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Arg Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575
```

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Ala Asn Thr Gly
580 585 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Ser Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 440
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 440
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcaggatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcgggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg ttgctatggc aacgcataag gacgacgagg aacgtttctt tccatcgagc 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta tagcagcgtt 1680

atgctaacca gcgaggaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaagccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaaa ttcctcacac ggacggcaat tttcacccgt ctcctctgat gggcggcttt 1920

ggactgaagc acccacctcc ccagatcctg atcaagaata cgccggtacc tgcggatcct 1980

ccaacgacgt tcagccaggc aaaattggct tccttcatca cgcagtacag caccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgatg gaacccagaa 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caattctgag 2160

ggtacatatt cagagcctcg ccccattggt actcgttatc tgacacgtaa tctgtaa 2217

<210> 441
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 441
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gcctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcg aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccagtaga gcagtcaccc caagaaccag actcctcctc gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaattttg gccagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

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aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttccc agtaacggga 1620

tcctgttttt ggcaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct acagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccgccccat tggcacccgt tacctcaccc gtaatctgta a 2211

<210> 442
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 442

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

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

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445
```

```
Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Val Thr Gly Ser Cys Phe Trp
    530                 535                 540

Gln Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 443
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 443

```
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcagcgc ggcggacgca gcggccctcg agcacgacaa ggcctgcgac      240

cagcggctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct      420

ggaaagaagg gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc      480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca      540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga      600

tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacga gggcgccgac      660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc      720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaatcacct ctacaagcaa      780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc      840
```

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac agctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga cgaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 444
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 444

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Cys Asp
65                  70                  75                  80

Gln Arg Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

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

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220
```

```
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655
```

```
Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Asp Glu Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 445
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 445

```
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct      420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc      480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca      540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga      600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac      660
```

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg 1140

actctcaaca acggtagtca ggccgtggga cgttcctcct tctactgcct ggagtacttc 1200

ccctctcaga tgctgagaac gggcaacaac ttttccttca gctacacttt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agtttggaca ggctgatgaa tcctctcatc 1320

gaccagtacc tgtactacct gtcaagaacc cagtctacgg gaggcacagc gggaacccag 1380

cagttgctgt tttctcaggc cgggcctagc aacatgtcga ctcaggccag aaactggctg 1440

cctggaccct gctacagaca gcagcgcgtc tccacgacac tgtcgcaaaa caacaacagc 1500

aactttgcct ggactggtgc caccaagtat catctgaacg gcagagactc tctggtgaat 1560

ccgggcgtcg ccatggcaac caacaaggac gacgaggacc gcttcttccc atccagcggc 1620

atcctcatgt ttggcaagca gggagctgga aaagacaacg tggactatag caacgtgatg 1680

ctaaccagcg aggaagaaat caagaccacc aaccccgtgg ccacagaaca gtatggcgtg 1740

gtggctgata acctacagca gcaaaacacc gctcctattg tgggggccgt caacagccag 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcctatttgg 1860

gccaagattc ctcacacaga tggcaacttt cacccgtctc ctttaatggg cggctttgga 1920

cttaaacatc cgcctcctca gatccttatc aaaaacactc ctgttcctgc ggatcctcca 1980

acagcgttca accaggccaa gctgaattct ttcatcacgc agtacagcac cggacaagtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatactt ccaactacta caaatctaca aatgtggact ttgctgttaa tactgagggt 2160

gcttactctg agcctcgccc cattggcact cgttacctca cccgtaatct gtaa 2214

<210> 446

<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 446

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

```
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr Thr
                405                 410                 415
```

```
Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe
    450                 455                 460

Ser Gln Ala Gly Pro Ser Asn Met Ser Thr Gln Ala Arg Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr Asn
        515                 520                 525

Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met Phe
    530                 535                 540

Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620
```

```
His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Ala Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 447
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 447

```
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc      480
```

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaaggcc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 448
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 448

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

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

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
```

```
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 449
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 449
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagcacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgctga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacggttc aggtcttttc ggactcggaa taccagctgc cctacgtcct cggctccgca 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

ctgactctga acaatggcag ccaatcggtg ggtcgttcct ctttctactg cctggaatat 1200

ttcccttctc aaatgctgag aacgggcaac aacttcacct tcagctacac cttcgaggac 1260

gttcccttcc acagcagcta cgcacacagc cagagcctgg accggctgat gaatcctctt 1320

atcgaccagt acctgtatta cctggccaga acacagagca acgcaggagg cacagctggc 1380

aatcgggaac tgcagtttta tcagggcggg cctaccacca tggccgaaca agccaaaaac 1440

tggctgcctg gaccttgctt ccggcaacaa agagtctcca agacgctgga tcaaaacaac 1500

aacagcaact ttgcttggac tggtgccacc aaataccatc taaatggaag aaattcattg 1560

gttaatcccg gtgtcgccat ggcaacccac aaggacgacg aggaacgctt cttcccttcg 1620

agcggagtcc tgatttttgg aaaaactgga gcagctaata agactacact ggaaaatgtg 1680

ttaatgacaa atgaagagga aattcgtcct accaacccgg tagccaccga ggaatacggg 1740

actgttagca gcaacctgca ggcggctaac actgcagccc agacacaagt tgtcaacaac 1800

cagggagcct tacctggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac tttcacccgt ctccgctgat gggcggcttt 1920

ggactgaagc atccgcctcc tcagatcctg atcaaaaaca ctcctgttcc tgctaatccc 1980

ccggaggtgt ttacgcctgc caagtttgct tctttcatca cacagtacag caccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cctccaattt tgacaaacag actggtgtgg actttgccgt tgacagccag 2160

ggtgtttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 450
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 450

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys His Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


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


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


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


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
```

```
Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ala Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu
    450                 455                 460

Gln Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn
465                 470                 475                 480

Trp Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu
                485                 490                 495

Asp Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr
            500                 505                 510

His Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala
        515                 520                 525

Thr His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu
    530                 535                 540

Ile Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val
545                 550                 555                 560

Leu Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr
                565                 570                 575
```

```
Glu Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala
            580                 585                 590

Ala Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 451
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 451

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
```

```
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445
```

```
Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
```

660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 452
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 452

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 453
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 453

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro

```
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
```

610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 454
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 454

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270
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Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480
```

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Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700
```

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 455
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 455
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacaa gggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca gcaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 456
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 456
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgcac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acttatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggcaac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acatgggcta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacgg caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 457
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 457

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro His Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg

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    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Leu Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350
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Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Asn Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Met Gly Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
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565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Gly Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 458
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 458
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccggaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

gtcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gagcccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 459
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 459

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
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                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540
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Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Ser Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 460

<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 460
atggttgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcagggc 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctta aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagctt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgcg ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gccagcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagccgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 461
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 461

Met Val Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Leu Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Gln Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
```

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        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Pro Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735
```

Asn Leu

<210> 462
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 462
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa tagcctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactccca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgtcttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacttgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 463
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 463

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
```

```
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Ser Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Pro Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Ser Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495
```

```
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
```

705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 464
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 464

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
```

```
Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Val His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Ser Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575
```

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Pro Thr Arg
725 730 735

Asn Leu

<210> 465
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 465
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgtgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aattcgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc ccacccgtaa tctgtaa 2217

<210> 466
<211> 734
<212> PRT
<213> Adeno-associated virus

<400> 466

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Arg Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
```

```
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
    450                 455                 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
                485                 490                 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr Tyr Leu Asn Gly Arg
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540

Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560
```

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
565 570 575

Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
580 585 590

Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
610 615 620

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
645 650 655

Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
690 695 700

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 467
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 467
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct cttcaacatc 960

caagtcaagg aggtcacgac gaatgacggc gtcacgacca tcgctaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggagtac cagctgccgt acgtcctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg 1140

actctgaaca atggcagcca atcggtggga cgttcatcct tctactgcct ggaatacttc 1200

ccttctcagg tgctgagaac gggtaacaac ttcaccttca gttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agcctagacc ggctgatgaa tcccctcatc 1320

gaccagtacc tgtattacct ggctagaaca cagagtaacc caggaggcac atctggcaat 1380

cgggaactgc agttttacca gggcgggcct tccaccatgg ccgaacaagc caagaactgg 1440

ttacctggac cttgcttccg gcaacaaaga gtttccaaaa cactggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggcagaaa ctcattggtg 1560

aatcctggtg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc 1620

ggagtcctga tttttggaaa aactggagca accaacaaga ctacattgga aaacgtgtta 1680

atgacaaatg aagaagaaat tcgtcctact aatcctgtgg ccacagaaga atacgggata 1740

gtcagcagca atttacaagc ggccaatact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaaaattc ctcacacaga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 468
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 468

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Val Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ser Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540
```

```
Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 469
<211> 2214

<212> DNA
<213> Adeno-associated virus

<400> 469
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca cacggctggg cgacagagtc 720

atcaccacca gcacccggac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacgaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 470
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 470

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Arg Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735
```

Leu

<210> 471
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 471
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cttcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggcccagccc acctacaaca accacctcta caagcaaatc 780

tcaagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa aacacaatca aatagtggag ctcttcagca gtctcggcta 1380

ctgtttagtc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctacctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtaccaccta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccgaggagcg 1800

ttacctggca tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tgggctcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaagagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 472
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 472

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Gln Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Ala Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Arg Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 473
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 473
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgcg ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

acctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgcgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 474
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 474

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

```
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495
```

```
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Ala Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 475
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 475
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggccgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagctgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaagca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagtgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 476
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 476

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460
```

```
Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Ser Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685
```

```
Leu Gln Lys Glu Asn Ser Lys Cys Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 477
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 477

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
```

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
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Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
```

545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Ser Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 478
<211> 2217
<212> DNA

<213> Adeno-associated virus

<400> 478
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacga gggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccctaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 479
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 479

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
```

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305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Pro Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 480
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 480
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcac 60

gagtggtggg acccgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacccaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaacg tctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgtcact tctcaccacg tgaccggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cggaaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc ctcagatcct gatcaaaaac actcctgttc ctgctaatcc cccggaggtg 1980

tttacgcctg ccaagtttgc ttctttcatc acacagtaca gcaccggcca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaagcgct ggaacccaga gattcagtat 2100

acctccaatt ttgacaaaca gactggtgtg gactttgccg ttgacagcca gggtgtttat 2160

tctgagcctc gccccattgg tactcgttac ctcacccgta atctgtaa 2208

<210> 481
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 481

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile His Glu Trp Trp Asp Pro Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr His Asn Asn His
                245                 250                 255

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

Asn Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
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```
Arg Phe His Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Glu Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
```

```
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Phe
    690                 695                 700

Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 482
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 482

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

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

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Pro Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
```

```
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Pro Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asp Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

```
Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Val Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 483
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 483

```
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccg aaacccaagg ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt      300
```

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgacccatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctaccc tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaagac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcaggtcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 484
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 484
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttc 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggctgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gagccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacaa gggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gggtgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atgacagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 485
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 485

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Ala Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Gly Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Asp Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
```

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465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685
```

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 486
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 486
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgtgtg ggagctgcag aaggagaaca gcaagcgcag gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 487
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 487

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
```

```
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
```

```
Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
```

660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Val Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Arg Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 488
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 488

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320
```

```
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 489
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 489

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


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


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
```

```
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
```

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
```

610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Val Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 490
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 490

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270
```

```
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480
```

```
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 491
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 491
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctagac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 492
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 492

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
```

```
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460
```

```
Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Arg Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670
```

```
Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 493
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 493

```
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accatgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcctccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct      420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc      480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca      540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga      600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac      660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc      720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa      780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc      840
```

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac agctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 494
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 494

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220
```

```
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655
```

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 495
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 495

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Leu Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
```

```
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735
```

Leu

<210> 496
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 496
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccacccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg tgatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcttcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 497
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 497

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
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        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495
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```
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Pro Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Val Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
```

705 710 715 720

Gly Val Tyr Ser Glu Leu Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 498
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 498
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgcc ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccatca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

caggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacaga tggcaacttt cacccgtctc ctttaatggg cggctttgga 1920

cttaaacatc cgcctcctca gatcctcatc aaaaacactc ctgttcctgc ggatcctcca 1980

acagcgttca accaggccaa gctgaattct ttcatcacgc agtacagcac cggacaagtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatactt ccaactacta caaatctaca aatgtggact ttgctgttaa tactgagggt 2160

gtttactctg agcctcgccc cattggcact cgttacctca cccgtaatct gtaa 2214

<210> 499
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 499

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

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

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Ile Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Gln Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
```

```
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685
```

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 500
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 500
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccgcctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gatgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga gcggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tcttccatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tttgtaa 2217

<210> 501
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 501

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
```

```
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Ala Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
```

```
Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Ser Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Ser
```

660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 502
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 502

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 503
<211> 2217

<212> DNA
<213> Adeno-associated virus

<400> 503
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 504
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 504

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

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

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Arg Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735
```

Asn Leu

<210> 505
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 505

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Leu Asn Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Asp Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Gly
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Lys Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Asp Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Ser Gly Ile
145 150 155 160

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

```
Thr Gly Glu Ala Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ser Asp Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

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

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

```
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
        435                 440                 445

Thr Gln Gly Thr Asn Ala Thr Val Gln Gly Ala Lys Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Asn Met Arg Asp Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Glu Tyr Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met Asn Gly Thr Leu Val Phe Gly
    530                 535                 540

Lys Asn Gly Ala Gly Asn Ser Asn Val Asp Ile Glu Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Val Val Ser Asp Asn Leu Gln Ser Ser Asn Thr Arg Pro Ile
            580                 585                 590

Thr Gly Asp Val Asp Ser Gln Gly Val Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 506
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 506

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270
```

```
Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  507
<211>  736
<212>  PRT
<213>  Adeno-associated virus

<400>  507

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


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


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160
```

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
```

```
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 508
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 508

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460
```

```
Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 509
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 509

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
```

```
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Arg Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  510
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide
```

<400> 510

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
```

```
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Ala Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 511
<211> 1803
<212> DNA
<213> Bovine adeno-associated virus

<400> 511
acggcgcctg cggcaaaaaa gaggcctcta gagcagagtc ctcaagagcc agactcctcg 60

agcggagttg gcaagaaagg caaacagcct gccagaaaga gactcaactt tgacgacgaa 120

cctggagccg gagacgggcc tcccccagaa ggaccatctt ccggagctat gtctactgag 180

actgaaatgc gtgcagcagc tggcggaaat ggtggcgatg cgggacaagg tgccgaggga 240

gtgggtaatg cctccggtga ttggcattgc gattccactt ggtcagagag ccacgtcacc 300

accacctcaa cccgcacctg ggtcctgccg acctacaaca accacctgta cctgcggctc 360

ggctcgagca acgccagcga caccttcaac ggattctcca ccccctgggg atactttgac 420

tttaaccgct tccactgcca cttctcgcca agagactggc aaaggctcat caacaaccac 480

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<213> Bovine adeno-associated virus

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<213> Bovine adeno-associated virus

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<213> Bovine adeno-associated virus

<400> 514
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<213> Bovine adeno-associated virus

<400> 515
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<211> 4694
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<213> Bovine adeno-associated virus

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<211> 390
<212> PRT
<213> Bovine adeno-associated virus

<400> 517

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35 40 45

Ile Met Ser Leu Thr Lys Ser Ala Ser Asp Tyr Leu Val Gly Gln Thr
50 55 60

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Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Leu Tyr Gly Trp Cys
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Thr Arg Ala Phe Gly Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ser His Thr Val Pro
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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
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Cys Val Glu Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Ser
145                 150                 155                 160

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

Val Asp Gln Lys Cys Lys Ser Ser Val Gln Val Asp Ser Thr Pro Val
            180                 185                 190

Ile Ile Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
        195                 200                 205

Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Arg Phe
    210                 215                 220

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

Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
                245                 250                 255

Thr His Glu Phe Met Val Pro Lys Lys Val Ala Gly Thr Glu Arg Ala
            260                 265                 270

Glu Thr Ser Arg Lys Arg Pro Leu Asp Asp Val Thr Asn Thr Asn Tyr
        275                 280                 285
```

```
Lys Ser Pro Glu Lys Arg Ala Arg Leu Ser Val Val Pro Glu Thr Pro
    290                 295                 300

Arg Ser Ser Asp Val Pro Val Glu Pro Ala Pro Leu Arg Pro Leu Asn
305                 310                 315                 320

Trp Ser Ser Arg Tyr Glu Cys Arg Cys Asp Tyr His Ala Lys Phe Asp
                325                 330                 335

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

Asn Gly Cys Ile Phe His Asn Ala Thr His Cys Gln Ile Cys His Ala
        355                 360                 365

Val Pro Pro Trp Glu Lys Glu Asn Val Ser Asp Phe Asn Asp Phe Asp
    370                 375                 380

Asp Cys Asn Lys Glu Gln
385                 390
```

<210> 518
<211> 610
<212> PRT
<213> Bovine adeno-associated virus

<400> 518

```
Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
1               5                   10                  15

Glu His Leu Pro Gly Ile Ser Asp Asn Phe Val Asp Trp Val Thr Gly
            20                  25                  30

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

Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
    50                  55                  60

Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
```

```
65                  70                  75                  80

Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
                85                  90                  95

Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
            100                 105                 110

Ala Gln Leu Val Lys Val Val Phe Gln Asn Ile Glu Pro Arg Ile Asn
        115                 120                 125

Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
    130                 135                 140

Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
145                 150                 155                 160

Glu Leu Gln Trp Ala Trp Thr Asn Leu Glu Glu Tyr Lys Leu Ala Ala
                165                 170                 175

Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Gln Leu Glu
            180                 185                 190

Ser Ser Gln Arg Ser Gln Glu Ala Ser Ser Gln Arg Asp Val Ser Ala
        195                 200                 205

Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
    210                 215                 220

Ser Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
225                 230                 235                 240

Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
                245                 250                 255

Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys Ile Met Ser Leu
            260                 265                 270

Thr Lys Ser Ala Ser Asp Tyr Leu Val Gly Gln Thr Val Pro Glu Asp
        275                 280                 285
```

```
Ile Ser Glu Asn Arg Ile Trp Gln Ile Phe Asp Leu Asn Gly Tyr Asp
    290                 295                 300

Pro Ala Tyr Ala Gly Ser Val Leu Tyr Gly Trp Cys Thr Arg Ala Phe
305                 310                 315                 320

Gly Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
                325                 330                 335

Thr Asn Ile Ala Glu Ala Ile Ser His Thr Val Pro Phe Tyr Gly Cys
            340                 345                 350

Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Glu Lys
        355                 360                 365

Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Ser Lys Val Val Glu
    370                 375                 380

Pro Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg Val Asp Gln Lys
385                 390                 395                 400

Cys Lys Ser Ser Val Gln Val Asp Ser Thr Pro Val Ile Ile Thr Ser
                405                 410                 415

Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
            420                 425                 430

His Gln Gln Pro Leu Glu Asp Arg Met Phe Arg Phe Glu Leu Met Arg
        435                 440                 445

Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
    450                 455                 460

Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
465                 470                 475                 480

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

Lys Arg Pro Leu Asp Asp Val Thr Asn Thr Asn Tyr Lys Ser Pro Glu
```

```
            500                 505                 510

Lys Arg Ala Arg Leu Ser Val Val Pro Glu Thr Pro Arg Ser Ser Asp
        515                 520                 525

Val Pro Val Glu Pro Ala Pro Leu Arg Pro Leu Asn Trp Ser Ser Arg
    530                 535                 540

Tyr Glu Cys Arg Cys Asp Tyr His Ala Lys Phe Asp Ser Val Thr Gly
545                 550                 555                 560

Glu Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys Asn Gly Cys Ile
                565                 570                 575

Phe His Asn Ala Thr His Cys Gln Ile Cys His Ala Val Pro Pro Trp
            580                 585                 590

Glu Lys Glu Asn Val Ser Asp Phe Asn Asp Phe Asp Asp Cys Asn Lys
        595                 600                 605

Glu Gln
    610
```

<210> 519
<211> 538
<212> PRT
<213> Bovine adeno-associated virus

<400> 519

```
Met Arg Ala Ala Ala Gly Gly Asn Gly Gly Asp Ala Gly Gln Gly Ala
1               5                   10                  15

Glu Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
            20                  25                  30

Ser Glu Ser His Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro
        35                  40                  45

Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Ser Ser Asn Ala Ser
    50                  55                  60
```

```
Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
65                  70                  75                  80

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

Asn His Trp Gly Leu Arg Pro Lys Ser Met Gln Val Arg Ile Phe Asn
            100                 105                 110

Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ser
        115                 120                 125

Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp Ser Thr Tyr Glu
    130                 135                 140

Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser Leu Pro Pro Phe
145                 150                 155                 160

Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Leu Val
                165                 170                 175

Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys
            180                 185                 190

Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu
        195                 200                 205

Met Val Tyr Lys Phe Glu Asn Val Pro Phe His Ser Met Tyr Ala His
    210                 215                 220

Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp Gln Tyr Leu
225                 230                 235                 240

Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly Thr Leu Asn Gln Gly Asn
                245                 250                 255

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

Arg Lys Asn Trp Leu Pro Gly Pro Met Met Lys Gln Gln Arg Phe Ser
        275                 280                 285
```

```
Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Gln Gly Arg Asn Asn Ser
    290                 295                 300

Leu Leu His Tyr Glu Thr Arg Thr Thr Leu Asp Gly Arg Trp Ser Asn
305                 310                 315                 320

Phe Ala Pro Gly Thr Ala Met Ala Thr Ala Ala Asn Asp Ala Thr Asp
                325                 330                 335

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

Thr Thr Thr Asp Ala Asn Asn Leu Met Phe Thr Ser Glu Asp Glu Leu
        355                 360                 365

Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu Phe Gly His Leu Ala Thr
    370                 375                 380

Asn Gln Gln Asn Ala Thr Thr Val Pro Thr Val Asp Asp Val Asp Gly
385                 390                 395                 400

Val Gly Val Tyr Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Tyr
                405                 410                 415

Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His
            420                 425                 430

Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys Ser Pro Pro Pro Gln
        435                 440                 445

Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala Thr Thr Phe
    450                 455                 460

Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln
465                 470                 475                 480

Val Ala Val Lys Ile Glu Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg
                485                 490                 495
```

Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Ala Gln Asp Ser
500 505 510

Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala Tyr Lys Glu Pro Arg Ala
515 520 525

Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
530 535

<210> 520
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 520

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Ser Ile Gly Asp
1 5 10 15

Gly Phe Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

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

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Asp Pro Val
50 55 60

Asn Phe Ala Asp Glu Val Ala Arg Glu His Asp Leu Ser Tyr Gln Lys
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Ser Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
115 120 125

```
Gly Leu Val Glu Thr Pro Asp Lys Thr Ala Pro Ala Ala Lys Lys Arg
    130                 135                 140

Pro Leu Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Asp Asp Glu
                165                 170                 175

Pro Gly Ala Gly Asp Gly Pro Pro Pro Glu Gly Pro Ser Ser Gly Ala
            180                 185                 190

Met Ser Thr Glu Thr Glu Met Arg Ala Ala Ala Gly Gly Asn Gly Gly
        195                 200                 205

Asp Ala Gly Gln Gly Ala Glu Gly Val Gly Asn Ala Ser Gly Asp Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Ser Glu Ser His Val Thr Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu
                245                 250                 255

Gly Ser Ser Asn Ala Ser Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp
            260                 265                 270

Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
        275                 280                 285

Trp Gln Arg Leu Ile Asn Asn His Trp Gly Leu Arg Pro Lys Ser Met
    290                 295                 300

Gln Val Arg Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
305                 310                 315                 320

Gly Glu Thr Thr Val Ser Asn Asn Leu Thr Ser Thr Val His Ile Phe
                325                 330                 335

Ala Asp Ser Thr Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
            340                 345                 350
```

```
Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
        355                 360                 365

Gly Tyr Cys Gly Leu Val Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp
    370                 375                 380

Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Met Val Tyr Lys Phe Glu Asn Val Pro Phe
                405                 410                 415

His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Leu Asp Gln Tyr Leu Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly
        435                 440                 445

Thr Leu Asn Gln Gly Asn Ser Ala Thr Asn Phe Ala Lys Leu Thr Asn
    450                 455                 460

Lys Asn Phe Ser Gly Tyr Arg Lys Asn Trp Leu Pro Gly Pro Met Met
465                 470                 475                 480

Lys Gln Gln Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro
                485                 490                 495

Gln Gly Gly Asn Asn Ser Leu Leu His Tyr Glu Thr Arg Thr Thr Leu
            500                 505                 510

Asp Arg Arg Trp Ser Asn Phe Ala Pro Gly Thr Ala Met Ala Thr Ala
        515                 520                 525

Ala Asn Asp Ala Thr Asp Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly
    530                 535                 540

Pro Asn Ile Thr Gly Asn Thr Thr Thr Asp Ala Asn Asn Leu Met Phe
545                 550                 555                 560
```

```
Thr Ser Glu Asp Glu Leu Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu
                565                 570                 575

Phe Gly His Leu Ala Thr Asn Gln Gln Asn Ala Thr Thr Val Pro Thr
            580                 585                 590

Val Asp Asp Val Asp Gly Val Gly Val Tyr Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Ser Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ala Thr Thr Phe Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ala Val Lys Ile Glu Trp Glu Ile Gln
        675                 680                 685

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
    690                 695                 700

Tyr Gly Ala Gln Asp Ser Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala
705                 710                 715                 720

Tyr Lys Glu Pro Arg Ala Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730                 735
```

<210> 521
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 521

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Ser Ile Gly Asp
1               5                  10                  15

Gly Phe Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

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

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Asp Pro Val
    50                  55                  60

Asn Phe Ala Asp Glu Val Ala Arg Glu His Asp Leu Ser Tyr Gln Lys
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Ser Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
        115                 120                 125

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

Pro Leu Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Asp Asp Glu
                165                 170                 175

Pro Gly Ala Gly Asp Gly Pro Pro Pro Glu Gly Pro Ser Ser Gly Ala
            180                 185                 190

Met Ser Thr Glu Thr Glu Met Arg Ala Ala Ala Gly Gly Asn Gly Gly
        195                 200                 205

Asp Ala Gly Gln Gly Ala Glu Gly Val Gly Asn Ala Ser Gly Asp Trp
    210                 215                 220
```

```
His Cys Asp Ser Thr Trp Ser Glu Ser His Val Thr Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu
                245                 250                 255

Gly Ser Ser Asn Ala Ser Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp
            260                 265                 270

Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
        275                 280                 285

Trp Gln Arg Leu Ile Asn Asn His Trp Gly Leu Arg Pro Lys Ser Met
    290                 295                 300

Gln Val Arg Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
305                 310                 315                 320

Gly Glu Thr Thr Val Ser Asn Asn Leu Thr Ser Thr Val Gln Ile Phe
                325                 330                 335

Ala Asp Ser Thr Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
            340                 345                 350

Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
        355                 360                 365

Gly Tyr Cys Gly Leu Val Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp
    370                 375                 380

Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Met Val Tyr Lys Phe Glu Asn Val Pro Phe
                405                 410                 415

His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430
```

```
Leu Leu Asp Gln Tyr Leu Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly
        435                 440                 445

Thr Leu Asn Gln Gly Asn Ser Ala Thr Asn Phe Ala Lys Leu Thr Lys
    450                 455                 460

Thr Asn Phe Ser Gly Tyr Arg Lys Asn Trp Leu Pro Gly Pro Met Met
465                 470                 475                 480

Lys Gln Gln Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro
                485                 490                 495

Gln Gly Arg Asn Asn Ser Leu Leu His Tyr Glu Thr Arg Thr Thr Leu
            500                 505                 510

Asp Gly Arg Trp Ser Asn Phe Ala Pro Gly Thr Ala Met Ala Thr Ala
        515                 520                 525

Ala Asn Asp Ala Thr Asp Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly
    530                 535                 540

Pro Asn Ile Thr Gly Asn Thr Thr Thr Asp Ala Asn Asn Leu Met Phe
545                 550                 555                 560

Thr Ser Glu Asp Glu Leu Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu
                565                 570                 575

Phe Gly His Leu Ala Thr Asn Gln Gln Asn Ala Thr Thr Val Pro Thr
            580                 585                 590

Val Asp Asp Val Asp Gly Val Gly Val Tyr Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Ser Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Ala Thr Thr Phe Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ala Val Lys Ile Glu Trp Glu Ile Gln
        675                 680                 685

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
    690                 695                 700

Tyr Gly Ala Gln Asp Ser Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala
705                 710                 715                 720

Tyr Lys Glu Pro Arg Ala Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730                 735
```

<210> 522
<211> 736
<212> PRT
<213> Bovine adeno-associated virus

<400> 522

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Ser Ile Gly Asp
1               5                   10                  15

Gly Phe Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

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

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Asp Pro Val
    50                  55                  60

Asn Phe Ala Asp Glu Val Ala Arg Glu His Asp Leu Ser Tyr Gln Lys
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Ser Asp Thr Ser Phe Gly Gly Asn
```

```
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
        115                 120                 125

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

Pro Leu Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Asp Asp Glu
                165                 170                 175

Pro Gly Ala Gly Asp Gly Pro Pro Pro Glu Gly Pro Ser Ser Gly Ala
            180                 185                 190

Met Ser Thr Glu Thr Glu Met Arg Ala Ala Ala Gly Gly Asn Gly Gly
        195                 200                 205

Asp Ala Gly Gln Gly Ala Glu Gly Val Gly Asn Ala Ser Gly Asp Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Ser Glu Ser His Val Thr Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu
                245                 250                 255

Gly Ser Ser Asn Ala Ser Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp
            260                 265                 270

Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
        275                 280                 285

Trp Gln Arg Leu Ile Asn Asn His Trp Gly Leu Arg Pro Lys Ser Met
    290                 295                 300

Gln Val Arg Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
305                 310                 315                 320
```

```
Gly Glu Thr Thr Val Ser Asn Asn Leu Thr Ser Thr Val Gln Ile Phe
                325                 330                 335

Ala Asp Ser Thr Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
            340                 345                 350

Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
        355                 360                 365

Gly Tyr Cys Gly Leu Val Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp
    370                 375                 380

Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Met Val Tyr Lys Phe Glu Asn Val Pro Phe
                405                 410                 415

His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Leu Asp Gln Tyr Leu Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly
        435                 440                 445

Thr Leu Asn Gln Gly Asn Ser Ala Thr Asn Phe Ala Lys Leu Thr Lys
    450                 455                 460

Thr Asn Phe Ser Gly Tyr Arg Lys Asn Trp Leu Pro Gly Pro Met Met
465                 470                 475                 480

Lys Gln Gln Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro
                485                 490                 495

Gln Gly Arg Asn Asn Ser Leu Leu His Tyr Glu Thr Arg Thr Thr Leu
            500                 505                 510

Asp Gly Arg Trp Ser Asn Phe Ala Pro Gly Thr Ala Met Ala Thr Ala
        515                 520                 525

Ala Asn Asp Ala Thr Asp Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly
```

```
    530                 535                 540

Pro Asn Ile Thr Gly Asn Thr Thr Thr Asp Ala Asn Asn Leu Met Phe
545                 550                 555                 560

Thr Ser Glu Asp Glu Leu Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu
                565                 570                 575

Phe Gly His Leu Ala Thr Asn Gln Gln Asn Ala Thr Thr Val Pro Thr
            580                 585                 590

Val Asp Asp Val Asp Gly Val Gly Val Tyr Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Ser Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ala Thr Thr Phe Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ala Val Lys Ile Glu Trp Glu Ile Gln
        675                 680                 685

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
    690                 695                 700

Tyr Gly Ala Gln Asp Ser Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala
705                 710                 715                 720

Tyr Lys Glu Pro Arg Ala Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730                 735

<210>  523
<211>  600
<212>  PRT
```

<213> Bovine adeno-associated virus

<400> 523

```
Thr Ala Pro Ala Ala Lys Lys Arg Pro Leu Glu Gln Ser Pro Gln Glu
1               5                  10                  15


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


Lys Arg Leu Asn Phe Asp Asp Glu Pro Gly Ala Gly Asp Gly Pro Pro
        35                  40                  45


Pro Glu Gly Pro Ser Ser Gly Ala Met Ser Thr Glu Thr Glu Met Arg
    50                  55                  60


Ala Ala Ala Gly Gly Asn Gly Gly Asp Ala Gly Gln Gly Ala Glu Gly
65                  70                  75                  80


Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Ser Glu
                85                  90                  95


Ser His Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Thr Tyr
            100                 105                 110


Asn Asn His Leu Tyr Leu Arg Leu Gly Ser Ser Asn Ala Ser Asp Thr
        115                 120                 125


Phe Asn Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
    130                 135                 140


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn His
145                 150                 155                 160


Trp Gly Leu Arg Pro Lys Ser Met Gln Val Arg Ile Phe Asn Ile Gln
                165                 170                 175


Val Lys Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ser Asn Asn
            180                 185                 190


Leu Thr Ser Thr Val Gln Ile Phe Ala Asp Ser Thr Tyr Glu Leu Pro
        195                 200                 205
```

```
Tyr Val Met Asp Ala Gly Gln Glu Gly Ser Leu Pro Pro Phe Pro Asn
    210                 215                 220

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Leu Val Thr Gly
225                 230                 235                 240

Gly Ser Ser Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys Leu Glu
                245                 250                 255

Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Met Val
            260                 265                 270

Tyr Lys Phe Glu Asn Val Pro Phe His Ser Met Tyr Ala His Ser Gln
        275                 280                 285

Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp Gln Tyr Leu Trp Glu
    290                 295                 300

Leu Gln Ser Thr Thr Ser Gly Gly Thr Leu Asn Gln Gly Asn Ser Ala
305                 310                 315                 320

Thr Asn Phe Ala Lys Leu Thr Lys Thr Asn Phe Ser Gly Tyr Arg Lys
                325                 330                 335

Asn Trp Leu Pro Gly Pro Met Met Lys Gln Gln Arg Phe Ser Lys Thr
            340                 345                 350

Ala Ser Gln Asn Tyr Lys Ile Pro Gln Gly Arg Asn Asn Ser Leu Leu
        355                 360                 365

His Tyr Glu Thr Arg Thr Thr Leu Asp Gly Arg Trp Ser Asn Phe Ala
    370                 375                 380

Pro Gly Thr Ala Met Ala Thr Ala Ala Asn Asp Ala Thr Asp Phe Ser
385                 390                 395                 400

Gln Ala Gln Leu Ile Phe Ala Gly Pro Asn Ile Thr Gly Asn Thr Thr
                405                 410                 415
```

```
Thr Asp Ala Asn Asn Leu Met Phe Thr Ser Glu Asp Glu Leu Arg Ala
            420                 425                 430

Thr Asn Pro Arg Asp Thr Asp Leu Phe Gly His Leu Ala Thr Asn Gln
        435                 440                 445

Gln Asn Ala Thr Thr Val Pro Thr Val Asp Asp Val Asp Gly Val Gly
    450                 455                 460

Val Tyr Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Tyr Gln Gly
465                 470                 475                 480

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser
                485                 490                 495

Pro Leu Ile Gly Gly Phe Gly Leu Lys Ser Pro Pro Pro Gln Ile Phe
            500                 505                 510

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala Thr Thr Phe Ser Pro
        515                 520                 525

Ala Arg Ile Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ala
    530                 535                 540

Val Lys Ile Glu Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg Trp Asn
545                 550                 555                 560

Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Ala Gln Asp Ser Leu Leu
                565                 570                 575

Trp Ala Pro Asp Asn Ala Gly Ala Tyr Lys Glu Pro Arg Ala Ile Gly
            580                 585                 590

Ser Arg Tyr Leu Thr Asn His Leu
        595                 600
```

<210> 524
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 524
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gtttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ttggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 525
<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 525

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

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

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510
```

```
Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735
```

Leu

<210> 526
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 526

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590
```

```
Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210>  527
<211>  736
<212>  PRT
<213>  Artificial Sequence

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

<400>  527

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30
```

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Glu Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460
```

```
Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 528
<211> 2181
<212> DNA
<213> Artificial Sequence

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

<400> 528

```
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag       60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa      120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga      180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag      240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag      300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc      360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc      420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc      480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc      540

ccagcacaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca      600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc      660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgcacctg ggtgctgccc      720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc      780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc      840

cactggagcc cccgagactg gcaaagactc atcaacaact attggggctt cagaccccgg      900
```

tctctcagag tcaaaatctt caacatccaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccaa 1020

ctcccgtacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc cccgcaggtc 1080

tttacgctgc cgcagtacgg ctacgcgacg ctgaaccgag acaacggaga caacccgaca 1140

gagcggagca gcttcttttg cctagagtac tttcccagca agatgctgag gacgggcaac 1200

aactttgagt ttacctacag ctttgaagag gtgcccttcc actgcagctt cgccccgagc 1260

cagaacctct ttaagctggc caacccgctg gtggaccagt acctgtaccg cttcgtgagc 1320

acctcggcca cgggcgccat ccagttccaa aagaacctgg cgggcagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacac gagctctggg 1440

gtcagcagca ccaacagagt cagcgtcaac aacttttccg tctcaaaccg gatgaacctg 1500

gaggggggca gctaccaagt gaacccccag cccaacggga tgacaaacac gctccaaggc 1560

agcaaccgct acgcgctgga aaacaccatg atcttcaacg ctcaaaacgc cacgccggga 1620

actacctcgg tgtacccaga ggacaatcta ctgctgacca gcgagagcga gactcagccc 1680

gtcaaccggg tggcttacaa cacgggcggt cagatggcca ccaacgccca gaacgccacc 1740

acggctccca cggtcgggac ctacaacctc caggaagtgc ttcctggcag cgtatggatg 1800

gagagggacg tgtacctcca aggacccatc tgggccaaga tcccagagac gggggcgcac 1860

tttcacccct ctccggccat gggcggattc ggactcaaac acccgccgcc catgatgctc 1920

atcaaaaaca cgccggtgcc cggcaacatc accagcttct cggacgtgcc cgtcagcagc 1980

ttcatcaccc agtacagcac cgggcaggtc accgtggaga tggaatggga gctcaaaaag 2040

gaaaactcca agaggtggaa cccagagatc cagtacacca acaactacaa cgacccccag 2100

tttgtggact ttgctccaga cggctccggc gaatacagaa ccaccagagc catcggaacc 2160

cgatacctca cccgacccct t 2181

<210> 529
<211> 726
<212> PRT
<213> Artificial Sequence

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

<400> 529

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
195 200 205

```
Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Gly Asp Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Ser Phe Glu Glu Val Pro Phe His Cys Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430
```

```
Gln Tyr Leu Tyr Arg Phe Val Ser Thr Ser Ala Thr Gly Ala Ile Gln
        435                 440                 445

Phe Gln Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Thr Ser Ser Gly
465                 470                 475                 480

Ser Ser Thr Asn Arg Val Ser Val Asn Asn Phe Ser Val Ser Asn Arg
                485                 490                 495

Met Asn Leu Glu Gly Ala Ser Tyr Gln Val Asn Pro Gln Pro Asn Gly
            500                 505                 510

Met Thr Asn Thr Leu Gln Gly Ser Asn Arg Tyr Ala Leu Glu Asn Thr
        515                 520                 525

Met Ile Phe Asn Ala Gln Asn Ala Thr Pro Gly Thr Thr Ser Val Tyr
    530                 535                 540

Pro Glu Asp Asn Leu Leu Leu Thr Ser Glu Ser Glu Thr Gln Pro Val
545                 550                 555                 560

Asn Arg Val Ala Tyr Asn Thr Gly Gly Gln Met Ala Thr Asn Ala Gln
                565                 570                 575

Asn Ala Thr Thr Ala Pro Thr Val Gly Thr Tyr Asn Leu Gln Glu Val
            580                 585                 590

Leu Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro
        595                 600                 605

Ile Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro
    610                 615                 620

Ala Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile
625                 630                 635                 640
```

```
Lys Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro
                645                 650                 655

Val Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu
            660                 665                 670

Met Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
        675                 680                 685

Ile Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala
    690                 695                 700

Pro Asp Gly Ser Gly Glu Tyr Arg Thr Thr Arg Ala Ile Gly Thr Arg
705                 710                 715                 720

Tyr Leu Thr Arg Pro Leu
                725
```

<210> 530
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 530

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 531
<211> 1797
<212> DNA
<213> Artificial Sequence

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

<400> 531
acggctccga ccggagacaa gcggaaaggc gaagacgaac ctcgtttgcc cgacacttct 60

tcacagactc ccaagaaaaa caagaagcct cgcaaggaaa gaccttccgg cggggcagaa 120

gatccgggcg aaggcacctc ttccaacgct ggagcagcag cacccgcctc tagtgtggga 180

tcatctatca tggctgaagg aggtggcggc ccagtgggcg atgcaggcca gggtgccgat 240

ggagtgggca attcctccgg aaattggcat tgcgattccc aatggctgga aaacggagtc 300

gtcactcgaa ccacccgaac ctgggtcttg cccagctaca acaaccacct gtacaaacga 360

atccaaggac ccagcggagg cgacaacaac aacaaattct ttggattcag cacccctgg 420

ggatactttg actacaatcg attccactgc cacttttccc cgcgagactg gcaacgactc 480

atcaacaaca actggggcat ccgtcccaaa gcgatgcgct ttagactctt taacatccag 540

gttaaagagg tcacggtcca agacttcaac accaccatcg gcaacaacct caccagtacg 600

gtccaggtct ttgcggacaa ggactaccaa ctgccgtacg tcctcggatc ggctaccgaa 660

ggcaccttcc cgccgttccc agcggatatc tacacgatcc cgcagtacgg gtactgcacg 720

ctaaactaca acaacgaggc ggtggatcgt tcggccttct actgtctgga ctactttccc 780

tcagacatgc tgcggacagg aaataacttt gagtttactt acaccttcga ggacgttcct 840

ttccatagca tgtttgccca caaccagacg ctagaccggc tgatgaatcc cctcgtggat 900

cagtacctct gggctttcag ctccgtcagc caagcaggct catctggacg agctcttcat 960

tactcgcggg cgactaaaac caacatggcg gctcaatata ggaactggtt acctgggcct 1020

ttcttccgtg atcagcaaat ctttacgggc gctagcaaca tcactaaaaa taacgtcttt 1080

agcgtttggg aaaaaggcaa gcaatgggaa ctcgacaatc ggaccaacct aatgcagccc 1140

ggtcctgcgg cagcgaccac ctttagcgga gaacctgacc gtcaagccat gcaaaacacg 1200

ctggctttta gcaggaccgt ctacgatcaa acgaccgcca cgaccgatcg taaccagata 1260

ctcatcacca acgaagacga aatcagaccc accaactcgg tcggtatcga cgcgtgggga 1320

gcagttccca ccaacaacca gtcgatcgtg acccccggca ctcgcgcggc cgtcaacaat 1380

caaggggcgc ttcccgggat ggtgtggcaa aacagagaca tttaccctac agggacccat 1440

ttggccaaaa ttcccgacac tgacaatcac ttccatccgt ccccgcttat tgggcggttt 1500

ggctgcaagc atccccctcc ccagattttc attaaaaaca cacccgtccc tgccaaccct 1560

tcggaaacgt tccagacggc caaagtggcc tccttcatca accagtactc gaccggacag 1620

tgcaccgtcg aaatcttttg ggaactcaag aaggaaacct ccaagcgctg gaaccccgaa 1680

atccagttca cctccaactt tggcaacgcg gccgacatcc agtttgccgt ctccgacacg 1740

ggatcctatt ccgaacctcg tcccatcggt acccgttacc ttaccaaacc tctgtaa 1797

<210> 532
<211> 1989
<212> DNA
<213> Artificial Sequence

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

<400> 532
atgaggtcgt actacgaggt catcgttcag ctgcccaacg acgtcgagag tcaggtacct 60

ggaatctccg attcgttcgt caactggatt acgtcgcgag aatggacgtt gcctgaggac 120

gccgattggg atttggacca ggtcgatcaa gttcaactga cgctcggcga caaaatccaa 180

cgggagattc gaactcattg ggggacgatg gccaaagaac cggactttca ctattttatc 240

caactggaac aaggtgaggt gttctttcat ttacacgtcc tgctggaaac gtgttccgta 300

aagccgatgg tactcggaag atatatccga catattcaac aaaaaattgt gagtaaagtc 360

tactgcgcca cgagcctacg atggaaggat ggatgcgtgg tgaccaagac caaaaatttc 420

gggggcgcga acaaggtccg ggccgagtcg tatattcccg cctacctgat cccgaaacag 480

caaccggaag tgcagtgggc gtggactaac gtgcccgagt atataaaagc gtgcttgcac 540

cgagaactgc gtgccagtct cgcgcgactt cacttcgagg aggcgggcgt ctcgcaatcc 600

aaggaaaatc tcgcgagaac tgcagacggc gctcccgtga tgccgacccg cgtcagcaaa 660

cgctacatgg agctcgtgga ttggctcgtg gagaagggga tcaccaccga gaaggaatgg 720

ctgctggaaa acagagaaag ctttcggagc tttcaggcct cgagcaactc ggcgcgtcag 780

atcaagacgg ccctgcaagg cgccattcag gagatgcttc tgaccaagac ggcggaggac 840

tacctcgtcg gaaaggatcc cgtctcggac gacgacatcc gtcagaaccg catctacaag 900

attctggaac tgaaccacta cgacccagcg tacgtgggga gtattttggt cgggtggtgc 960

cagaagaaat ggggcaagcg aaacacgctg tggctgttcg gacatgcgac caccggcaag 1020

accaacatcg cggaggctat tgcccatgct gtgccgttct atggatgcgt taactggacc 1080

aacgagaact ttccgttcaa cgactgcgtc gaaaaaatga ttatctggtg ggaggagggc 1140

aaaatgaccg ccaaagtggt ggaaacagcc aaggcgattc tgggaggatc tcgggtgaga 1200

gtggaccaaa aatgcaaagc ttcggttccg atcgaaccga cgccggtcat tattaccagt 1260

aacaccaaca tgtgttatgt catcgacggg aacacgacca cgttcgagca taagcagccg 1320

ttggaggaca ggatgtttaa gctcgaattg ctgactcggt tgcctgatga ctttggtaag 1380

gtgaccaaac aggaggtgcg tcaattcttc aggtggtctc aggatcacct gacccctgtg 1440

atcccagaat tcctagtgcg gaaggcggag tctcgcaaaa gacccgcccc ttccggggaa 1500

ggctatataa gcccgacaaa gcggcccgcg ctcgcagagc agcagcaggc gtcggagagc 1560

gcggacccgg ttcccaccag gtatcgtatc aaatgctcga aacattgcgg tatggataaa 1620

atgttgtttc cttgccaaat ttgtgaatcg atgaacagag atattaatat ttgtgctatt 1680

cataaaacga ccgactgtaa agagtgtttc cccgactacg gggataaaga tgatgtagaa 1740

ctacccccct gtacagaaca caacgtgtct cgttgttatc aatgtcattc gggcgaattg 1800

tatcgcgtga cttcggactc tgacgagaaa cctgcccccg agagtgatga aggcaccgag 1860

ccatcctatg ctccctgcac gattcaccac ctgatgggca agagtcacgg gttagtcact 1920

tgcgcggcgt gtcggttgaa aaatagtacg ttgcatgatg acttggatga cggtgatctc 1980

gaacaataa 1989

<210> 533
<211> 1626
<212> DNA
<213> Artificial Sequence

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

<400> 533
atgaggtcgt actacgaggt catcgttcag ctgcccaacg acgtcgagag tcaggtacct 60

ggaatctccg attcgttcgt caactggatt acgtcgcgag aatggacgtt gcctgaggac 120

gccgattggg atttggacca ggtcgatcaa gttcaactga cgctcggcga caaaatccaa 180

cgggagattc gaactcattg ggggacgatg gccaaagaac cggactttca ctattttatc 240

caactggaac aaggtgaggt gttctttcat ttacacgtcc tgctggaaac gtgttccgta 300

aagccgatgg tactcggaag atatatccga catattcaac aaaaaattgt gagtaaagtc 360

tactgcgcca cgagcctacg atggaaggat ggatgcgtgg tgaccaagac caaaaatttc 420

gggggcgcga acaaggtccg ggccgagtcg tatattcccg cctacctgat cccgaaacag 480

caaccggaag tgcagtgggc gtggactaac gtgcccgagt atataaaagc gtgcttgcac 540

cgagaactgc gtgccagtct cgcgcgactt cacttcgagg aggcgggcgt ctcgcaatcc 600

aaggaaaatc tcgcgagaac tgcagacggc gctcccgtga tgccgacccg cgtcagcaaa 660

cgctacatgg agctcgtgga ttggctcgtg gagaagggga tcaccaccga gaaggaatgg 720

ctgctggaaa acagagaaag ctttcggagc tttcaggcct cgagcaactc ggcgcgtcag 780

atcaagacgg ccctgcaagg cgccattcag gagatgcttc tgaccaagac ggcggaggac 840

tacctcgtcg gaaaggatcc cgtctcggac gacgacatcc gtcagaaccg catctacaag 900

attctggaac tgaaccacta cgacccagcg tacgtgggga gtattttggt cgggtggtgc 960

cagaagaaat ggggcaagcg aaacacgctg tggctgttcg gacatgcgac caccggcaag 1020

accaacatcg cggaggctat tgcccatgct gtgccgttct atggatgcgt taactggacc 1080

aacgagaact ttccgttcaa cgactgcgtc gaaaaaatga ttatctggtg ggaggagggc 1140

aaaatgaccg ccaaagtggt ggaaacagcc aaggcgattc tgggaggatc tcgggtgaga 1200

gtggaccaaa aatgcaaagc ttcggttccg atcgaaccga cgccggtcat tattaccagt 1260

aacaccaaca tgtgttatgt catcgacggg aacacgacca cgttcgagca taagcagccg 1320

ttggaggaca ggatgtttaa gctcgaattg ctgactcggt tgcctgatga ctttggtaag 1380

gtgaccaaac aggaggtgcg tcaattcttc aggtggtctc aggatcacct gacccctgtg 1440

atcccagaat tcctagtgcg gaaggcggag tctcgcaaaa gacccgcccc ttccggggaa 1500

ggctatataa gcccgacaaa gcggcccgcg ctcgcagagc agcagcaggc gtcggagagc 1560

gcggacccgg ttcccaccag attggttgga gcggttggtc aaaaagggag tgaatgctgc 1620

agctga 1626

<210> 534
<211> 1323
<212> DNA
<213> Artificial Sequence

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

<400> 534
atggagctcg tggattggct cgtggagaag gggatcacca ccgagaagga atggctgctg 60

gaaaacagag aaagctttcg gagctttcag gcctcgagca actcggcgcg tcagatcaag 120

acggccctgc aaggcgccat tcaggagatg cttctgacca agacggcgga ggactacctc 180

gtcggaaagg atcccgtctc ggacgacgac atccgtcaga accgcatcta caagattctg 240

gaactgaacc actacgaccc agcgtacgtg gggagtattt tggtcgggtg gtgccagaag 300

aaatggggca agcgaaacac gctgtggctg ttcggacatg cgaccaccgg caagaccaac 360

atcgcggagg ctattgccca tgctgtgccg ttctatggat gcgttaactg gaccaacgag 420

aactttccgt tcaacgactg cgtcgaaaaa atgattatct ggtgggagga gggcaaaatg 480

accgccaaag tggtggaaac agccaaggcg attctgggag gatctcgggt gagagtggac 540

caaaaatgca aagcttcggt tccgatcgaa ccgacgccgg tcattattac cagtaacacc 600

aacatgtgtt atgtcatcga cgggaacacg accacgttcg agcataagca gccgttggag 660

gacaggatgt ttaagctcga attgctgact cggttgcctg atgactttgg taaggtgacc 720

aaacaggagg tgcgtcaatt cttcaggtgg tctcaggatc acctgacccc tgtgatccca 780

gaattcctag tgcggaaggc ggagtctcgc aaaagacccg ccccttccgg ggaaggctat 840

ataagcccga caaagcggcc cgcgctcgca gagcagcagc aggcgtcgga gagcgcggac 900

ccggttccca ccaggtatcg tatcaaatgc tcgaaacatt gcggtatgga taaaatgttg 960

tttccttgcc aaatttgtga atcgatgaac agagatatta atatttgtgc tattcataaa 1020

acgaccgact gtaaagagtg tttccccgac tacggggata aagatgatgt agaactaccc 1080

ccctgtacag aacacaacgt gtctcgttgt tatcaatgtc attcgggcga attgtatcgc 1140

gtgacttcgg actctgacga gaaacctgcc cccgagagtg atgaaggcac cgagccatcc 1200

tatgctccct gcacgattca ccacctgatg ggcaagagtc acgggttagt cacttgcgcg 1260

gcgtgtcggt tgaaaaatag tacgttgcat gatgacttgg atgacggtga tctcgaacaa 1320

taa 1323

<210> 535
<211> 960
<212> DNA
<213> Artificial Sequence

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

<400> 535
atggagctcg tggattggct cgtggagaag gggatcacca ccgagaagga atggctgctg 60

gaaaacagag aaagctttcg gagctttcag gcctcgagca actcggcgcg tcagatcaag 120

acggccctgc aaggcgccat tcaggagatg cttctgacca agacggcgga ggactacctc 180

gtcggaaagg atcccgtctc ggacgacgac atccgtcaga accgcatcta caagattctg 240

gaactgaacc actacgaccc agcgtacgtg gggagtattt tggtcgggtg gtgccagaag 300

aaatggggca agcgaaacac gctgtggctg ttcggacatg cgaccaccgg caagaccaac 360

atcgcggagg ctattgccca tgctgtgccg ttctatggat gcgttaactg gaccaacgag 420

aactttccgt tcaacgactg cgtcgaaaaa atgattatct ggtgggagga gggcaaaatg 480

accgccaaag tggtggaaac agccaaggcg attctgggag gatctcgggt gagagtggac 540

caaaaatgca aagcttcggt tccgatcgaa ccgacgccgg tcattattac cagtaacacc 600

aacatgtgtt atgtcatcga cgggaacacg accacgttcg agcataagca gccgttggag 660

gacaggatgt ttaagctcga attgctgact cggttgcctg atgactttgg taaggtgacc 720

aaacaggagg tgcgtcaatt cttcaggtgg tctcaggatc acctgacccc tgtgatccca 780

gaattcctag tgcggaaggc ggagtctcgc aaaagacccg ccccttccgg ggaaggctat 840

ataagcccga caaagcggcc cgcgctcgca gagcagcagc aggcgtcgga gagcgcggac 900

ccggttccca ccagattggt tggagcggtt ggtcaaaaag ggagtgaatg ctgcagctga 960

<210> 536
<211> 1608
<212> DNA
<213> Artificial Sequence

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

<400> 536
atggctgaag gaggtggcgg cccagtgggc gatgcaggcc agggtgccga tggagtgggc 60

aattcctccg gaaattggca ttgcgattcc caatggctgg aaaacggagt cgtcactcga 120

accacccgaa cctgggtctt gcccagctac aacaaccacc tgtacaaacg aatccaagga 180

cccagcggag gcgacaacaa caacaaattc tttggattca gcacccccctg gggatacttt 240

gactacaatc gattccactg ccacttttcc ccgcgagact ggcaacgact catcaacaac 300

aactggggca tccgtcccaa agcgatgcgc tttagactct ttaacatcca ggttaaagag 360

gtcacggtcc aagacttcaa caccaccatc ggcaacaacc tcaccagtac ggtccaggtc 420

tttgcggaca aggactacca actgccgtac gtcctcggat cggctaccga aggcaccttc 480

ccgccgttcc cagcggatat ctacacgatc ccgcagtacg ggtactgcac gctaaactac 540

aacaacgagg cggtggatcg ttcggccttc tactgtctgg actactttcc ctcagacatg 600

ctgcggacag gaaataactt tgagtttact tacaccttcg aggacgttcc tttccatagc 660

atgtttgccc acaaccagac gctagaccgg ctgatgaatc ccctcgtgga tcagtacctc 720

tgggctttca gctccgtcag ccaagcaggc tcatctggac gagctcttca ttactcgcgg 780

gcgactaaaa ccaacatggc ggctcaatat aggaactggt tacctgggcc tttcttccgt 840

gatcagcaaa tctttacggg cgctagcaac atcactaaaa ataacgtctt tagcgtttgg 900

gaaaaaggca agcaatggga actcgacaat cggaccaacc taatgcagcc cggtcctgcg 960

gcagcgacca cctttagcgg agaacctgac cgtcaagcca tgcaaaacac gctggctttt 1020

agcaggaccg tctacgatca aacgaccgcc acgaccgatc gtaaccagat actcatcacc 1080

aacgaagacg aaatcagacc caccaactcg gtcggtatcg acgcgtgggg agcagttccc 1140

accaacaacc agtcgatcgt gacccccggc actcgcgcgg ccgtcaacaa tcaaggggcg 1200

cttcccggga tggtgtggca aaacagagac atttacccta cagggaccca tttggccaaa 1260

attcccgaca ctgacaatca cttccatccg tccccgctta ttgggcggtt tggctgcaag 1320

catccccctc cccagatttt cattaaaaac acacccgtcc ctgccaaccc ttcggaaacg 1380

ttccagacgg ccaaagtggc ctccttcatc aaccagtact cgaccggaca gtgcaccgtc 1440

gaaatctttt gggaactcaa gaaggaaacc tccaagcgct ggaaccccga aatccagttc 1500

acctccaact ttggcaacgc ggccgacatc cagtttgccg tctccgacac gggatcctat 1560

tccgaacctc gtcccatcgg tacccgttac cttaccaaac ctctgtaa 1608

<210> 537
<211> 2232
<212> DNA
<213> Artificial Sequence

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

<400> 537
atgtctctca tttctgatgc gattccagat tggttggagc ggttggtcaa aaagggagtg 60

aatgctgcag ctgatttcta ccatttggaa agcggtcctc ctcgtcctaa ggcaaatcag 120

caaactcaag aatctcttga aaaggacgat tcgagaggtc tcgtgttccc aggctacaat 180

tatctaggcc ctttcaacgg tctagataaa ggagaacccg tcaacgaggc agacgctgcc 240

gccttagaac acgacaaggc ttacgacctc gaaatcaagg acgggcacaa cccgtacttt 300

gagtacaacg aggccgacag acgtttccag gaacgtctca aagacgatac ctcctttgga 360

ggcaatttag gtaaagccat cttccaggcc aaaaagaggg ttctcgaacc ctttggtctg 420

gtggaagact caaagacggc tccgaccgga gacaagcgga aaggcgaaga cgaacctcgt 480

ttgcccgaca cttcttcaca gactcccaag aaaaacaaga agcctcgcaa ggaaagacct 540

tccggcgggg cagaagatcc gggcgaaggc acctcttcca acgctggagc agcagcaccc 600

gcctctagtg tgggatcatc tatcatggct gaaggaggtg gcggcccagt gggcgatgca 660

ggccagggtg ccgatggagt gggcaattcc tccggaaatt ggcattgcga ttcccaatgg 720

ctggaaaacg gagtcgtcac tcgaaccacc cgaacctggg tcttgcccag ctacaacaac 780

cacctgtaca aacgaatcca aggacccagc ggaggcgaca acaacaacaa attctttgga 840

ttcagcaccc cctggggata ctttgactac aatcgattcc actgccactt ttccccgcga 900

gactggcaac gactcatcaa caacaactgg ggcatccgtc ccaaagcgat gcgctttaga 960

ctctttaaca tccaggttaa agaggtcacg gtccaagact tcaacaccac catcggcaac 1020

aacctcacca gtacggtcca ggtctttgcg gacaaggact accaactgcc gtacgtcctc 1080

ggatcggcta ccgaaggcac cttcccgccg ttcccagcgg atatctacac gatcccgcag 1140

tacgggtact gcacgctaaa ctacaacaac gaggcggtgg atcgttcggc cttctactgt 1200

ctggactact ttccctcaga catgctgcgg acaggaaata actttgagtt tacttacacc 1260

ttcgaggacg ttcctttcca tagcatgttt gcccacaacc agacgctaga ccggctgatg 1320

aatcccctcg tggatcagta cctctgggct ttcagctccg tcagccaagc aggctcatct 1380

ggacgagctc ttcattactc gcgggcgact aaaaccaaca tggcggctca atataggaac 1440

tggttacctg ggcctttctt ccgtgatcag caaatcttta cgggcgctag caacatcact 1500

aaaaataacg tctttagcgt ttgggaaaaa ggcaagcaat gggaactcga caatcggacc 1560

aacctaatgc agcccggtcc tgcggcagcg accaccttta gcggagaacc tgaccgtcaa 1620

gccatgcaaa acacgctggc ttttagcagg accgtctacg atcaaacgac cgccacgacc 1680

gatcgtaacc agatactcat caccaacgaa gacgaaatca gacccaccaa ctcggtcggt 1740

atcgacgcgt ggggagcagt tcccaccaac aaccagtcga tcgtgacccc cggcactcgc 1800

gcggccgtca acaatcaagg ggcgcttccc gggatggtgt ggcaaaacag agacatttac 1860

cctacaggga cccatttggc caaaattccc gacactgaca atcacttcca tccgtccccg 1920

cttattgggc ggtttggctg caagcatccc cctccccaga ttttcattaa aaacacaccc 1980

gtccctgcca acccttcgga aacgttccag acggccaaag tggcctcctt catcaaccag 2040

tactcgaccg gacagtgcac cgtcgaaatc ttttgggaac tcaagaagga aacctccaag 2100

cgctggaacc ccgaaatcca gttcacctcc aactttggca acgcggccga catccagttt 2160

gccgtctccg acacgggatc ctattccgaa cctcgtccca tcggtacccg ttaccttacc 2220

aaacctctgt aa 2232

<210> 538
<211> 535
<212> PRT
<213> Artificial Sequence

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

<400> 538

Met Ala Glu Gly Gly Gly Gly Pro Val Gly Asp Ala Gly Gln Gly Ala
1 5 10 15

Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp
20 25 30

Leu Glu Asn Gly Val Val Thr Arg Thr Thr Arg Thr Trp Val Leu Pro
35 40 45

```
Ser Tyr Asn Asn His Leu Tyr Lys Arg Ile Gln Gly Pro Ser Gly Gly
    50                  55                  60

Asp Asn Asn Asn Lys Phe Phe Gly Phe Ser Thr Pro Trp Gly Tyr Phe
65                  70                  75                  80

Asp Tyr Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg
                85                  90                  95

Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Ala Met Arg Phe Arg
            100                 105                 110

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

Thr Ile Gly Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp Lys
    130                 135                 140

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

Pro Pro Phe Pro Ala Asp Ile Tyr Thr Ile Pro Gln Tyr Gly Tyr Cys
                165                 170                 175

Thr Leu Asn Tyr Asn Asn Glu Ala Val Asp Arg Ser Ala Phe Tyr Cys
            180                 185                 190

Leu Asp Tyr Phe Pro Ser Asp Met Leu Arg Thr Gly Asn Asn Phe Glu
        195                 200                 205

Phe Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Met Phe Ala His
    210                 215                 220

Asn Gln Thr Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu
225                 230                 235                 240

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

His Tyr Ser Arg Ala Thr Lys Thr Asn Met Ala Ala Gln Tyr Arg Asn
            260                 265                 270
```

```
Trp Leu Pro Gly Pro Phe Phe Arg Asp Gln Gln Ile Phe Thr Gly Ala
        275                 280                 285

Ser Asn Ile Thr Lys Asn Asn Val Phe Ser Val Trp Glu Lys Gly Lys
    290                 295                 300

Gln Trp Glu Leu Asp Asn Arg Thr Asn Leu Met Gln Pro Gly Pro Ala
305                 310                 315                 320

Ala Ala Thr Thr Phe Ser Gly Glu Pro Asp Arg Gln Ala Met Gln Asn
                325                 330                 335

Thr Leu Ala Phe Ser Arg Thr Val Tyr Asp Gln Thr Thr Ala Thr Thr
            340                 345                 350

Asp Arg Asn Gln Ile Leu Ile Thr Asn Glu Asp Glu Ile Arg Pro Thr
        355                 360                 365

Asn Ser Val Gly Ile Asp Ala Trp Gly Ala Val Pro Thr Asn Asn Gln
    370                 375                 380

Ser Ile Val Thr Pro Gly Thr Arg Ala Ala Val Asn Asn Gln Gly Ala
385                 390                 395                 400

Leu Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Pro Thr Gly Thr
                405                 410                 415

His Leu Ala Lys Ile Pro Asp Thr Asp Asn His Phe His Pro Ser Pro
            420                 425                 430

Leu Ile Gly Arg Phe Gly Cys Lys His Pro Pro Pro Gln Ile Phe Ile
        435                 440                 445

Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Glu Thr Phe Gln Thr Ala
    450                 455                 460

Lys Val Ala Ser Phe Ile Asn Gln Tyr Ser Thr Gly Gln Cys Thr Val
465                 470                 475                 480
```

Glu Ile Phe Trp Glu Leu Lys Lys Glu Thr Ser Lys Arg Trp Asn Pro
485 490 495

Glu Ile Gln Phe Thr Ser Asn Phe Gly Asn Ala Ala Asp Ile Gln Phe
500 505 510

Ala Val Ser Asp Thr Gly Ser Tyr Ser Glu Pro Arg Pro Ile Gly Thr
515 520 525

Arg Tyr Leu Thr Lys Pro Leu
530 535

<210> 539
<211> 440
<212> PRT
<213> Artificial Sequence

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

<400> 539

Met Glu Leu Val Asp Trp Leu Val Glu Lys Gly Ile Thr Thr Glu Lys
1 5 10 15

Glu Trp Leu Leu Glu Asn Arg Glu Ser Phe Arg Ser Phe Gln Ala Ser
20 25 30

Ser Asn Ser Ala Arg Gln Ile Lys Thr Ala Leu Gln Gly Ala Ile Gln
35 40 45

Glu Met Leu Leu Thr Lys Thr Ala Glu Asp Tyr Leu Val Gly Lys Asp
50 55 60

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

Glu Leu Asn His Tyr Asp Pro Ala Tyr Val Gly Ser Ile Leu Val Gly
85 90 95

Trp Cys Gln Lys Lys Trp Gly Lys Arg Asn Thr Leu Trp Leu Phe Gly
100 105 110

```
His Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala
        115                 120                 125


Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe
    130                 135                 140


Asn Asp Cys Val Glu Lys Met Ile Ile Trp Trp Glu Glu Gly Lys Met
145                 150                 155                 160


Thr Ala Lys Val Val Glu Thr Ala Lys Ala Ile Leu Gly Gly Ser Arg
                165                 170                 175


Val Arg Val Asp Gln Lys Cys Lys Ala Ser Val Pro Ile Glu Pro Thr
            180                 185                 190


Pro Val Ile Ile Thr Ser Asn Thr Asn Met Cys Tyr Val Ile Asp Gly
        195                 200                 205


Asn Thr Thr Thr Phe Glu His Lys Gln Pro Leu Glu Asp Arg Met Phe
    210                 215                 220


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


Lys Gln Glu Val Arg Gln Phe Phe Arg Trp Ser Gln Asp His Leu Thr
                245                 250                 255


Pro Val Ile Pro Glu Phe Leu Val Arg Lys Ala Glu Ser Arg Lys Arg
            260                 265                 270


Pro Ala Pro Ser Gly Glu Gly Tyr Ile Ser Pro Thr Lys Arg Pro Ala
        275                 280                 285


Leu Ala Glu Gln Gln Gln Ala Ser Glu Ser Ala Asp Pro Val Pro Thr
    290                 295                 300


Arg Tyr Arg Ile Lys Cys Ser Lys His Cys Gly Met Asp Lys Met Leu
305                 310                 315                 320


Phe Pro Cys Gln Ile Cys Glu Ser Met Asn Arg Asp Ile Asn Ile Cys
                325                 330                 335
```

```
Ala Ile His Lys Thr Thr Asp Cys Lys Glu Cys Phe Pro Asp Tyr Gly
            340                 345                 350

Asp Lys Asp Asp Val Glu Leu Pro Pro Cys Thr Glu His Asn Val Ser
        355                 360                 365

Arg Cys Tyr Gln Cys His Ser Gly Glu Leu Tyr Arg Val Thr Ser Asp
    370                 375                 380

Ser Asp Glu Lys Pro Ala Pro Glu Ser Asp Glu Gly Thr Glu Pro Ser
385                 390                 395                 400

Tyr Ala Pro Cys Thr Ile His His Leu Met Gly Lys Ser His Gly Leu
                405                 410                 415

Val Thr Cys Ala Ala Cys Arg Leu Lys Asn Ser Thr Leu His Asp Asp
            420                 425                 430

Leu Asp Asp Gly Asp Leu Glu Gln
        435                 440
```

<210> 540
<211> 319
<212> PRT
<213> Artificial Sequence

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

<400> 540

```
Met Glu Leu Val Asp Trp Leu Val Glu Lys Gly Ile Thr Thr Glu Lys
1               5                   10                  15

Glu Trp Leu Leu Glu Asn Arg Glu Ser Phe Arg Ser Phe Gln Ala Ser
            20                  25                  30

Ser Asn Ser Ala Arg Gln Ile Lys Thr Ala Leu Gln Gly Ala Ile Gln
        35                  40                  45

Glu Met Leu Leu Thr Lys Thr Ala Glu Asp Tyr Leu Val Gly Lys Asp
    50                  55                  60
```

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

Glu Leu Asn His Tyr Asp Pro Ala Tyr Val Gly Ser Ile Leu Val Gly
                85                  90                  95

Trp Cys Gln Lys Lys Trp Gly Lys Arg Asn Thr Leu Trp Leu Phe Gly
            100                 105                 110

His Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala
        115                 120                 125

Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe
    130                 135                 140

Asn Asp Cys Val Glu Lys Met Ile Ile Trp Trp Glu Glu Gly Lys Met
145                 150                 155                 160

Thr Ala Lys Val Val Glu Thr Ala Lys Ala Ile Leu Gly Gly Ser Arg
                165                 170                 175

Val Arg Val Asp Gln Lys Cys Lys Ala Ser Val Pro Ile Glu Pro Thr
            180                 185                 190

Pro Val Ile Ile Thr Ser Asn Thr Asn Met Cys Tyr Val Ile Asp Gly
        195                 200                 205

Asn Thr Thr Thr Phe Glu His Lys Gln Pro Leu Glu Asp Arg Met Phe
    210                 215                 220

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

Lys Gln Glu Val Arg Gln Phe Phe Arg Trp Ser Gln Asp His Leu Thr
                245                 250                 255

Pro Val Ile Pro Glu Phe Leu Val Arg Lys Ala Glu Ser Arg Lys Arg
            260                 265                 270
```

Pro Ala Pro Ser Gly Glu Gly Tyr Ile Ser Pro Thr Lys Arg Pro Ala
        275   280   285

Leu Ala Glu Gln Gln Gln Ala Ser Glu Ser Ala Asp Pro Val Pro Thr
    290   295   300

Arg Leu Val Gly Ala Val Gly Gln Lys Gly Ser Glu Cys Cys Ser
305   310   315

<210> 541
<211> 662
<212> PRT
<213> Artificial Sequence

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

<400> 541

Met Arg Ser Tyr Tyr Glu Val Ile Val Gln Leu Pro Asn Asp Val Glu
1   5   10   15

Ser Gln Val Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Ile Thr Ser
            20   25   30

Arg Glu Trp Thr Leu Pro Glu Asp Ala Asp Trp Asp Leu Asp Gln Val
        35   40   45

Asp Gln Val Gln Leu Thr Leu Gly Asp Lys Ile Gln Arg Glu Ile Arg
    50   55   60

Thr His Trp Gly Thr Met Ala Lys Glu Pro Asp Phe His Tyr Phe Ile
65   70   75   80

Gln Leu Glu Gln Gly Glu Val Phe Phe His Leu His Val Leu Leu Glu
                85   90   95

Thr Cys Ser Val Lys Pro Met Val Leu Gly Arg Tyr Ile Arg His Ile
            100   105   110

Gln Gln Lys Ile Val Ser Lys Val Tyr Cys Ala Thr Ser Leu Arg Trp
        115   120   125

```
Lys Asp Gly Cys Val Val Thr Lys Thr Lys Asn Phe Gly Gly Ala Asn
    130                 135                 140

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

Gln Pro Glu Val Gln Trp Ala Trp Thr Asn Val Pro Glu Tyr Ile Lys
                165                 170                 175

Ala Cys Leu His Arg Glu Leu Arg Ala Ser Leu Ala Arg Leu His Phe
            180                 185                 190

Glu Glu Ala Gly Val Ser Gln Ser Lys Glu Asn Leu Ala Arg Thr Ala
        195                 200                 205

Asp Gly Ala Pro Val Met Pro Thr Arg Val Ser Lys Arg Tyr Met Glu
    210                 215                 220

Leu Val Asp Trp Leu Val Glu Lys Gly Ile Thr Thr Glu Lys Glu Trp
225                 230                 235                 240

Leu Leu Glu Asn Arg Glu Ser Phe Arg Ser Phe Gln Ala Ser Ser Asn
                245                 250                 255

Ser Ala Arg Gln Ile Lys Thr Ala Leu Gln Gly Ala Ile Gln Glu Met
            260                 265                 270

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

Ser Asp Asp Asp Ile Arg Gln Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290                 295                 300

Asn His Tyr Asp Pro Ala Tyr Val Gly Ser Ile Leu Val Gly Trp Cys
305                 310                 315                 320

Gln Lys Lys Trp Gly Lys Arg Asn Thr Leu Trp Leu Phe Gly His Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350
```

```
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Glu Lys Met Ile Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Thr Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ala Ser Val Pro Ile Glu Pro Thr Pro Val
                405                 410                 415

Ile Ile Thr Ser Asn Thr Asn Met Cys Tyr Val Ile Asp Gly Asn Thr
            420                 425                 430

Thr Thr Phe Glu His Lys Gln Pro Leu Glu Asp Arg Met Phe Lys Leu
        435                 440                 445

Glu Leu Leu Thr Arg Leu Pro Asp Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Arg Gln Phe Phe Arg Trp Ser Gln Asp His Leu Thr Pro Val
465                 470                 475                 480

Ile Pro Glu Phe Leu Val Arg Lys Ala Glu Ser Arg Lys Arg Pro Ala
                485                 490                 495

Pro Ser Gly Glu Gly Tyr Ile Ser Pro Thr Lys Arg Pro Ala Leu Ala
            500                 505                 510

Glu Gln Gln Gln Ala Ser Glu Ser Ala Asp Pro Val Pro Thr Arg Tyr
        515                 520                 525

Arg Ile Lys Cys Ser Lys His Cys Gly Met Asp Lys Met Leu Phe Pro
    530                 535                 540

Cys Gln Ile Cys Glu Ser Met Asn Arg Asp Ile Asn Ile Cys Ala Ile
545                 550                 555                 560
```

```
His Lys Thr Thr Asp Cys Lys Glu Cys Phe Pro Asp Tyr Gly Asp Lys
                565                 570                 575


Asp Asp Val Glu Leu Pro Pro Cys Thr Glu His Asn Val Ser Arg Cys
            580                 585                 590


Tyr Gln Cys His Ser Gly Glu Leu Tyr Arg Val Thr Ser Asp Ser Asp
        595                 600                 605


Glu Lys Pro Ala Pro Glu Ser Asp Glu Gly Thr Glu Pro Ser Tyr Ala
    610                 615                 620


Pro Cys Thr Ile His His Leu Met Gly Lys Ser His Gly Leu Val Thr
625                 630                 635                 640


Cys Ala Ala Cys Arg Leu Lys Asn Ser Thr Leu His Asp Asp Leu Asp
                645                 650                 655


Asp Gly Asp Leu Glu Gln
            660
```

<210> 542
<211> 541
<212> PRT
<213> Artificial Sequence

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

<400> 542

```
Met Arg Ser Tyr Tyr Glu Val Ile Val Gln Leu Pro Asn Asp Val Glu
1               5                   10                  15


Ser Gln Val Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Ile Thr Ser
            20                  25                  30


Arg Glu Trp Thr Leu Pro Glu Asp Ala Asp Trp Asp Leu Asp Gln Val
        35                  40                  45


Asp Gln Val Gln Leu Thr Leu Gly Asp Lys Ile Gln Arg Glu Ile Arg
    50                  55                  60
```

```
Thr His Trp Gly Thr Met Ala Lys Glu Pro Asp Phe His Tyr Phe Ile
65                  70                  75                  80

Gln Leu Glu Gln Gly Glu Val Phe Phe His Leu His Val Leu Leu Glu
                85                  90                  95

Thr Cys Ser Val Lys Pro Met Val Leu Gly Arg Tyr Ile Arg His Ile
            100                 105                 110

Gln Gln Lys Ile Val Ser Lys Val Tyr Cys Ala Thr Ser Leu Arg Trp
        115                 120                 125

Lys Asp Gly Cys Val Val Thr Lys Thr Lys Asn Phe Gly Gly Ala Asn
    130                 135                 140

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

Gln Pro Glu Val Gln Trp Ala Trp Thr Asn Val Pro Glu Tyr Ile Lys
                165                 170                 175

Ala Cys Leu His Arg Glu Leu Arg Ala Ser Leu Ala Arg Leu His Phe
            180                 185                 190

Glu Glu Ala Gly Val Ser Gln Ser Lys Glu Asn Leu Ala Arg Thr Ala
        195                 200                 205

Asp Gly Ala Pro Val Met Pro Thr Arg Val Ser Lys Arg Tyr Met Glu
    210                 215                 220

Leu Val Asp Trp Leu Val Glu Lys Gly Ile Thr Thr Glu Lys Glu Trp
225                 230                 235                 240

Leu Leu Glu Asn Arg Glu Ser Phe Arg Ser Phe Gln Ala Ser Ser Asn
                245                 250                 255

Ser Ala Arg Gln Ile Lys Thr Ala Leu Gln Gly Ala Ile Gln Glu Met
            260                 265                 270

Leu Leu Thr Lys Thr Ala Glu Asp Tyr Leu Val Gly Lys Asp Pro Val
        275                 280                 285
```

```
Ser Asp Asp Asp Ile Arg Gln Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290                 295                 300

Asn His Tyr Asp Pro Ala Tyr Val Gly Ser Ile Leu Val Gly Trp Cys
305                 310                 315                 320

Gln Lys Lys Trp Gly Lys Arg Asn Thr Leu Trp Leu Phe Gly His Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Glu Lys Met Ile Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Thr Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ala Ser Val Pro Ile Glu Pro Thr Pro Val
                405                 410                 415

Ile Ile Thr Ser Asn Thr Asn Met Cys Tyr Val Ile Asp Gly Asn Thr
            420                 425                 430

Thr Thr Phe Glu His Lys Gln Pro Leu Glu Asp Arg Met Phe Lys Leu
        435                 440                 445

Glu Leu Leu Thr Arg Leu Pro Asp Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Arg Gln Phe Phe Arg Trp Ser Gln Asp His Leu Thr Pro Val
465                 470                 475                 480

Ile Pro Glu Phe Leu Val Arg Lys Ala Glu Ser Arg Lys Arg Pro Ala
                485                 490                 495
```

Pro Ser Gly Glu Gly Tyr Ile Ser Pro Thr Lys Arg Pro Ala Leu Ala
500 505 510

Glu Gln Gln Gln Ala Ser Glu Ser Ala Asp Pro Val Pro Thr Arg Leu
515 520 525

Val Gly Ala Val Gly Gln Lys Gly Ser Glu Cys Cys Ser
530 535 540

<210> 543
<211> 743
<212> PRT
<213> Artificial Sequence

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

<400> 543

Met Ser Leu Ile Ser Asp Ala Ile Pro Asp Trp Leu Glu Arg Leu Val
1 5 10 15

Lys Lys Gly Val Asn Ala Ala Ala Asp Phe Tyr His Leu Glu Ser Gly
20 25 30

Pro Pro Arg Pro Lys Ala Asn Gln Gln Thr Gln Glu Ser Leu Glu Lys
35 40 45

Asp Asp Ser Arg Gly Leu Val Phe Pro Gly Tyr Asn Tyr Leu Gly Pro
50 55 60

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

Ala Leu Glu His Asp Lys Ala Tyr Asp Leu Glu Ile Lys Asp Gly His
85 90 95

Asn Pro Tyr Phe Glu Tyr Asn Glu Ala Asp Arg Arg Phe Gln Glu Arg
100 105 110

Leu Lys Asp Asp Thr Ser Phe Gly Gly Asn Leu Gly Lys Ala Ile Phe
115 120 125

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

Lys Thr Ala Pro Thr Gly Asp Lys Arg Lys Gly Glu Asp Glu Pro Arg
145                 150                 155                 160

Leu Pro Asp Thr Ser Ser Gln Thr Pro Lys Lys Asn Lys Lys Pro Arg
                165                 170                 175

Lys Glu Arg Pro Ser Gly Gly Ala Glu Asp Pro Gly Glu Gly Thr Ser
            180                 185                 190

Ser Asn Ala Gly Ala Ala Ala Pro Ala Ser Ser Val Gly Ser Ser Ile
        195                 200                 205

Met Ala Glu Gly Gly Gly Gly Pro Val Gly Asp Ala Gly Gln Gly Ala
    210                 215                 220

Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp
225                 230                 235                 240

Leu Glu Asn Gly Val Val Thr Arg Thr Thr Arg Thr Trp Val Leu Pro
                245                 250                 255

Ser Tyr Asn Asn His Leu Tyr Lys Arg Ile Gln Gly Pro Ser Gly Gly
            260                 265                 270

Asp Asn Asn Asn Lys Phe Phe Gly Phe Ser Thr Pro Trp Gly Tyr Phe
        275                 280                 285

Asp Tyr Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg
    290                 295                 300

Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Ala Met Arg Phe Arg
305                 310                 315                 320

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

Thr Ile Gly Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp Lys
            340                 345                 350
```

```
Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala Thr Glu Gly Thr Phe
        355                 360                 365

Pro Pro Phe Pro Ala Asp Ile Tyr Thr Ile Pro Gln Tyr Gly Tyr Cys
    370                 375                 380

Thr Leu Asn Tyr Asn Asn Glu Ala Val Asp Arg Ser Ala Phe Tyr Cys
385                 390                 395                 400

Leu Asp Tyr Phe Pro Ser Asp Met Leu Arg Thr Gly Asn Asn Phe Glu
                405                 410                 415

Phe Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Met Phe Ala His
            420                 425                 430

Asn Gln Thr Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu
        435                 440                 445

Trp Ala Phe Ser Ser Val Ser Gln Ala Gly Ser Ser Gly Arg Ala Leu
    450                 455                 460

His Tyr Ser Arg Ala Thr Lys Thr Asn Met Ala Ala Gln Tyr Arg Asn
465                 470                 475                 480

Trp Leu Pro Gly Pro Phe Phe Arg Asp Gln Gln Ile Phe Thr Gly Ala
                485                 490                 495

Ser Asn Ile Thr Lys Asn Asn Val Phe Ser Val Trp Glu Lys Gly Lys
            500                 505                 510

Gln Trp Glu Leu Asp Asn Arg Thr Asn Leu Met Gln Pro Gly Pro Ala
        515                 520                 525

Ala Ala Thr Thr Phe Ser Gly Glu Pro Asp Arg Gln Ala Met Gln Asn
    530                 535                 540

Thr Leu Ala Phe Ser Arg Thr Val Tyr Asp Gln Thr Thr Ala Thr Thr
545                 550                 555                 560
```

```
Asp Arg Asn Gln Ile Leu Ile Thr Asn Glu Asp Glu Ile Arg Pro Thr
                565                 570                 575

Asn Ser Val Gly Ile Asp Ala Trp Gly Ala Val Pro Thr Asn Asn Gln
            580                 585                 590

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

Leu Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Pro Thr Gly Thr
    610                 615                 620

His Leu Ala Lys Ile Pro Asp Thr Asp Asn His Phe His Pro Ser Pro
625                 630                 635                 640

Leu Ile Gly Arg Phe Gly Cys Lys His Pro Pro Pro Gln Ile Phe Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Glu Thr Phe Gln Thr Ala
            660                 665                 670

Lys Val Ala Ser Phe Ile Asn Gln Tyr Ser Thr Gly Gln Cys Thr Val
        675                 680                 685

Glu Ile Phe Trp Glu Leu Lys Lys Glu Thr Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Phe Thr Ser Asn Phe Gly Asn Ala Ala Asp Ile Gln Phe
705                 710                 715                 720

Ala Val Ser Asp Thr Gly Ser Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735

Arg Tyr Leu Thr Lys Pro Leu
            740
```

<210> 544
<211> 598
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 544

```
Thr Ala Pro Thr Gly Asp Lys Arg Lys Gly Glu Asp Glu Pro Arg Leu
1               5                  10                  15


Pro Asp Thr Ser Ser Gln Thr Pro Lys Lys Asn Lys Lys Pro Arg Lys
            20                  25                  30


Glu Arg Pro Ser Gly Gly Ala Glu Asp Pro Gly Glu Gly Thr Ser Ser
        35                  40                  45


Asn Ala Gly Ala Ala Ala Pro Ala Ser Ser Val Gly Ser Ser Ile Met
    50                  55                  60


Ala Glu Gly Gly Gly Gly Pro Val Gly Asp Ala Gly Gln Gly Ala Asp
65                  70                  75                  80


Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu
                85                  90                  95


Glu Asn Gly Val Val Thr Arg Thr Thr Arg Thr Trp Val Leu Pro Ser
            100                 105                 110


Tyr Asn Asn His Leu Tyr Lys Arg Ile Gln Gly Pro Ser Gly Gly Asp
        115                 120                 125


Asn Asn Asn Lys Phe Phe Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp
    130                 135                 140


Tyr Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu
145                 150                 155                 160


Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Ala Met Arg Phe Arg Leu
                165                 170                 175


Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Phe Asn Thr Thr
            180                 185                 190


Ile Gly Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp Lys Asp
        195                 200                 205
```

```
Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala Thr Glu Gly Thr Phe Pro
    210                 215                 220

Pro Phe Pro Ala Asp Ile Tyr Thr Ile Pro Gln Tyr Gly Tyr Cys Thr
225                 230                 235                 240

Leu Asn Tyr Asn Asn Glu Ala Val Asp Arg Ser Ala Phe Tyr Cys Leu
                245                 250                 255

Asp Tyr Phe Pro Ser Asp Met Leu Arg Thr Gly Asn Asn Phe Glu Phe
            260                 265                 270

Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Met Phe Ala His Asn
        275                 280                 285

Gln Thr Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Trp
    290                 295                 300

Ala Phe Ser Ser Val Ser Gln Ala Gly Ser Ser Gly Arg Ala Leu His
305                 310                 315                 320

Tyr Ser Arg Ala Thr Lys Thr Asn Met Ala Ala Gln Tyr Arg Asn Trp
                325                 330                 335

Leu Pro Gly Pro Phe Phe Arg Asp Gln Gln Ile Phe Thr Gly Ala Ser
            340                 345                 350

Asn Ile Thr Lys Asn Asn Val Phe Ser Val Trp Glu Lys Gly Lys Gln
        355                 360                 365

Trp Glu Leu Asp Asn Arg Thr Asn Leu Met Gln Pro Gly Pro Ala Ala
    370                 375                 380

Ala Thr Thr Phe Ser Gly Glu Pro Asp Arg Gln Ala Met Gln Asn Thr
385                 390                 395                 400

Leu Ala Phe Ser Arg Thr Val Tyr Asp Gln Thr Thr Ala Thr Thr Asp
                405                 410                 415
```

```
Arg Asn Gln Ile Leu Ile Thr Asn Glu Asp Glu Ile Arg Pro Thr Asn
            420                 425                 430

Ser Val Gly Ile Asp Ala Trp Gly Ala Val Pro Thr Asn Asn Gln Ser
        435                 440                 445

Ile Val Thr Pro Gly Thr Arg Ala Ala Val Asn Asn Gln Gly Ala Leu
    450                 455                 460

Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Pro Thr Gly Thr His
465                 470                 475                 480

Leu Ala Lys Ile Pro Asp Thr Asp Asn His Phe His Pro Ser Pro Leu
                485                 490                 495

Ile Gly Arg Phe Gly Cys Lys His Pro Pro Pro Gln Ile Phe Ile Lys
            500                 505                 510

Asn Thr Pro Val Pro Ala Asn Pro Ser Glu Thr Phe Gln Thr Ala Lys
        515                 520                 525

Val Ala Ser Phe Ile Asn Gln Tyr Ser Thr Gly Gln Cys Thr Val Glu
    530                 535                 540

Ile Phe Trp Glu Leu Lys Lys Glu Thr Ser Lys Arg Trp Asn Pro Glu
545                 550                 555                 560

Ile Gln Phe Thr Ser Asn Phe Gly Asn Ala Ala Asp Ile Gln Phe Ala
                565                 570                 575

Val Ser Asp Thr Gly Ser Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg
            580                 585                 590

Tyr Leu Thr Lys Pro Leu
        595
```

<210> 545
<211> 4694
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 545
tggccagttt ccaagacagg ctcgctcgct cactcgggcc ggggccccaa aggggcccct 60

agcgaccgct tcgcggtcgc ggcccgagtg agcgagcgag cctgtcttgg aaactggcca 120

gcactccggt gaggtaatgc cgtcacgtgg tcgggaatgg gaacgggaaa tctcgcgaga 180

acgtaaacaa atataagacg gcgccacacg gcgctgcgtc atacgcgcgc gcgcaccggc 240

gagatgaggt cgtactacga ggtcatcgtt cagctgccca acgacgtcga gagtcaggta 300

cctggaatct ccgattcgtt cgtcaactgg attacgtcgc gagaatggac gttgcctgag 360

gacgccgatt gggatttgga ccaggtcgat caagttcaac tgacgctcgg cgacaaaatc 420

caacgggaga ttcgaactca ttgggggacg atggccaaag aaccggactt tcactatttt 480

atccaactgg aacaaggtga ggtgttcttt catttacacg tcctgctgga aacgtgttcc 540

gtaaagccga tggtactcgg aagatatatc cgacatattc aacaaaaaat tgtgagtaaa 600

gtctactgcg ccacgagcct acgatggaag gatggatgcg tggtgaccaa gaccaaaaat 660

ttcgggggcg cgaacaaggt ccgggccgag tcgtatattc ccgcctacct gatcccgaaa 720

cagcaaccgg aagtgcagtg ggcgtggact aacgtgcccg agtatataaa agcgtgcttg 780

caccgagaac tgcgtgccag tctcgcgcga cttcacttcg aggaggcggg cgtctcgcaa 840

tccaaggaaa atctcgcgag aactgcagac ggcgctcccg tgatgccgac ccgcgtcagc 900

aaacgctaca tggagctcgt ggattggctc gtggagaagg ggatcaccac cgagaaggaa 960

tggctgctgg aaaacagaga aagctttcgg agctttcagg cctcgagcaa ctcggcgcgt 1020

cagatcaaga cggccctgca aggcgccatt caggagatgc ttctgaccaa gacggcggag 1080

gactacctcg tcggaaagga tcccgtctcg gacgacgaca tccgtcagaa ccgcatctac 1140

aagattctgg aactgaacca ctacgaccca gcgtacgtgg ggagtatttt ggtcgggtgg 1200

tgccagaaga aatggggcaa gcgaaacacg ctgtggctgt tcggacatgc gaccaccggc 1260

aagaccaaca tcgcggaggc tattgcccat gctgtgccgt tctatggatg cgttaactgg 1320

accaacgaga actttccgtt caacgactgc gtcgaaaaaa tgattatctg gtgggaggag 1380

ggcaaaatga ccgccaaagt ggtggaaaca gccaaggcga ttctgggagg atctcgggtg 1440

agagtggacc aaaaatgcaa agcttcggtt ccgatcgaac cgacgccggt cattattacc 1500

agtaacacca acatgtgtta tgtcatcgac gggaacacga ccacgttcga gcataagcag 1560

ccgttggagg acaggatgtt taagctcgaa ttgctgactc ggttgcctga tgactttggt 1620

aaggtgacca aacaggaggt gcgtcaattc ttcaggtggt ctcaggatca cctgaccct 1680

gtgatcccag aattcctagt gcggaaggcg gagtctcgca aaagacccgc cccttccggg 1740

gaaggctata taagcccgac aaagcggccc gcgctcgcag agcagcagca ggcgtcggag 1800

agcgcggacc cggttcccac caggtatcgt atcaaatgct cgaaacattg cggtatggat 1860

aaaatgttgt ttccttgcca aatttgtgaa tcgatgaaca gagatattaa tatttgtgct 1920

attcataaaa cgaccgactg taaagagtgt ttccccgact acggggataa agatgatgta 1980

gaactacccc cctgtacaga acacaacgtg tctcgttgtt atcaatgtca ttcgggcgaa 2040

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gagccatcct atgctccctg cacgattcac cacctgatgg gcaagagtca cgggttagtc 2160

acttgcgcgg cgtgtcggtt gaaaaatagt acgttgcatg atgacttgga tgacggtgat 2220

ctcgaacaat aaatgattga aatgtagcca tgtctctcat ttctgatgcg attccagatt 2280

ggttggagcg gttggtcaaa aagggagtga atgctgcagc tgatttctac catttggaaa 2340

gcggtcctcc tcgtcctaag gcaaatcagc aaactcaaga atctcttgaa aaggacgatt 2400

cgagaggtct cgtgttccca ggctacaatt atctaggccc tttcaacggt ctagataaag 2460

gagaacccgt caacgaggca gacgctgccg ccttagaaca cgacaaggct tacgacctcg 2520

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gaacctgggt cttgcccagc tacaacaacc acctgtacaa acgaatccaa ggacccagcg 3060

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atcgattcca ctgccacttt tccccgcgag actggcaacg actcatcaac aacaactggg 3180

gcatccgtcc caaagcgatg cgctttagac tctttaacat ccaggttaaa gaggtcacgg 3240

tccaagactt caacaccacc atcggcaaca acctcaccag tacggtccag gtctttgcgg 3300

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aaatctttac gggcgctagc aacatcacta aaaataacgt ctttagcgtt tgggaaaaag 3780

gcaagcaatg ggaactcgac aatcggacca acctaatgca gcccggtcct gcggcagcga 3840

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ggatggtgtg gcaaaacaga gacatttacc ctacagggac ccatttggcc aaaattcccg 4140

acactgacaa tcacttccat ccgtccccgc ttattgggcg gtttggctgc aagcatcccc 4200

ctccccagat tttcattaaa aacacacccg tccctgccaa cccttcggaa acgttccaga 4260

cggccaaagt ggcctccttc atcaaccagt actcgaccgg acagtgcacc gtcgaaatct 4320

tttgggaact caagaaggaa acctccaagc gctggaaccc cgaaatccag ttcacctcca 4380

actttggcaa cgcggccgac atccagtttg ccgtctccga cacgggatcc tattccgaac 4440

ctcgtcccat cggtacccgt taccttacca aacctctgta aattaaaccc ttcaataaac 4500

cgtttatgcg taactgtatt tccgtctcct gtcgttattc agtcacatga tgcggcatta 4560

cctcaccgga gtgctggcca gtttccaaga caggctcgct cgctcactcg ggccggggcc 4620

ccaaaggggc ccctagcgac cgcttcgcgg tcgcggcccg agtgagcgag cgagcctgtc 4680

ttggaaactg gcca 4694

<210> 546
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 546
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgcggagttc 300

cagcagcggc ttcagggcga cacatcgttt gggggcaacc tcggcagagc agtcttccag 360

gccaaaaaga gggttcttga acctcttggt ctggttgagc aagcgggtga gacggctcct 420

ggaaagaaga gaccgttgat tgaatccccc cagcagcccg actcctccac gggtatcggc 480

aaaaaaggca agcagccggc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

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ggctgcctcc cgccgttccc agcagacgtc ttcatggtgc cacagtatgg atacctcacc 1140

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ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

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gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 547
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 547

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

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Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

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

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 548
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 548
atggcttccg atggttatct tccagattgg ctcgaggaca acctctctga gggcatccgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca gagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

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gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attctactgg ccaagtcagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgtcccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 549
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 549

Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Arg Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460
```

```
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
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<210> 550
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 550

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atggctgctg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgcggagttc      300

cagcagcggc ttcagggcga cacatcgttt gggggcaacc tcggcagagc agtcttccag      360

gccaaaaaga gggttcttga acctcttggt ctggttgagc aagcgggtga gacggctcct      420

ggaaagaaga gaccgttgat tgaatccccc cagcagcccg actcctccac gggtatcggc      480

aaaaaaggca agcagccggc taaaaagaga ctcaattttg gtcagactgg cgactcagag      540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct      600

actacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga      660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc      720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc      780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg       840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc      900
```

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc cgccgttccc agcagacgtc ttcatggtgc cacagtatgg atacctcacc 1140

ctgaacaacg ggagtcaggc agtaggacgc tcttcatttt actgcctgga gtactttcct 1200

tctcagatgc tgcgtaccgg aaacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccaactggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ctgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgccatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 551
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 551

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

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

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Thr Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 552
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 552
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcaatcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt cgacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgat 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca taaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac attgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtccccagta a 2211

<210> 553
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 553

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

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

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

```
Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Ile Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Gln
                725                 730                 735
```

<210> 554
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 554
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac cttcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga gggttctcga acctctcggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt accggcagca gtgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 555
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 555

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
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Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Cys Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575
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Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 556
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 556
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gaatggtggg acttgaaacc tggagccccg aaacccaaag tcaaccagca aaagcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac cttcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggacgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccaactggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ctgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgccatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 557
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 557

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
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Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Thr Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

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Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
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<210> 558
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (955)..(955)
<223> n is a, c, t, or g

<220>
<221> misc_feature
<222> (971)..(972)
<223> n is a, c, t, or g

<220>
<221> misc_feature
<222> (981)..(981)
<223> n is a, c, t, or g

<220>
<221> misc_feature
<222> (986)..(986)
<223> n is a, c, t, or g

<220>
<221> misc_feature
<222> (1235)..(1235)
<223> n is a, c, t, or g

<220>
<221> misc_feature
<222> (1694)..(1696)
<223> n is a, c, t, or g

<220>
<221> misc_feature
<222> (1698)..(1698)
<223> n is a, c, t, or g

<220>
<221> misc_feature
<222> (1763)..(1765)
<223> n is a, c, t, or g

<220>
<221> misc_feature
<222> (1778)..(1778)
<223> n is a, c, t, or g

<220>
<221> misc_feature
<222> (2204)..(2204)
<223> n is a, c, t, or g

<400> 558

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gaatggtggg acttgaaacc tggagccccg aaacccaaag tcaaccagca aaagcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac cttcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggacgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaataaca attggggatt ccggcccaag agactcaact tcaaactctt caacntccaa 960

gtcaaggagg nnacgacgaa ngatgncgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt acctncagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccaactggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag agannncnaa gccactaacc ccgtggccac tgaaagattt gggactgtgg 1740

cagtcaatct ccaagcagca cannnaccct gcgaccgnag atgtgcatgc catgggagcc 1800

ttacctggaa tggtgtggca agacagagac gtatacctgc agggtcctat ttgggccaaa 1860

attcctcaca cggatggaca ctttcacccg tctcctctca tgggcggctt tggacttaag 1920

cacccgcctc ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcagag 1980

ttttcggcta caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg 2040

gagattgaat gggagctgca gaaagaaaac agcaaacgct ggaatcccga agtgcagtat 2100

acatctaact atgcaaaatc tgccaacgtt gatttcactg tggacaacaa tggactttat 2160

actgagcctc gccccattgg cacccgttac ctcacccgtc cccngtaa 2208

<210> 559
<211> 723
<212> PRT
<213> Artificial Sequence

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

<400> 559

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

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Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Gln Val
```

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305                 310                 315                 320

Lys Glu Thr Thr Asp Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Thr Ser Tyr Thr Phe Glu Asp Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser
        435                 440                 445

Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Thr
    450                 455                 460

Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe
                485                 490                 495

Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile
            500                 505                 510

Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys
        515                 520                 525
```

Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly
    530   535   540

Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile Thr Asp Glu Glu Ala
545   550   555   560

Thr Asn Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Leu
                565   570   575

Gln Ser Ser Pro Ala Thr Asp Val His Ala Met Gly Ala Leu Pro Gly
            580   585   590

Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
        595   600   605

Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly
    610   615   620

Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr
625   630   635   640

Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala
                645   650   655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu
            660   665   670

Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln
        675   680   685

Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp
    690   695   700

Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu
705   710   715   720

Thr Arg Pro

<210> 560

<211> 2208
<212> DNA
<213> Artificial Sequence

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

<400> 560
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctatgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggtc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaagttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggtaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacagacgct ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca agtgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga agttcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 561
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 561

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
```

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        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Lys Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asp Ala Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Ser Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
```

705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 562
<211> 2208
<212> DNA
<213> Artificial Sequence

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

<400> 562
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctatgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcaaac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaagttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcgggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggtaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacagacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca agtgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac gaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga agttcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

acagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 563
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 563

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asn Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
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                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Lys Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Arg Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asp Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
```

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Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Ser Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
```

675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 564
<211> 2211
<212> DNA
<213> Artificial Sequence

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

<400> 564
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt cgacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaata actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgat 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acggacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcactcaat actccacagg acaagtgagc 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 565
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 565

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

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                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 566
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 566

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
```

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                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Lys Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asp Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asn Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
```

```
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Ser Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Gln
                725                 730                 735
```

<210> 567
<211> 2208
<212> DNA
<213> Artificial Sequence

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

<400> 567
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctatgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggaacgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaagttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggtaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacagacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cggaaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca agtgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga agttcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atcagtaa 2208

<210> 568
<211> 2208
<212> DNA
<213> Artificial Sequence

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

<400> 568
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctatgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg atccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaagttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtatgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggtaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacagacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca agtgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga agttcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 569
<211> 735
<212> PRT
<213> Artificial Sequence

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

<400> 569

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly

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145                 150                 155                 160

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

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Lys Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
```

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Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asp Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Ser Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
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580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 570
<211> 2601
<212> DNA
<213> Artificial Sequence

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

<400> 570
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atgactgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aaggggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctgggggа cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcaactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctggagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 571
<211> 2601
<212> DNA
<213> Artificial Sequence

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

<400> 571
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aaggggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

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cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

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gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacgggcgg 2220

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gtctaataat gttgaatttg ctgttaatac tggaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 572
<211> 2601
<212> DNA
<213> Artificial Sequence

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

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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

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gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

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gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

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gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 573
<211> 2601
<212> DNA
<213> Artificial Sequence

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

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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aaggggggagc cggtcaacgc 540

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caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcctccag gccaaaaaga ggcttcttga 720

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gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

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gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 574

<211> 2601
<212> DNA
<213> Artificial Sequence

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

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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

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gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

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caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

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cgtttcagtt gaactgcggc c 2601

<210> 575
<211> 2601
<212> DNA
<213> Artificial Sequence

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

<400> 575
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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

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gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

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gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 576
<211> 2601
<212> DNA
<213> Artificial Sequence

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

<400> 576
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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

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tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctgggggа cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

atttcggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

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aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 577
<211> 2580
<212> DNA
<213> Artificial Sequence

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

<400> 577
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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aaggggggagc cggtcaacgc 540

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caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

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gcagtctcct cgggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

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cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

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aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

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gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggaact 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

<210> 578
<211> 2601
<212> DNA
<213> Artificial Sequence

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

<400> 578
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tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aaggggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtctttcag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcatgtgg 960

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cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

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aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

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ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

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gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 579
<211> 2601
<212> DNA
<213> Artificial Sequence

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

<400> 579
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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aaggggggagc cgatcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

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cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

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caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

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ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacgtacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 580
<211> 2601
<212> DNA
<213> Artificial Sequence

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

<400> 580

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tctcgccacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

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caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

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gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 581
<211> 2601
<212> DNA
<213> Artificial Sequence

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

<400> 581
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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

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caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

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acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

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<210> 582
<211> 2601
<212> DNA
<213> Artificial Sequence

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

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tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

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gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

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cgtttcagtt gaactgcggc c 2601

<210> 583
<211> 2601
<212> DNA
<213> Artificial Sequence

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

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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aaggggggagc cggtcaacgc 540

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caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

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cgtttcagtt gaactgcggc c 2601

<210> 584
<211> 2601
<212> DNA
<213> Artificial Sequence

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

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tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

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tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

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cgtttcagtt gaactgcggc c 2601

<210> 585
<211> 2601
<212> DNA
<213> Artificial Sequence

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

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gatgtctgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

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cgtttcagtt gaactgcggc c 2601

<210> 586
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 586

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1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro

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Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Gln Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
```

```
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 587
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 587

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
```

```
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Gly Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Gly Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 588
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 588

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Asp
145   150   155   160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly

```
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
```

625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 589
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 589

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Leu Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Ser Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
```

```
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 590
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 590

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
```

```
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Lys Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  591
<211>  736
<212>  PRT
<213>  Artificial Sequence

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

<400>  591

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
               245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Arg Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 592
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 592

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Val Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
```

```
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  593
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide
```

<400> 593

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Arg Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
```

```
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640
```

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 594
<211> 736
<212> PRT
<213> Artificial Sequence

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

<400> 594

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Cys Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
```

```
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 595
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 595

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Ile Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
```

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Tyr Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 596
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 596

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro His Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Asn
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
```

```
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Met Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 597
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 597

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
```

```
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
```

```
Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 598
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 598

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

```
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Arg Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  599
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  599

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
```

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
```

```
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 600
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 600

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
```

```
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Ile Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Cys Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 601
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 601

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
```

```
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480
```

```
Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
```

690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 602
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 602
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttcg gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctgggaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 603
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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aagcacccgc ctcctcagat cctcatcaaa aacgcccctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 604
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 605
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 606
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 606
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcggctca acttcaagct cttcaacatt 960

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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cacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 607

<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaggct cttcaacatt 960

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 608
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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cccagctacc gacaacaacg tgtctcaacc actgtgactc aaaacaacaa cagcgaattt 1500

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cctgctatgg ccagccacaa agaaggagag gaccgtttct ttcctttgtc tggatcttta 1620

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attcctcaca cggacggcaa ctttcaccct tctccgctga tgggagggtt tggaatgaag 1920

cacccgcctc ctcagatcct catcaaaaac acacctgtac ctgcggatcc tccaacggcc 1980

ttcaacaagg acgagctgaa ctctttcatc acccagtatt ctactggcca agtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaagcgct ggaacccgga gatccagtac 2100

acttccaact attacaagtc taataatgtt gaatttgctg ttaatactga aggtgtatat 2160

agtgaacccc gccccattgg caccagatac ctgactcgta atctg 2205

<210> 609
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gacaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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ctcatcaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

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aaattcagtg tggccggacc cagcaacatg gctgtccagg gaagaaacta catacctgga 1440

cccagctacc gacaacaacg tgtctcaacc actgtgactc aaaacaacaa cagcgaattt 1500

gcttggcctg gagcttcttc ttgggctctc aatggacgta atagcttgat gaatcctgga 1560

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cacccgcctc ctcagatcct catcaaaaac acacctgtac ctgcggatcc tccaacggcc 1980

ttcaacaagg acaagctgaa ctctttcatc acccagtatt ctactggcca agtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaagcgct ggaacccgga gatccagtac 2100

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<210> 610
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagccatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 611
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

accaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg gctcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 612
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa tctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 613
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 614
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 615
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 616

<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caagaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 617
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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<222> (1325)..(1325)
<223> n is a, c, t, or g

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 618
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 619
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 620
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

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gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 621
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 621
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taagaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatggtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 622
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 622
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ccggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 623

<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcagccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc aattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaag aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 624
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 624
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac agataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtatcggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtggac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 625
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 626
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

agatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacgggcgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 627
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 627
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gcctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 628
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacaacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcctcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgagatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 629
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg tgcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcacga ttcctcagta cgggtatctg 1140

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tgggccccga tacctgactc gtaatttt 2208

<210> 630
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 630
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgagatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 631
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 631
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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

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ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggcgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcgagct cttcaacatt 960

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acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 632

<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

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ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccccccagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcggaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atactttcgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 633
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 634
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 634
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 635
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcagggcaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 636
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 636
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 637
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaggct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 638
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcggaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggagtg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 639
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 639
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acttacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcaccaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

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tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggagtg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 640
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 640
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttta gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

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ttaatttctg gcaaacaagg aactggaaga gacaacgtgg atgcgaacaa agtcatgata 1680

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttgaaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 641

<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 641
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatag cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcgaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct tttcaacatt 960

cgggtcaaag aggttacgga caacaatgga gtcaagacca tcaccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgcttgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggagtg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 642
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 642
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggcg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

ccagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcgggc gttttcatga ttcctcagta cgggtatctg 1140

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 643
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 643
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag tccctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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ttaatttttg gcaaacaagg agctggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 644
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (377)..(377)
<223> n is a, c, t, or g

<400> 644
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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gccaaaaaga ggcttcntga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcggggaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggagtg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 645
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 645
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

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ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 646
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 646
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccag agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

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tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct ggactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggtgatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 647
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 647
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtggggcct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgtcgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtt acaaccatcg ctaataacct taccagcacg 1020

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ccacaaagct tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 648

<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 648
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagagac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

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atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcgttc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 649
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 649
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ccgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgggg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tcccatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 650
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 650
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacgacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgcgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggcc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acggacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 651
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 651
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cggctcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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caatacctgt attacctgaa cagaactcaa aatcagtccg ggagtgccca aaacaaggac 1380

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aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgacttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 652
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 652
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caagagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccgcaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

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aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 653
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 653
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcaactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccgac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 654
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 654
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caagagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

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actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgacgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 655
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 655
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca agagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

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actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

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atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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aagaacccgc ctcctcagat cctcatcaaa accacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

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tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacga caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 656
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

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ggaaagaaac gtccggtaga gcagtcgcta caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacga caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 657

<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 657
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagctccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagcgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcgaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccgt tggcacccgt taccttaccc gtcccctg 2208

<210> 658
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 658
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccatac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaaa tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg 840

gggtattttg atttcaacag attccactgc cactttccac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgtcgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggtccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 659
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 659
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc acgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgggc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 660
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 660
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg ccccaggaaa ttggcattgc gactccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcacagcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 661
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 661
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cagactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaggaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcgcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatatagc ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gggcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgccatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 662
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 662
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcgg cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaactct accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

acattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 663
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 663
atggctgccg atggttatct cccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcagcgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaagagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ccaataacct taccagcacg 1020

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

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gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 664
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 664
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag gggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 665
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 665
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

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aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 666

<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 666
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tacaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

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aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 667
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 667
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcagggc 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

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actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccaaca ctcgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

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gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtttgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

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gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 668
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 668
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccaaca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaatg 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgcggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 669
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 669
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacgggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtccgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 670
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (305)..(305)
<223> n is a, c, t, or g

<400> 670
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggngcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcgg cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggccacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

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tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag caacacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 671
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 671
atggctgccg atggttattt tccagattgg ctcgaggaca acctttctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aggacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcga cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

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gcagtcaatt tccagagcag cagcccagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatagtgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 672
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 672
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaacc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagactacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 673

<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 673
atggctgccg atggttatcc tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagtcccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 674
<211> 2196
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 674
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagcct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

ccatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

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atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

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gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctt 2196

<210> 675
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 675
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactctcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 676
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 676
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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ctatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

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aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 677
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 677
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacgatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 678
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 678
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacgggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

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gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 679
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 679
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

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tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

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tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc gggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

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gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctg 2205

<210> 680
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 680

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Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Asp Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Val Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
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Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Gly Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
```

```
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Pro
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640
```

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 681
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 681

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Arg Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
```

```
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Ile Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Leu Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 682
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 682

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Thr Glu Ser Val Ser Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Ser Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asp Val Asp Ala Asp Lys Val Ile Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
```

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 683
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 683

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Gly Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Gly Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Val
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gly Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Ser Tyr Ile Pro
```

```
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 684
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 684

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Val
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
```

```
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser His Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly His Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
```

```
Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Gly Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 685
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 685

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn Arg Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Pro Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
```

```
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  686
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  686

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
```

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
```

```
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 687
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 687

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
```

```
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 688
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 688

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Leu Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
```

```
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Lys Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
```

690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 689
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 689

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
```

565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 690
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 690

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Gly Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
```

```
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asp Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 691
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 691

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys Arg Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
```

```
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Ala Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 692

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 692

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro

```
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 693
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 693

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270
```

```
Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Thr Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
```

```
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 694
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 694

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
```

```
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Ser Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Ala Ala Thr Glu Ser
                565                 570                 575
```

```
Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln His Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  695
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  695

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
```

```
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Arg Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445
```

```
Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
```

660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 696
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 696

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Arg Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Ala Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe
                405                 410                 415

Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
        435                 440                 445

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val
    450                 455                 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu
        515                 520                 525

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys
```

```
    530                 535                 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr
545                 550                 555                 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr
            580                 585                 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
                645                 650                 655

Pro Pro Thr Ala Phe Asn Lys Asp Glu Leu Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210>  697
<211>  735
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 697

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Asp Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

```
Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe
```

```
                405                 410                 415

Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
        435                 440                 445

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val
    450                 455                 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu
        515                 520                 525

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr
545                 550                 555                 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr
            580                 585                 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
645 650 655

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 698
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 698

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Ala Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
```

```
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Thr
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
```

705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 699
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 699

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Thr Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Gly Ser Ser Ala Gly Ile Gly

```
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
```

580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 700
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 700

Met Ala Ala Asp Gly Tyr Phe Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Ser Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Leu
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
```

```
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Val Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  701
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  701

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Pro Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
```

```
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Ala Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 702
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 702

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Pro Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly

```
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Arg Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
```

625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 703
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 703

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Leu Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
```

```
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 704
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 704

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
```

```
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 705
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> MOD_RES
<222> (442)..(442)
<223> Xaa = any amino acid

<400> 705

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
```

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Thr Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Xaa Tyr Leu His Tyr Leu Ser
```

```
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Asp Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 706
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 706

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
```

```
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525
```

```
Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 707

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 707

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro

```
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Gly Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asp Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 708
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 708

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Arg Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270
```

```
Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Cys Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Thr Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
```

```
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

His Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 709
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 709

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
```

```
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Pro Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575
```

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Gly Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 710
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 710

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
```

```
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445
```

```
Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
```

660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 711
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 711

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asn Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Gly Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
```

```
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210>  712
<211>  736
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 712

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

```
Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Val Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
```

```
               405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
               485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
               565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Gly Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  713
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  713

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
```

```
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
```

705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 714
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 714

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln Arg Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Gly Asn Pro Cys Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly

```
145                 150                 155                 160

Arg Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Ala Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asp Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asp Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
```

580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Gly Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 715
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 715

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
```

```
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Pro Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 716
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 716

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asn Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Pro Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Arg Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
```

```
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Thr Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 717
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 717

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Val His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly

```
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Thr Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
```

625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Pro Arg Tyr Leu Thr Arg Asn Phe
725 730 735

<210> 718
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 718

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asn Lys Ala Tyr Asp

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Arg Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
```

```
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 719
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 719

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Glu Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
```

```
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Ser Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Ala Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  720
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  720

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Pro Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Ser Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Ser Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Ser Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 721
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 721

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
```

```
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 722
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 722

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
```

```
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640
```

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 723
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 723

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Asp Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
```

```
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 724
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 724

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
```

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 725
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 725

Met Ala Ala Asp Gly Tyr Pro Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro His Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
```

```
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Arg Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  726
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  726

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
```

```
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
```

```
Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  727
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  727
```

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Thr Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Ile
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

```
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  728
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  728

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
```

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
```

```
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Ser Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asn Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Glu Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 729
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 729

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Ile Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Arg Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Arg Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Thr Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
```

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385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Arg Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 730
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 730

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
```

```
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Gly Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480
```

```
Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Ala Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
```

```
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210>  731
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  731

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Gly Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
```

```
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Val Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
```

565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 732
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> MOD_RES

<222> (126)..(126)
<223> Xaa = any amino acid

<400> 732

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Arg Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Xaa Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
```

```
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Pro
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
```

625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 733
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 733

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
```

```
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 734
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 734

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
```

```
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asp Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Val Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  735
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  735

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Val Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460
```

```
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Leu Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 736
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 736

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Arg Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
```

```
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 737
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 737

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Gly Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
```

```
            420                 425                 430

Arg Leu Met Asn Pro Pro Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 738
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 738

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Arg Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
```

```
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Pro Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510
```

```
Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
```

725 730 735

<210> 739
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 739

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Gly Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Pro Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
```

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 740
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 740

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
```

```
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 741
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 741

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Gln Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
```

```
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560
```

```
Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Thr Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asp Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 742
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 742

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Pro Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly His Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Thr Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 743
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 743

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Glu Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
```

```
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Thr Gly Thr Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Thr Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asp Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 744
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 744

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Leu Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

```
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asp Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 745
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 745

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
```

```
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Ala Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
```

690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Val Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 746
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 746

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asn Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Pro Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Ser Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
```

565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 747
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 747

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
```

```
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Thr Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Gly Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 748
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 748

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Pro Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
```

```
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Gly Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 749

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 749

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Arg Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Arg Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro

```
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Gly Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Ser Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Gly Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Ala Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 750
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 750

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Gly Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Ser Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
```

```
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Thr Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210>  751
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  751

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Glu Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
```

```
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575
```

```
Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 752
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 752

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
```

```
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Gly Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
```

660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 753
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 753

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Pro Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
```

```
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Asn Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735

<210>  754
<211>  736
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 754

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
```

```
               405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Asp Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 755
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 755

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Gly Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Asn Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
```

```
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Gly His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Leu Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Phe Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
```

705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 756
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 756

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly

```
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Asn Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Met Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Ala Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
```

580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 757
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 757

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
```

```
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 758
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> MOD_RES
<222> (102)..(102)
<223> Xaa = any amino acid

<400> 758

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala

```
               85                  90                  95

Asp Ala Glu Phe Gln Xaa Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Gly Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly His Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Ser Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
```

```
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Asn Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 759
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 759

Met Ala Ala Asp Gly Tyr Phe Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Arg Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

```
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Pro Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 760
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 760

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Thr Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
```

```
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Tyr
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
```

690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 761
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 761

Met Ala Ala Asp Gly Tyr Pro Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Val Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
```

565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 762
<211> 732
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 762

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Ala Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Pro Tyr Leu Tyr Tyr Leu Asn Arg
```

```
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu
725 730

<210> 763
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 763

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
```

```
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Ser His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 764

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 764

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro

```
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Leu Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Thr Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 765
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 765

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Ser Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Pro Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Gln Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
```

```
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 766
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 766

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
```

```
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575
```

```
Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210>  767
<211>  735
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  767

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
```

```
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
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Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Arg
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
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660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 768
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 768
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gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tcctttact gcccggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgctttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcaccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 769
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 769
atggctgctg atggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actgttgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcaactc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tcctttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 770
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 770
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gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccggccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

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aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

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caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

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cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acggcaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagtg tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 771
<211> 2212
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (1283)..(1283)
<223> n is a, c, t, or g

<400> 771
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aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gaccgggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg gagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca gccatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

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cacggcagct acgctcacag ccngagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagacttttc aaagactgct aacgacaaca acaacagtaa 1500

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aggaccagct atggccagtc acaaggacga tgaagaaaaa tttttcccta tgcacggcaa 1620

tctaatattt ggcaaagaag ggacaacggc aagtaacgca gaattagata atgtaatgat 1680

tacggatgaa gaagagattc gtaccaccaa tcctgtggca acagagcagt atggaactgt 1740

ggcaaataac ttgcagagct caaatacagc tcccacgact agaactgtca atgatcaggg 1800

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gaaacatccg cctcctcaaa tcatgatcaa aaatactccg gtaccggcaa atcctccgac 1980

gactttcagc ccggccaagt ttgcttcatt tatcactcag tactccactg gacaggtcag 2040

cgtggaaatt gagtgggagc tacagaaaga aaacagcaaa cgttggaatc cagagattca 2100

gtacacttcc aactacaaca agtctgttaa tgtggacttt actgtagaca ctaatggtgt 2160

ttatagtgaa cctcgcccta ttggaacccg gtatctcaca cgaaactcgt aa 2212

<210> 772
<211> 2212
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 772
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg gagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcttgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca gccatctcta caagcaaatc 780

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aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

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cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatccc 1560

aggaccagct atggccagtc acaaggacga tgaagaaaaa tttttcccta tgcacggcaa 1620

tctaatattt ggcaaagaag ggacaacggc aagtaacgca gaattagata atgtaatgat 1680

tacggatgaa gaagagattc gtaccaccaa tcctgtggca acagagcagt atggaactgt 1740

ggcaaataac ttgcagagct caaatacagc tcccacgact agaactgtca atgatcaggg 1800

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gactttcagc ccggccaagt ttgcttcatt tatcactcag tactccactg gacaggtcag 2040

cgtggaaatt gagtgggagc tacagaaaga aaacagcaaa cgttggaatc cagagattca 2100

gtacacttcc aactacaaca agtctgttaa tgtggacttt actgtagaca ctaatggtgt 2160

ttatagtgaa cctcgcccta ttggaacccg gtatctcaca cgaaacttgt aa 2212

<210> 773
<211> 2212
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 773
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gaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtgc ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tagcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tggatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgctttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaaggacga tgaagaaaaa tttttcccta tgcacggcaa 1620

tctaatattt ggcaaagaag ggacaacggc aagtaacgca gaattagata atgtaatgat 1680

tacggatgaa gaagagattc gtaccaccaa tcctgtggca acagagcagt atggaactgt 1740

ggcaaataac ttgcagagct caaatacagc tcccacgact agaactgtca atgatcaggg 1800

ggccttacct ggcatggtgt ggcaagatcg tgacgtgtac cttcaaggac ctatctgggc 1860

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gaaacatccg cctcctcaaa tcatgatcaa aaatactccg gtaccggcaa atcctccgac 1980

gactttcagc ccggccaagt ttgcttcatt tatcactcag tactccactg gacaggtcag 2040

cgtggaaatt gagtgggagc tacagaaaga aaacagcaaa cgttggaatc cagagattca 2100

gtacacttcc aactacaaca agtctgttaa tgtggacttt actgtagaca ctaatggtgt 2160

ttatagtgaa cctcgcccta ttggaacccg gtatctcaca cgaaacctgt aa 2212

<210> 774
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 774
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gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

gaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcaa cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

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cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

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tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 775
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 775
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

gaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

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tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

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cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgctttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagtgcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 776
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 776
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gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaagg ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

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aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

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cacagcagct acgctcacag ccagagttcg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgaa cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

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acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

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aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 777
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 777
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gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

gaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg gagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

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tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

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tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

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acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

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aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 778
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 778
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gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg gagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca gccatctcta caagcaaatc 780

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acaacggaag tcaagcggtg ggacgctcat ccttttactg cctggagtac ttcccttcgc 1200

agatgctaag gactggaaat aacttccaat tcagctatac cctcgaggat gtacctttc 1260

acagcagcta cgctcacagc cagagtttgg atcgcttgat gaatcctctt attgatcagt 1320

atctgtacta cctgaacaga acgcaaggaa caacctctgg aacaaccaac caatcacggc 1380

tgctttttag ccaggctggg cctcagtcta tgtctttgca ggccagaaat tggctacctg 1440

ggccctgcta ccggcaacag agactttcaa agactgctaa cgacaacaac aacagtaact 1500

ttccttggac agcggccagc aaatatcatc tcaatggccg cgactcgctg gtgaatccag 1560

gaccagctat ggccagtcac aaaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagatag tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 779
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 779
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tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

actggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acctttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgctacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc gacgaccttc 1980

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tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 780
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 780
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tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

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tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccccctgg ggatactttg acttcaaccg cttccactgc 840

cacttcttac cacgtgactg gcagcgactc atcaacaaca actggggcgt gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcgacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc gacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 781
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 781
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacgag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgctacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc gacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 782
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 782
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tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acggaactgg agcaggcgac 540

ggaccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

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cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

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actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

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agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 783
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 783
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tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

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actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

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cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

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tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 784
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 784
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tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttca gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc ccttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggaccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ccggtctgag ggccacgtca cgaccaccag caccagaacc 720

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actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgcccg gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

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cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

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tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 785
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 785
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaggctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 786
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 786
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atcctccggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgcta gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 787
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 787
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgaca ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagagc 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 788
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 788
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tttttgggcc ctgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg tccggaccga agaggactcc 480

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgccgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

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gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctattggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 789
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 789
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ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

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aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

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acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

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gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 790
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 790
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacggggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

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acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

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gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 791
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 791
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ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

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aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

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acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

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gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

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<210> 792
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

gagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

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acccgacccc tttaa 2175

<210> 793
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

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acccgacccc tttaa 2175

<210> 794
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

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cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

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acccgacccc tttaa 2175

<210> 795
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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acccgacccc tttaa 2175

<210> 796
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

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acccgacccc tttaa 2175

<210> 797
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

cacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gtcgaacggc atgaccaaca acctccgggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

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tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 798
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 798
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

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acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 799
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

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aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

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tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc gcgaccaata ggatggagct cgagggcgcg 1500

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tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatac caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 800
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 800
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggtagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggggcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

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cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 801
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 801
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga      180
ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag      240
cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag      300
gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc      360
aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc      420
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aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc      540
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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc      660
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aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc      840
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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

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tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatgcaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 802
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 802
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

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tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggc caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 803
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 803
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ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

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accatcatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgcccccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 804
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 804
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcctc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 805
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 805
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg ccaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcgggcgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

ggctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataata ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 806
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 806
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagcctccca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccgcc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

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gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 807
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 807
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gccgcaaatc 540

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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

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aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

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tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgcgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 808
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 808
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagcctccca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 809
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 809
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgccgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt cgccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 810
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 810
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga      180
ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag      240
cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag      300
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aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc      420
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tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgcgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 811
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 811
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gctgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag ccaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

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gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccggagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 812
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 812
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

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aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgggactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

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cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa gggaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 813
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 813
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ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac gtccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

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aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

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cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 814
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (1652)..(1652)
<223> n is a, c, t, or g

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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

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cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

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cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 815
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

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cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 816
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 816
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggaccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc aacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 817
<211> 2234
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 817
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

ttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgacccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaaccgtgta ttcgtgtcag 2220

taaaatactg cctc 2234

<210> 818
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 818

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

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Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
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305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Pro Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
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Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 819

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 819

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145 150 155 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro

```
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Val Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
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Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 820
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 820

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Gly Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
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Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Gly Asn
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                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Cys Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 821
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 821

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gly Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Ser His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
```

```
        355                 360                 365

Ala Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Gly Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575
```

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
580 585 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Ser
725 730 735

<210> 822
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 822

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gly Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Leu Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
```

```
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Ser His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Gly Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445
```

```
Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
```

660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 823
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 823

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asp Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Cys Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Ser
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asp Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
```

530 535 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
565 570 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
580 585 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 824
<211> 736
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 824

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asp Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asn Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
```

```
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 825
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 825

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asp Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
```

```
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Val Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
```

705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 826
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 826

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Gly Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly

```
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Phe Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
```

```
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Ser Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Thr Ala Ala Ser Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr Thr
```

580 585 590

Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 827
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 827

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Glu Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gly Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Ser His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
```

```
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 828
<211> 668
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 828

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gly Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Ser His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Ile Leu Thr Leu Thr Asp Ser Thr
        275                 280                 285

Ala Thr Ser His His Val Thr Gly Ser Asp Ser Leu Thr Thr Thr Gly
    290                 295                 300

Asp Ser Gly Pro Arg Asn Ser Ala Ser Ser Ser Ser Thr Ser Lys Leu
305                 310                 315                 320

Lys Arg Ser Arg Arg Thr Met Ala Arg Arg Leu Leu Pro Ile Thr Leu
```

```
                325                 330                 335

Pro Ala Arg Phe Lys Cys Leu Arg Thr Arg Ser Ile Ser Ser Arg Thr
            340                 345                 350

Cys Ser Gly Arg Arg Thr Lys Ala Val Ser Arg Arg Phe Gln Arg Thr
        355                 360                 365

Pro Ser Trp Ser Leu Ser Met Asp Thr Ser Pro Thr Thr Glu Val Lys
    370                 375                 380

Arg Trp Asp Ala His Pro Phe Thr Ala Trp Ser Thr Ser Leu Arg Arg
385                 390                 395                 400

Cys Gly Leu Glu Ile Thr Ser Asn Ser Ala Ile Pro Ser Arg Met Tyr
                405                 410                 415

Leu Phe Thr Ala Ala Thr Leu Thr Ala Arg Val Trp Ile Ala Ile Leu
            420                 425                 430

Leu Leu Ile Ser Ile Cys Thr Thr Thr Glu Arg Lys Glu Gln Pro Leu
        435                 440                 445

Glu Gln Pro Thr Asn His Gly Cys Phe Leu Ala Arg Leu Gly Leu Ser
    450                 455                 460

Leu Cys Leu Cys Arg Pro Glu Ile Gly Tyr Leu Gly Pro Ala Thr Gly
465                 470                 475                 480

Asn Arg Asp Phe Gln Arg Leu Leu Thr Thr Thr Thr Thr Val Thr Phe
                485                 490                 495

Leu Gly Gln Arg Pro Ala Asn Ile Ile Ser Met Ala Ala Thr Arg Trp
            500                 505                 510

Ile Gln Asp Gln Leu Trp Pro Val Thr Arg Thr Met Lys Lys Asn Phe
        515                 520                 525

Ser Leu Cys Thr Ala Ile Arg Gly Pro Tyr Leu Ala Trp Cys Gly Lys
    530                 535                 540
```

```
Ile Val Thr Cys Thr Phe Lys Asp Leu Ser Gly Gln Arg Phe Leu Thr
545                 550                 555                 560


Arg Met Asp Thr Phe Ile Leu Leu Leu Trp Glu Ala Leu Asp Asn Ile
                565                 570                 575


Arg Leu Leu Lys Ser Ser Lys Ile Leu Arg Tyr Arg Gln Ile Leu Arg
            580                 585                 590


Arg Leu Ser Ala Arg Pro Ser Leu Leu His Leu Ser Leu Ser Thr Pro
        595                 600                 605


Leu Asp Arg Ser Ala Trp Lys Leu Ser Gly Ser Tyr Arg Lys Lys Thr
    610                 615                 620


Ala Asn Val Gly Ile Gln Arg Phe Ser Thr Leu Pro Thr Thr Thr Ser
625                 630                 635                 640


Leu Leu Met Trp Thr Leu Leu Thr Leu Met Val Phe Ile Val Asn Leu
                645                 650                 655


Ala Leu Leu Glu Pro Gly Ile Ser His Glu Thr Cys
            660                 665


<210>  829
<211>  734
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  829

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1               5                   10                  15


Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20                  25                  30


Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45
```

```
Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50                  55                  60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Thr Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
```

```
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Leu Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480
```

```
Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
```

690 695 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705 710 715 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730

<210> 830
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 830

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
115 120 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro

```
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Leu Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Val Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350
```

```
Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asp Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
```

565 570 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
580 585 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
595 600 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
610 615 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
645 650 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
675 680 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
690 695 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705 710 715 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730

<210> 831
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 831

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu

```
1               5                   10                  15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20                  25                  30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Glu Gly Glu Pro Val
    50                  55                  60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220
```

```
Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
```

```
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655
```

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
675 680 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
690 695 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705 710 715 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730

<210> 832
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 832

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

```
Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Gly Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Pro Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
```

```
305                 310                 315                 320

Thr Thr Ala Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525
```

```
Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730
```

<210> 833

<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 833

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
115 120 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
130 135 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145 150 155 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
165 170 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser

```
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Arg Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400
```

```
Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
```

610 615 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
645 650 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
675 680 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
690 695 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705 710 715 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730

<210> 834
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 834

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Gln Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val

```
    50                  55                  60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Arg Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270
```

```
Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
```

```
               485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Arg Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
               565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
               645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700
```

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705 710 715 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730

<210> 835
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 835

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Arg Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

```
Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
```

```
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575
```

```
Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Glu Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 836
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 836

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15
```

```
Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Ser Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
```

```
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445
```

```
Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
```

660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 837
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 837

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn

```
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320
```

```
Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
```

530 535 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Ser
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 838
<211> 724
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 838

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                  10                  15


Gly Leu Arg Glu Phe Leu Gly Pro Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Val Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190
```

```
Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Pro Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
```

```
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Cys Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620
```

```
Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu
```

<210> 839
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 839

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60
```

```
Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
```

```
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495
```

```
Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Ala Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
```

705 710 715 720

Thr Arg Pro Leu

<210> 840
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 840

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Gly Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser

```
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Ala Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365
```

```
Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
```

580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 841
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 841

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys

```
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240
```

```
Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
```

```
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Val Pro Pro Gln Pro Asn Gly Met Thr Asn
            500                 505                 510

Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe
        515                 520                 525

Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly
    530                 535                 540

Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg Val
545                 550                 555                 560

Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser Thr
                565                 570                 575

Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly
            580                 585                 590

Ser Val Trp Met Glu Gly Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
        595                 600                 605

Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met Gly
    610                 615                 620

Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn Thr
625                 630                 635                 640

Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser Ser
                645                 650                 655

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu Trp
            660                 665                 670
```

Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr
675 680 685

Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser
690 695 700

Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr
705 710 715 720

Arg Pro Leu

<210> 842
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 842

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

```
Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Val Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
```

```
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540
```

```
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Glu Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 843
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 843

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1   5   10   15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20   25   30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50   55   60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Ser Glu
65   70   75   80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100   105   110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115   120   125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130   135   140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145   150   155   160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165   170   175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180   185   190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala

```
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415
```

```
Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
```

625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Ala Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 844
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 844

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Pro Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu

```
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285
```

```
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
```

```
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Thr Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Pro Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720
```

Thr Arg Pro Leu

<210> 845
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 845

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

```
Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
```

```
    370                 375                 380

Phe Leu Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

Gly Ser Val Trp Met Lys Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 846
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 846

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

```
Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Pro Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
```

```
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460
```

```
Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
```

675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 847
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 847

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe

```
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335
```

```
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr His Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Ser Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Arg Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
```

545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 848
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 848

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                  10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205
```

```
Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
```

```
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Ser Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Thr Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Arg Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640
```

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 849
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 849

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

```
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
```

```
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Ala Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510
```

```
Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Gly Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Thr Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 850
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 850

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1   5   10   15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20   25   30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50   55   60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65   70   75   80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100   105   110

Leu Gly Lys Val Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115   120   125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130   135   140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145   150   155   160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln

```
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Gly Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Gly Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Leu Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
```

595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 851
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 851

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly

```
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255
```

```
Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
```

```
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Ala
        595                 600                 605

Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met Gly
    610                 615                 620

Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn Thr
625                 630                 635                 640

Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser Ser
                645                 650                 655

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu Trp
            660                 665                 670

Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr
        675                 680                 685
```

Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser
690 695 700

Thr Gly Glu Cys Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr
705 710 715 720

Arg Pro Leu

<210> 852
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 852

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

```
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Leu Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
```

```
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Gly
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Glu Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560
```

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Ala Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 853
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 853

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                  10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
```

```
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Ile Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430
```

```
Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
```

645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 854
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 854

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp

```
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300
```

```
Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
```

```
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Leu Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 855
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 855

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Ala
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Gly
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

```
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Gly Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
```

```
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605
```

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 856
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 856

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

```
Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Pro Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
```

```
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Ala
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480
```

```
Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
```

690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 857
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 857

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile

```
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Pro Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350
```

```
Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
```

565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Ala Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 858
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 858

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu

```
1               5                   10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Pro Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220
```

```
Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
```

```
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655
```

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 859
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 859

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

```
Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Pro Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Pro Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
```

```
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525
```

```
Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ala Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 860

<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 860

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr

```
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400
```

```
Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
```

610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Ala Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 861
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 861

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val

```
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Ala Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270
```

```
Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Ala
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Leu Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
```

```
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Val His Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700
```

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 862
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 862

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

```
Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Gly Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
```

```
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575
```

```
Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Ala Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Gly Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 863
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 863

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15
```

```
Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
```

```
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445
```

```
Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Val His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
```

660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 864
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> MOD_RES
<222> (551)..(551)
<223> Xaa = any amino acid

<400> 864

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

```
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
```

```
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510
```

```
Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Ser Met Leu Ile Thr Xaa Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 865
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 865

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145   150   155   160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
```

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 866
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 866

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly

```
        35                  40                  45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50                  55                  60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255
```

```
Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
```

```
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685
```

```
Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730
```

<210> 867
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 867

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125
```

```
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala Asp
        195                 200                 205

Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Met
    210                 215                 220

Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro Ser
225                 230                 235                 240

Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp Gly
                245                 250                 255

Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe
            260                 265                 270

Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln Arg
        275                 280                 285

Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val Lys
    290                 295                 300

Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr Thr
305                 310                 315                 320

Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Asp
                325                 330                 335

Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys Leu
```

```
            340                 345                 350

Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr Ala
        355                 360                 365

Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser Phe
    370                 375                 380

Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn Asn
385                 390                 395                 400

Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser Phe
                405                 410                 415

Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp Gln
            420                 425                 430

Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln Phe
        435                 440                 445

Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe
    450                 455                 460

Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly Val
465                 470                 475                 480

Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu Leu
                485                 490                 495

Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr Asn
            500                 505                 510

Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe
        515                 520                 525

Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly
    530                 535                 540

Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg Val
545                 550                 555                 560
```

```
Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser Thr
                565                 570                 575

Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly
            580                 585                 590

Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
        595                 600                 605

Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met Gly
    610                 615                 620

Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn Thr
625                 630                 635                 640

Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser Ser
                645                 650                 655

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu Trp
            660                 665                 670

Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr
        675                 680                 685

Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser
    690                 695                 700

Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr
705                 710                 715                 720

Arg Pro Leu
```

<210> 868
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 868

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Thr Leu Ala Val
            580                 585                 590

Pro Phe Lys Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
```

645 650 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
660 665 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
675 680 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
690 695 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705 710 715 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
725 730 735

Arg Tyr Leu Thr Arg Asn Leu
740

<210> 869
<211> 2232
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 869
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctctagaact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg taccggcaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaaactttg gcggtgcctt ttaaggcaca ggcgcagacc 1800

ggttgggttc aaaaccaagg aatacttccg ggtatggttt ggcaggacag agatgtgtac 1860

ctgcaaggac ccatttgggc caaaattcct cacacggacg gcaactttca cccttctccg 1920

ctgatgggag ggtttggaat gaagcacccg cctcctcaga tcctcatcaa aaacacacct 1980

gtacctgcgg atcctccaac ggccttcaac aaggacaagc tgaactcttt catcacccag 2040

tattctactg gccaagtcag cgtggagatc gagtgggagc tgcagaagga aaacagcaag 2100

cgctggaacc cggagatcca gtacacttcc aactattaca agtctaataa tgttgaattt 2160

gctgttaata ctgaaggtgt atatagtgaa ccccgcccca ttggcaccag atacctgact 2220

cgtaatctgt aa 2232

<210> 870
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 870

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
```

```
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Gln Ser Ser Gln Thr Pro Arg Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  871
<211>  743
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  871

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Ile Leu Gly Thr Gly Thr Ser Gln Thr Leu Lys Phe Ser
    450                 455                 460
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Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Thr Arg Thr Asn
            580                 585                 590

Pro Glu Ala Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
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675 680 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
690 695 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705 710 715 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
725 730 735

Arg Tyr Leu Thr Arg Asn Leu
740

<210> 872
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 872

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

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            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
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```
Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Ile Leu Gly Thr Gly Thr Ser Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
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    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Asn Gly Gly Thr
            580                 585                 590

Ser Ser Ser Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735

Arg Tyr Leu Thr Arg Asn Leu
            740
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<210> 873
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 873

Thr Leu Ala Val Pro Phe Lys
1 5

<210> 874
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 874

Lys Phe Pro Val Ala Leu Thr
1 5

<210> 875
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 875

Leu Ala Val Pro Phe Lys
1 5

<210> 876
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 876

Ala Val Pro Phe Lys

1 5

<210> 877
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 877

Val Pro Phe Lys
1

<210> 878
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 878

Thr Leu Ala Val Pro Phe
1 5

<210> 879
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 879

Thr Leu Ala Val Pro
1 5

<210> 880
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 880

Thr Leu Ala Val
1

<210> 881
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 881

Ser Val Ser Lys Pro Phe Leu
1 5

<210> 882
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 882

Phe Thr Leu Thr Thr Pro Lys
1 5

<210> 883
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 883

Met Asn Ala Thr Lys Asn Val
1 5

<210> 884
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 884

Gln Ser Ser Gln Thr Pro Arg
1 5

<210> 885
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 885

Ile Leu Gly Thr Gly Thr Ser
1 5

<210> 886
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 886

Thr Arg Thr Asn Pro Glu Ala
1 5

<210> 887
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 887

Asn Gly Gly Thr Ser Ser Ser
1 5

<210> 888
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 888

Tyr Thr Leu Ser Gln Gly Trp
1   5

<210> 889
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 889
aagtttcctg tggcgttgac t   21

<210> 890
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 890
actttggcgg tgcctttaa g   21

<210> 891
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 891
agtgtgagta agccttttt g   21

<210> 892
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 892

tttacgttga cgacgcctaa g 21

<210> 893
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 893
atgaatgcta cgaagaatgt g 21

<210> 894
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 894
cagtcgtcgc agacgcctag g 21

<210> 895
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 895
attctgggga ctggtacttc g 21

<210> 896
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 896
acgcggacta atcctgaggc t 21

<210> 897
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 897
aatgggggga ctagtagttc t 21

<210> 898
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 898
tatactttgt cgcagggttg g 21

<210> 899
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 899

Ser Ala Asp Asn Asn Asn Ser Glu Tyr
1 5

<210> 900
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 900

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
1 5

<210> 901
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 901

Val Pro Gln Tyr Gly Tyr Leu Thr Leu
1   5

<210> 902
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 902

Thr Thr Ser Thr Arg Thr Trp Ala Leu
1   5

<210> 903
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 903

Tyr His Leu Asn Gly Arg Asp Ser Leu
1   5

<210> 904
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 904

Ser Gln Ala Val Gly Arg Ser Ser Phe
1   5

<210> 905
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 905

Val Pro Ala Asn Pro Ser Thr Thr Phe
1 5

<210> 906
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 906

Phe Pro Gln Ser Gly Val Leu Ile Phe
1 5

<210> 907
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 907

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
1 5 10 15

<210> 908
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 908

Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met
1 5 10 15

<210> 909

<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 909

Gln Phe Ser Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg
1 5 10 15

<210> 910
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 910

Gly Ala Ser Asp Ile Arg Gln Ser Arg Asn Trp Leu Pro
1 5 10

<210> 911
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 911

Gly Asn Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly Val
1 5 10 15

<210> 912
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 912

Leu Asp Arg Leu Met Asn Pro Leu Ile
1 5

<210> 913
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 913

Gln Pro Ala Lys Lys Arg Leu Asn Phe
1 5

<210> 914
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 914

Gln Ala Val Arg Thr Ser Leu
1 5

<210> 915
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 915

Leu Ala Lys Glu Arg Leu Ser
1 5

<210> 916
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature

<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 916
uuuauaggcc agaccuccgn n 21

<210> 917
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 917
uuuuauaggc cagaccuccn n 21

<210> 918
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 918
ucuuuauagg ccagaccucn n 21

<210> 919
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature

<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 919
uacuuuauag gccagaccun n 21

<210> 920
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 920
uuacuuuaua ggccagaccn n 21

<210> 921
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 921
uacuacuuua uaggccagan n 21

<210> 922
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature

<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 922
ugacuacuuu auaggccagn n 21

<210> 923
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 923
ucgacuacuu uauaggccan n 21

<210> 924
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 924
ugcgacuacu uuauaggccn n 21

<210> 925
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature

<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 925
ucgcgacuac uuuauaggcn n 21

<210> 926
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 926
uccgcgacua cuuuauaggn n 21

<210> 927
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 927
ugcugcagga gacuacgacn n 21

<210> 928
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature

<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 928
uacgcugcag gagacuacgn n 21

<210> 929
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
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<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 929
ugacgcugca ggagacuacn n 21

<210> 930
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
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<220>
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<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 930
uagacgcugc aggagacuan n 21

<210> 931
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature

<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 931
ucacggccuu cgucgccaun n 21

<210> 932
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 932
ucgcacacgg ccuucgucgn n 21

<210> 933
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 933
uagcacgcac acggccuucn n 21

<210> 934
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature

<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 934
uuucagcacg cacacggccn n 21

<210> 935
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 935
ugcacugggc cgucgcccun n 21

<210> 936
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 936
uaauugauga ugcccugcan n 21

<210> 937
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature

<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 937
uaaauugaug augcccugcn n 21

<210> 938
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 938
ucgaaauuga ugaugcccun n 21

<210> 939
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 939
uucgaaauug augaugcccn n 21

<210> 940
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature

<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 940
ucucgaaauu gaugaugccn n 21

<210> 941
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 941
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<210> 1043
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<210> 1044
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<210> 1064
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<210> 1072
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<210> 1073
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<210> 1083
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<210> 1084
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<210> 1085
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<210> 1173
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<210> 1174
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<210> 1175
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<210> 1176
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<210> 1188
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<210> 1194
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<400> 1194
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<210> 1195
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<210> 1196
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<400> 1196
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<210> 1197
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<400> 1197
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<210> 1198
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<400> 1198
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<210> 1199
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<210> 1200
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<400> 1200
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<400> 1201
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<210> 1202
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<400> 1203
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<210> 1204
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<400> 1204
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<210> 1205
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<400> 1205
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<210> 1206
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<400> 1206
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<210> 1207
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<210> 1208
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<210> 1209
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<400> 1209
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<210> 1210
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<210> 1212
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<210> 1213
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<210> 1214
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<210> 1215
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<210> 1216
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<400> 1216
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<210> 1217
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<210> 1218
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<210> 1219
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<400> 1219
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<210> 1220
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<400> 1220
uuaaacacug uaaucuuacn n 21

<210> 1221
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<210> 1222
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<400> 1222
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<210> 1223
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<210> 1224
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<400> 1224
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<210> 1225
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<400> 1225
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<210> 1226
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<400> 1226
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<210> 1227
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uuaugaucac uuggaagacn n 21

<210> 1228
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<220>
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<222> (20)..(21)
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<400> 1228
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<210> 1229
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<400> 1229
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<210> 1230
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<210> 1231
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<222> (20)..(21)
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<400> 1231
uauaaaacuc aguuaaaacn n 21

<210> 1232
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<400> 1232
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<210> 1233
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<400> 1233
gucuguuuca augaccugcn n 21

<210> 1234
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<210> 1235
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accuguauuu ugccagaccn n 21

<210> 1236
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<400> 1236
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<210> 1237
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<222> (20)..(21)
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<400> 1237
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<210> 1238
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<400> 1238
aucacagaug gguauuaacn n 21

<210> 1239
<211> 21
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<400> 1239
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<210> 1240
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<210> 1241
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<210> 1242
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<400> 1242
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<210> 1243
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<400> 1243
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<210> 1244
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<400> 1244
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<210> 1245
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<210> 1246
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<210> 1247
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<400> 1247
aauaaaaacc cuguauggcn n 21

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<400> 1248
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<210> 1249
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<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature

<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 1249
aacccuguau ggcacuuacn n 21

<210> 1250
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 1250
acccuguaug gcacuuaucn n 21

<210> 1251
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 1251
gaggcuauua aaagaauccn n 21

<210> 1252
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature

<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 1252
aaagaaucca aauucaaacn n 21

<210> 1253
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (20)..(21)
<223> nn is a deoxythymidine dinucleotide

<400> 1253
gaauccaaau ucaaacuacn n 21

<210> 1254
<211> 981
<212> DNA
<213> Homo sapiens

<400> 1254
gtttggggcc agagtgggcg aggcgcggag gtctggccta taaagtagtc gcggagacgg 60

ggtgctggtt tgcgtcgtag tctcctgcag cgtctggggt ttccgttgca gtcctcggaa 120

ccaggacctc ggcgtggcct agcgagttat ggcgacgaag gccgtgtgcg tgctgaaggg 180

cgacggccca gtgcagggca tcatcaattt cgagcagaag gaaagtaatg gaccagtgaa 240

ggtgtgggga agcattaaag gactgactga aggcctgcat ggattccatg ttcatgagtt 300

tggagataat acagcaggct gtaccagtgc aggtcctcac tttaatcctc tatccagaaa 360

acacggtggg ccaaaggatg aagagaggca tgttggagac ttgggcaatg tgactgctga 420

caaagatggt gtggccgatg tgtctattga agattctgtg atctcactct caggagacca 480

ttgcatcatt ggccgcacac tggtggtcca tgaaaaagca gatgacttgg gcaaaggtgg 540

aaatgaagaa agtacaaaga caggaaacgc tggaagtcgt ttggcttgtg gtgtaattgg 600

gatcgcccaa taaacattcc cttggatgta gtctgaggcc ccttaactca tctgttatcc 660

tgctagctgt agaaatgtat cctgataaac attaaacact gtaatcttaa aagtgtaatt 720

gtgtgacttt ttcagagttg ctttaaagta cctgtagtga gaaactgatt tatgatcact 780

tggaagattt gtatagtttt ataaaactca gttaaaatgt ctgtttcaat gacctgtatt 840

ttgccagact taaatcacag atgggtatta aacttgtcag aatttctttg tcattcaagc 900

ctgtgaataa aaaccctgta tggcacttat tatgaggcta ttaaaagaat ccaaattcaa 960

actaaaaaaa aaaaaaaaaa a 981

<210> 1255
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1255
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaa 54

<210> 1256
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1256
gaagcaaaga aggggcagag ggagcccgtg agctgagtgg gccagggact gggagaagga 60

gtgaggaggc agggccggca tgcctctgct gctggccaga 100

<210> 1257
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1257
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctccac ggaa 54

<210> 1258
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1258
gggccctccc gcagaacacc atgcgctcca cggaa 35

<210> 1259
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1259
ctcccgcaga acaccatgcg ctccacggaa 30

<210> 1260
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1260
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctccac ggaag 55

<210> 1261
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1261
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcctc ggaa 54

<210> 1262
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1262
tttatgcctc atcctctgag tgctgaaggc ttgctgtagg ctgtatgctg 50

<210> 1263
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1263
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggga 54

<210> 1264
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1264
tgtgacctgg 10

<210> 1265
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1265
tgtgatttgg 10

<210> 1266
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1266
gtctgcacct gtcactag 18

<210> 1267
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1267
gtgacccaag 10

<210> 1268
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1268
gtggccactg agaag 15

<210> 1269
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1269
gtgacccaat 10

<210> 1270
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1270
gtgacccaac 10

<210> 1271
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1271
gtggccactg agaaa 15

<210> 1272
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1272
tataatttgg 10

<210> 1273
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1273
cctgacccag t 11

<210> 1274
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1274
ctgaggagcg ccttgacagc agccatggga gggccgcccc ctacctcagt ga 52

<210> 1275
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1275
ctgtggagcg ccttgacagc agccatggga gggccgcccc ctacctcagt ga 52

<210> 1276
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1276
tggccgtgta gtgctaccca gcgctggctg cctcctcagc attgcaattc ctctcccatc 60

tgggcaccag tcagctaccc tggtgggaat ctgggtagcc 100

<210> 1277
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1277
ctgaggagcg ccttgacagc agccatggga gggcc 35

<210> 1278
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1278
ctgcggagcg ccttgacagc agccatggga gggccgcccc ctacctcagt ga 52

<210> 1279
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1279
agtgtatgat gcctgttact agcattcaca tggaacaaat tgctgccgtg 50

<210> 1280
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1280
tcctgaggag cgccttgaca gcagccatgg gagggccgcc ccctacctca gtga 54

<210> 1281
<211> 152
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1281
tttatgcctc atcctctgag tgctgaaggc ttgctgtagg ctgtatgctg caatgtgact 60

gctgacaacc ctgtgacctg gtttgtcagc agtcacattg ttagtgtatg atgcctgtta 120

ctagcattca catggaacaa attgctgccg tg 152

<210> 1282
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1282
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aaccctgtga cctggtttgt cagcagtcac attgttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1283
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1283
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aatcctgtga cctggtttgt cagcagtcac attgttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1284
<211> 158

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1284
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aagcctgtga cctggtttgt cagcagtcac attgttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1285
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1285
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aaacctgtga cctggtttgt cagcagtcac attgttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1286
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1286
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gacagctgac aaacctgtga cctggtttgt cagcagtcac attgttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1287
<211> 157
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1287
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aacctgtgac ctggtttgtc agcagtcaca ttgttctgag gagcgccttg 120

acagcagcca tgggagggcc gccccctacc tcagtga 157

<210> 1288
<211> 159
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1288
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aatccctgtg acctggtttg tcagcagtca cattgttctg aggagcgcct 120

tgacagcagc catgggaggg ccgcccccta cctcagtga 159

<210> 1289
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1289
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aaccctgtga tttggtttgt cagcagtcac attgttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1290
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1290
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aaccctataa tttggtttgt cagcagtcac attgttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1291
<211> 159
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1291
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aacaccctga cccagttttg tcagcagtca cattgttctg aggagcgcct 120

tgacagcagc catgggaggg ccgcccccta cctcagtga 159

<210> 1292
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1292
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aaccctgtga cctggtttgt cagcagtcac attgttctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1293
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1293
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aatcctgtga cctggtttgt cagcagtcac attgttctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1294
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1294
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gacagctgac aaacctgtga cctggtttgt cagcagtcac attgttctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1295
<211> 159
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1295
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aacaccctga cccagttttg tcagcagtca cattgttctg tggagcgcct 120

tgacagcagc catgggaggg ccgcccccta cctcagtga 159

<210> 1296
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1296
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacaatgt 60

gactgctgac aagcctgtga cctggtttgt cagcagtcac attgttctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1297
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1297
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacgacga 60

aggccgtgtg cgccctgtga cctggtcgca cacggccttc gtcgttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1298
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1298
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaatgactt 60

gggcaaaggt ggccctgtga cctggtccac ctttgcccaa gtcattctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1299
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1299
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaaaactca 60

tctgttatcc tgccctgtga cctggtcagg ataacagatg agttttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1300
<211> 260
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1300
gaagcaaaga aggggcagag ggagcccgtg agctgagtgg gccagggact gggagaagga 60

gtgaggaggc agggccggca tgcctctgct gctggccaga caatgtgact gctgacaacc 120

cgtctgcacc tgtcactagt ttgtcagcag tcacattgtt tggccgtgta gtgctaccca 180

gcgctggctg cctcctcagc attgcaattc ctctcccatc tgggcaccag tcagctaccc 240

tggtgggaat ctgggtagcc 260

<210> 1301
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1301
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacccctt 60

aactcatctg ttccctgtga cctggtaaca gatgagttaa ggggttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1302
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1302
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaaccctta 60

actcatctgt taccctgtga cctggttaac agatgagtta agggttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1303
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1303
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaaaactca 60

tctgttatct tgccctgtga cctggtcagg ataacagatg agttttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1304
<211> 158

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1304
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaagctgtg 60

gaaatgtatc ttccctgtga cctggtagga tacatttcta cagcttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1305
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1305
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaatgactt 60

gggcaaaggt gagcctgtga cctggtccac ctttgcccaa gtcattctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1306
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1306
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacccctt 60

aactcatctg ttgcctgtga cctggtaaca gatgagttaa ggggttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1307
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1307
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaaccctta 60

actcatctgt tagcctgtga cctggttaac agatgagtta agggttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1308
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1308
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaaaactca 60

tctgttatct tagcctgtga cctggtcagg ataacagatg agttttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1309
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1309
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaagctgtg 60

gaaatgtatc ttgcctgtga cctggtagga tacatttcta cagcttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1310
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1310
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaatgactt 60

gggcaaaggt aggcctgtga cctggtccac ctttgcccaa gtcattctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1311
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1311
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacccctt 60

aactcatctg ttccctgtga tttggtaaca gatgagttaa ggggttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1312
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1312
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaaccctta 60

actcatctgt taccctgtga tttggttaac agatgagtta agggttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1313
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1313
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaaaactca 60

tctgttatct tgccctgtga tttggtcagg ataacagatg agttttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1314
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1314
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaagctgtg 60

gaaatgtatc ttccctgtga tttggtagga tacatttcta cagcttctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1315
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1315
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaatgactt 60

gggcaaaggt gagcctgtga tttggtccac ctttgcccaa gtcattctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1316
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1316
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacccctt 60

aacacatctg ttacctgtga cctggtaaca gatgagttaa ggggttctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1317
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1317
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaaccctta 60

actgatctgt taacctgtga cctggttaac agatgagtta agggttctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1318
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1318
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaaaactca 60

tctcttatct tgccctgtga cctggtcagg ataacagatg agttttctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1319
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1319
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaagctgtg 60

gaattgtatc ttgcctgtga cctggtagga tacatttcta cagcttctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1320
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1320
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaatgactt 60

ggggaaaggt gagcctgtga cctggtccac ctttgcccaa gtcattctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1321
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1321
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaacccctt 60

aactcatctg ttgcctgtga cctggtaaca gatgagttaa ggggttctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1322
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1322
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaaccctta 60

actcatctgt tagcctgtga cctggttaac agatgagtta agggttctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1323
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1323
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaaaactca 60

tctgttatct tggcctgtga cctggtcagg ataacagatg agttttctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1324
<211> 158
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1324
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaagctgtg 60

gaaatgtatc ttgcctgtga cctggtagga tacatttcta cagcttctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1325
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1325
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc ggaatgactt 60

gggcaaaggt aggcctgtga cctggtccac ctttgcccaa gtcattctgt ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1326
<211> 260
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1326
gaagcaaaga aggggcagag ggagcccgtg agctgagtgg gccagggact gggagaagga 60

gtgaggaggc agggccggca tgcctctgct gctggccaga ccccttaact catttgttcc 120

cgtctgcacc tgtcactagt aacagatgag ttaaggggtt tggccgtgta gtgctaccca 180

gcgctggctg cctcctcagc attgcaattc ctctcccatc tgggcaccag tcagctaccc 240

tggtgggaat ctgggtagcc 260

<210> 1327
<211> 260
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1327
gaagcaaaga aggggcagag ggagcccgtg agctgagtgg gccagggact gggagaagga 60

gtgaggaggc agggccggca tgcctctgct gctggccaga cccttaactc atctgttacc 120

cgtctgcacc tgtcactagt taacagatga gttaagggtt tggccgtgta gtgctaccca 180

gcgctggctg cctcctcagc attgcaattc ctctcccatc tgggcaccag tcagctaccc 240

tggtgggaat ctgggtagcc 260

<210> 1328
<211> 260
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1328
gaagcaaaga aggggcagag ggagcccgtg agctgagtgg gccagggact gggagaagga 60

gtgaggaggc agggccggca tgcctctgct gctggccaga aactcatctg ttatcttgcc 120

cgtctgcacc tgtcactagt caggataaca gatgagtttt tggccgtgta gtgctaccca 180

gcgctggctg cctcctcagc attgcaattc ctctcccatc tgggcaccag tcagctaccc 240

tggtgggaat ctgggtagcc 260

<210> 1329
<211> 260
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1329
gaagcaaaga aggggcagag ggagcccgtg agctgagtgg gccagggact gggagaagga 60

gtgaggaggc agggccggca tgcctctgct gctggccaga gctgtggaaa tgtatcttcc 120

cgtctgcacc tgtcactagt aggatacatt tctacagctt tggccgtgta gtgctaccca 180

gcgctggctg cctcctcagc attgcaattc ctctcccatc tgggcaccag tcagctaccc 240

tggtgggaat ctgggtagcc 260

<210> 1330
<211> 260

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1330
gaagcaaaga aggggcagag ggagcccgtg agctgagtgg gccagggact gggagaagga 60

gtgaggaggc agggccggca tgcctctgct gctggccaga tgacttgggc aaaggtagcc 120

cgtctgcacc tgtcactagt ccacctttgc ccaagtcatt tggccgtgta gtgctaccca 180

gcgctggctg cctcctcagc attgcaattc ctctcccatc tgggcaccag tcagctaccc 240

tggtgggaat ctgggtagcc 260

<210> 1331
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1331
caatgtgact gctgacaacc c 21

<210> 1332
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1332
tttgtcagca gtcacattgt t 21

<210> 1333
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1333
caatgtgact gctgacaatc c 21

<210> 1334
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1334
caatgtgact gctgacaagc c 21

<210> 1335
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1335
caatgtgact gctgacaaac c 21

<210> 1336
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1336
caatgtgaca gctgacaaac c 21

<210> 1337
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1337
caatgtgact gctgacaacc 20

<210> 1338
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1338
caatgtgact gctgacaaca c 21

<210> 1339
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1339
caatgtgact gctgacaatc cc 22

<210> 1340
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1340
cgacgaaggc cgtgtgcgcc c 21

<210> 1341
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1341
tcgcacacgg ccttcgtcgt t 21

<210> 1342
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1342
tgacttgggc aaaggtggcc c 21

<210> 1343
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1343
tccacctttg cccaagtcat t 21

<210> 1344
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1344
aactcatctg ttatcctgcc c 21

<210> 1345
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1345
tcaggataac agatgagttt t 21

<210> 1346
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1346
ccccttaact catctgttcc c 21

<210> 1347
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1347
taacagatga gttaaggggt t 21

<210> 1348
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1348
cccttaactc atctgttacc c 21

<210> 1349
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1349
ttaacagatg agttaagggt t 21

<210> 1350
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1350
aactcatctg ttatcttgcc c 21

<210> 1351
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1351
gctgtggaaa tgtatcttcc c 21

<210> 1352
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1352
taggatacat ttctacagct t 21

<210> 1353
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1353
tgacttgggc aaaggtgagc c 21

<210> 1354
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1354
ccccttaact catctgttgc c 21

<210> 1355
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1355
cccttaactc atctgttagc c 21

<210> 1356
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1356
aactcatctg ttatcttagc c 21

<210> 1357
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1357
gctgtggaaa tgtatcttgc c 21

<210> 1358
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1358
tgacttgggc aaaggtaggc c 21

<210> 1359
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1359
ccccttaaca catctgttac c 21

<210> 1360
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1360
cccttaactg atctgttaac c 21

<210> 1361
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1361
aactcatctc ttatcttgcc c 21

<210> 1362
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1362
gctgtggaat tgtatcttgc c 21

<210> 1363
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1363
tgacttgggg aaaggtgagc c 21

<210> 1364
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1364
aactcatctg ttatcttggc c 21

<210> 1365
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1365
ccccttaact catttgttcc c 21

<210> 1366
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1366
tgacttgggc aaaggtagcc c 21

<210> 1367
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1367
gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc gggatttgtc 60

agcagtcaca ttgtctgtga cctggcaatg tgactgctga caaatcctga ggagcgcctt 120

gacagcagcc atgggagggc cgccccctac ctcagtga 158

<210> 1368
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1368
tttgtcagca gtcacattgt c 21

<210> 1369
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1369
caatgtgact gctgacaaa 19

<210> 1370
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1370
cctgcaggca gctgcgcgct cgctcgctca ctgaggccgc ccgggcaaag cccgggcgtc 60

gggcgacctt tggtcgcccg gcctcagtga gcgagcgagc gcgcagagag ggagtggcca 120

actccatcac taggggttcc t 141

<210> 1371
<211> 105
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1371
ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgtcg ggcgaccttt 60

ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gagtg 105

<210> 1372
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<212> DNA
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<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1372
aggaacccct agtgatggag ttggccactc cctctctgcg cgctcgctcg ctcactgagg 60

ccgggcgacc aaaggtcgcc cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc 120

gagcgcgcag ctgcctgcag g 141

<210> 1373
<211> 130
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1373
aggaacccct agtgatggag ttggccactc cctctctgcg cgctcgctcg ctcactgagg 60

ccgggcgacc aaaggtcgcc cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc 120

gagcgcgcag 130

<210> 1374
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1374
gtcgacataa 10

<210> 1375
<211> 121
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1375
gtcgacataa cgcgtaattc gcccttgggc ctaggcaatt ggatccgccg gcagagaaaa 60

catcccaggg atttacagat cacatgcagg cagggaccag ctcaaccctt ctacgcgtat 120

a 121

<210> 1376
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1376
gtcgacataa cgcgtaattc gcccttgggc ctaggcaatt ggatccgccg gcagagaaaa 60

catcacgcgt ata 73

<210> 1377
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1377
gtcgacataa cgcgtata 18

<210> 1378
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1378
ctcgagagat ctac 14

<210> 1379
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<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1379
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cagggatgga ggggaggggt tgaggagcga gaggcagtta tttttgggtg ggattcacca 180

cttttcccat gaagagggga gacttggtat tttgttcaat cattaagaag acaaagggtt 240

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agaagcagag acacgttgta aggctgatcc caggcctcga gcaaggctca cgtggacacc 420

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tcataggcac cttcacggtg gtcacctggt ccacgtggaa gtcctcttcc tcggtgtcct 2820

tgacttcaaa gggtctctcc catttgcctg gagagagggg aaggtgggca tcaccagggg 2880

tgagtgaagg tttggaagag tgtagcagaa taagaaacca tgagtcccct ccctgagaag 2940

ccctgagccc ccttgacgac acacatccct cgaggctcag cttcatcatc tgtaaaaggt 3000

gctgaaactg acc 3013

<210> 1380
<211> 712
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1380
aattcgccct tgggcctagg caattggatc cgccggcaga gaaaacatcc cagggattta 60

cagatcacat gcaggcaggg accagctcaa cccttcttta atgtcatcca gggaggggc 120

cagggatgga ggggaggggt tgaggagcga gaggcagtta tttttgggtg ggattcacca 180

cttttcccat gaagagggga gacttggtat tttgttcaat cattaagaag acaaagggtt 240

tgttgaactt gacctcgggg gggatagaca tgggtatggc ctctaaaaac atggccccag 300

cagcttcagt ccctttctcg tcgatggtca gcacagcctt atgcacggcc tggaggggag 360

agaagcagag acacgttgta aggctgatcc caggcctcga gcaaggctca cgtggacacc 420

tcccaggaag cgctcactcc ccctggacgg ccctggccct gcacatcctc tccctccctg 480

tcacataggc cttgctcctc ctcaaggctt tggctgatgg ggctggctcc cctctgtcca 540

tcttcctgac aagcgcctct ccccctgctc aggtgcaccc acaactcaga acagggaaga 600

gcatcgtcac tccacgtctg cctccagggc tctctccttt ctagtacacg gcttgaagct 660

ccttgaggac acggaccctg gcagtgacct tcacagtgcc cagaccacgc gt 712

<210> 1381
<211> 2405
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1381
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cagatcacat gcaggcaggg accagctcaa cccttcttta atgtcatcca gggagggggc 120

cagggatgga ggggaggggt tgaggagcga gaggcagtta tttttgggtg ggattcacca 180

cttttcccat gaagagggga gacttggtat tttgttcaat cattaagaag acaaagggtt 240

tgttgaactt gacctcgggg gggatagaca tgggtatggc ctctaaaaac atggccccag 300

cagcttcagt ccctttctcg tcgatggtca gcacagcctt atgcacggcc tggaggggag 360

agaagcagag acacgttgta aggctgatcc caggcctcga gcaaggctca cgtggacacc 420

tcccaggaag cgctcactcc ccctggacgg ccctggccct gcacatcctc tccctccctg 480

tcacataggc cttgctcctc ctcaaggctt tggctgatgg ggctggctcc cctctgtcca 540

tcttcctgac aagcgcctct ccccctgctc aggtgcaccc acaactcaga acagggaaga 600

gcatcgtcac tccacgtctg cctccagggc tctctccttt ctagtacacg gcttgaagct 660

ccttgaggac acggaccctg gcagtgacct tcacagtgcc cagaccccaa gataatgcag 720

ccattcatgg aactgcagtt gttcattggt cgcctttagt tttccaaaat aagtgtcatc 780

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tgtctagaag gtcttgggca aagttgaaat tcagggtcag tgacacaacc tcaagggagg 960

ccccgaaagt gccagctgca cagcagtccc ctgcctggct ttgctgtttg accacgtccc 1020

gtgtcagtga atcacgggca tcttcaggag ctcagcctgg gtcttcattt gtttccctcg 1080

gccccttcct cagcctcagg acagagctgc agcccccaca cattcttccc tacagatacc 1140

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gtgaccccgg agaggtcagc cccattgctg aagaccttag tgatgcccag ttgacccagg 1260

acgctcttca gatcataggt tccagtaatg gacagtttgg gtaaatgtaa gctggcagac 1320

ctgtcgtgca gaaaagaaat tcaaggcatg gcacagcatt cctcttgttc ttctgggacc 1380

caccacagtg caagtgtttt cttttctgat tatttctgcc acttactcct gtgtcctcca 1440

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tcaaagaatg ttaacatcga atgaatcaca aaagcttgaa atgccacctc ctctgatatt 1560

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agacctcagg aggtgctggc atggaacaga gaaattccag cctcgattcc tattatgaac 1920

ccgacacctt ttgtattttc atcttggttt tacagtgtac aaaacgaact agatcagcag 1980

ggcatgggca taatcacgaa tgcacacaca tacactaatg tgtggctcat gtttaagtat 2040

cacttactac aggacaccca atctaacagc accgataaag tgacagagaa acgcaagcct 2100

tctgcgaaca tggcctggct gttccaattc cgaaccttgc ttttctgggc cttgccacac 2160

aggctcttcc cccgtccccc cagggacatt ctacccttga actccacact ccactgctgc 2220

ctttgccagg aagcccatct gttccttttt ggttctgcca gaacgtgtgg tggtgctgct 2280

gtccctgccc tgggcactgg atattgggaa gggacagtgt ccacactgga gtgggaagtc 2340

cccagggacg agacctttac ctcctcaccc ctgggtactg ttctcctcat ggagcatgga 2400

cgcgt 2405

<210> 1382
<211> 1203
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1382
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cagatcacat gcaggcaggg accagctcaa cccttcttta atgtcatcca gggaggggc 120

cagggatgga ggggaggggt tgaggagcga gaggcagtta tttttgggtg ggattcacca 180

cttttcccat gaagagggga gacttggtat tttgttcaat cattaagaag acaaagggtt 240

tgttgaactt gacctcgggg gggatagaca tgggtatggc ctctaaaaac atggccccag 300

cagcttcagt ccctttctcg tcgatggtca gcacagcctt atgcacggcc tggaggggag 360

agaagcagag acacgttgta aggctgatcc caggcctcga gcaaggctca cgtggacacc 420

tcccaggaag cgctcactcc ccctggacgg ccctggccct gcacatcctc tccctccctg 480

tcacataggc cttgctcctc ctcaaggctt tggctgatgg ggctggctcc cctctgtcca 540

tcttcctgac aagcgcctct ccccctgctc aggtgcaccc acaactcaga acagggaaga 600

gcatcgtcac tccacgtctg cctccagggc tctctccttt ctagtacacg gcttgaagct 660

ccttgaggac acggaccctg gcagtgacct tcacagtgcc cagaccccaa gataatgcag 720

ccattcatgg aactgcagtt gttcattggt cgcctttagt tttccaaaat aagtgtcatc 780

tttagctgaa atcattcatt aattcagaca ccaaatctca cagatcgaag gagtcagaaa 840

ttcctttgaa acaacttagc ccaaaccttt ctgtgtcagt atggataaat caaggcccaa 900

tgtctagaag gtcttgggca aagttgaaat tcagggtcag tgacacaacc tcaagggagg 960

ccccgaaagt gccagctgca cagcagtccc ctgcctggct ttgctgtttg accacgtccc 1020

gtgtcagtga atcacgggca tcttcaggag ctcagcctgg gtcttcattt gtttccctcg 1080

gccccttcct cagcctcagg acagagctgc agcccccaca cattcttccc tacagatacc 1140

agggtgcaac aaggtcgtca gggtgatctc accttggaga gcttcagggg tgcctccacg 1200

cgt 1203

<210> 1383
<211> 103
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1383
aattcgccct tgggcctagg caattggatc cgccggcaga gaaaacatcc cagggattta 60

cagatcacat gcaggcaggg accagctcaa cccttctacg cgt 103

<210> 1384
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1384
aattcgccct tgggcctagg caattggatc cgccggcaga gaaaacatca cgcgt 55

<210> 1385
<211> 1512
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1385
cgcgtaattc gcccttgggc ctaggcaatt ggatccgccg gcagagaaaa catcccaggg 60

atttacagat cacatgcagg cagggaccag ctcaaccctt ctttaatgtc atccagggag 120

ggggccaggg atggagggga ggggttgagg agcgagaggc agttattttt gggtgggatt 180

caccactttt cccatgaaga ggggagactt ggtattttgt tcaatcatta agaagacaaa 240

gggtttgttg aacttgacct cgggggggat agacatgggt atggcctcta aaaacatggc 300

cccagcagct tcagtccctt tctcgtcgat ggtcagcaca gccttatgca cggcctggag 360

gggagagaag cagagacacg ttgtaaggct gatcccaggc ctcgagcaag gctcacgtgg 420

acacctccca ggaagcgctc actccccctg gacggccctg gccctgcaca tcctctccct 480

ccctgtcaca taggccttgc tcctcctcaa ggctttggct gatggggctg gctcccctct 540

gtccatcttc ctgacaagcg cctctccccc tgctcaggtg cacccacaac tcagaacagg 600

gaagagcatc gtcactccac gtctgcctcc agggctctct cctttctagt acacggcttg 660

aagctccttg aggacacgga ccctggcagt gaccttcaca gtgcccagac cccaagataa 720

tgcagccatt catggaactg cagttgttca ttggtcgcct ttagttttcc aaaataagtg 780

tcatctttag ctgaaatcat tcattaattc agacaccaaa tctcacagat cgaaggagtc 840

agaaattcct ttgaaacaac ttagcccaaa cctttctgtg tcagtatgga taaatcaagg 900

cccaatgtct agaaggtctt gggcaaagtt gaaattcagg gtcagtgaca caacctcaag 960

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cagacctgtc gtgcagaaaa gaaattcaag gcatggcaca gcattcctct tgttcttctg 1380

ggacccacca cagtgcaagt gttttctttt ctgattattt ctgccactta ctcctgtgtc 1440

ctccacccac actaagatgg gaactcggct ttggtttgtt ctacttttag ctcttctaca 1500

ttgagtcaaa ga 1512

<210> 1386
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1386
aattcgccct tgggcctagg caattggatc cgccggcaga gaaaacatcc cagggattta 60

cagatcacat gcaggcaggg accagctcaa cccttcttta atgtcatcca gggaggggc 120

cagggatgga ggggaggggt tgaggagcga gaggcagtta tttttgggtg ggattcacca 180

cttttcccat gaagagggga gacttggtat tttgttcaat cattaagaag acaaagggtt 240

tgttgaactt gacctcgggg gggatagaca tgggtatggc ctctaaaaac atggccccag 300

cagcttcagt ccctttctcg tcgatggtca gcacagcctt atgcacggcc tggagggacg 360

cgt 363

<210> 1387
<211> 2395
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1387

aattcgccct tgggcctagg caattggatc cgccggcaga gaaaacatcc cagggattta 60

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cagggatgga ggggaggggt tgaggagcga gaggcagtta tttttgggtg ggattcacca 180

cttttcccat gaagagggga gacttggtat tttgttcaat cattaagaag acaaagggtt 240

tgttgaactt gacctcgggg gggatagaca tgggtatggc ctctaaaaac atggccccag 300

cagcttcagt ccctttctcg tcgatggtca gcacagcctt atgcacggcc tggaggggag 360

agaagcagag acacgttgta aggctgatcc caggcctcga gcaaggctca cgtggacacc 420

tcccaggaag cgctcactcc ccctggacgg ccctggccct gcacatcctc tccctccctg 480

tcacataggc cttgctcctc ctcaaggctt tggctgatgg ggctggctcc cctctgtcca 540

tcttcctgac aagcgcctct ccccctgctc aggtgcaccc acaactcaga acagggaaga 600

gcatcgtcac tccacgtctg cctccagggc tctctccttt ctagtacacg gcttgaagct 660

ccttgaggac acggaccctg gcagtgacct tcacagtgcc cagaccccaa gataatgcag 720

ccattcatgg aactgcaggt tgttcattgg tcgcctttag ttttccaaaa taagtgtcac 780

tttagctgaa atcattcatt aattcagaca ccaaatctca cagatcgaag gagtcagaaa 840

ttcctttgaa acaacttagc ccaaaccttt ctgtgtcagt atggataaat caaggcccaa 900

tgtctagaag gtcttgggca aagttgaaat tcagggtcag tgacacaacc tcaagggagg 960

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gtgtcagtga atcacgggca tcttcaggag ctcagcctgg gtcttcattt gtttccctcg 1080

gccccttcct cagcctcagg acagtgctgc agcccccaca cattcttccc tacagatacc 1140

atggtgcaac aaggtcgtca gggtgatctc accttggaga gcttcagggg tgcctcctct 1200

gtgaccccgg agaggtcagc cccattgctg aagaccttag tgatgcccag ttgacccagg 1260

acgctcttca gatcataggt tccagtaatg gacagtttgg gtaaatgtaa gctggcagac 1320

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cctcaggagg tgctggcatg gaacagagaa attccagcct cgattcctat tatgaacccg 1920

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cctgccttgg gcactggata ttgggaaggg acagtgtcca cactggagtg ggaagttccc 2340

agggacgaga cctttacctc ctcaccctgg gtactgttct cctcatggag catgg 2395

<210> 1388
<211> 97
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1388
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cagatcacat gcaggcaggg accagctcaa cccttct 97

<210> 1389
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1389
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cagatcacat gcaggcaggg accagctcaa cccttcttta atgtcatcca gggaggggc 120

cagggatgga ggggaggggt tgaggagcga gaggcagtta tttttgggtg ggattcacca 180

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tcacataggc cttgctcctc ctcaaggctt tggctgatgg ggctggctcc cctctgtcca 540

tcttcctgac aagcgcctct ccccctgctc aggtgcaccc acaactcaga acagggaaga 600

gcatcgtcac tccacgtctg cctccagggc tctctccttt ctagtacacg gcttgaagct 660

ccttgaggac acggaccctg gcagtgacct tcacagtgcc cagaccattt aaat 714

<210> 1390
<211> 3021
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1390
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cagatcacat gcaggcaggg accagctcaa cccttcttta atgtcatcca gggaggggc 120

cagggatgga ggggaggggt tgaggagcga gaggcagtta tttttgggtg ggattcacca 180

cttttcccat gaagagggga gacttggtat tttgttcaat cattaagaag acaaagggtt 240

tgttgaactt gacctcgggg gggatagaca tgggtatggc ctctaaaaac atggccccag 300

cagcttcagt ccctttctcg tcgatggtca gcacagcctt atgcacggcc tggaggggag 360

agaagcagag acacgttgta aggctgatcc caggcctcga gcaaggctca cgtggacacc 420

tcccaggaag cgctcactcc ccctggacgg ccctggccct gcacatcctc tccctccctg 480

tcacataggc cttgctcctc ctcaaggctt tggctgatgg ggctggctcc cctctgtcca 540

tcttcctgac aagcgcctct ccccctgctc aggtgcaccc acaactcaga acagggaaga 600

gcatcgtcac tccacgtctg cctccagggc tctctccttt ctagtacacg gcttgaagct 660

ccttgaggac acggaccctg gcagtgacct tcacagtgcc cagaccccaa gataatgcag 720

ccattcatgg aactgcaggt tgttcattgg tcgcctttag ttttccaaaa taagtgtcac 780

tttagctgaa atcattcatt aattcagaca ccaaatctca cagatcgaag gagtcagaaa 840

ttcctttgaa acaacttagc ccaaaccttt ctgtgtcagt atggataaat caaggcccaa 900

tgtctagaag gtcttgggca aagttgaaat tcagggtcag tgacacaacc tcaagggagg 960

ccccgaaagt gccagctgca cagcagcccc tgcctggctt tgctgtttgc ccaccgtccc 1020

gtgtcagtga atcacgggca tcttcaggag ctcagcctgg gtcttcattt gtttccctcg 1080

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gtgaccccgg agaggtcagc cccattgctg aagaccttag tgatgcccag ttgacccagg 1260

acgctcttca gatcataggt tccagtaatg gacagtttgg gtaaatgtaa gctggcagac 1320

ctgtcgtgca gaaaagaaat tcaaggcatg gcacagcatt cctcttgttc ttctgggacc 1380

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ctaggtgtcc tggaagcctg tctcatcttg ccctgtagtg ttgggtcacc tggcccccag 1620

cctgtaacat ccccagggcc ctacacccag agaaacacgg ggctggtggc agtgcccagt 1680

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caacatggct aagaggtgtg ggcagcttct tggtcaccct caggttgggg aatcaccttc 2580

tgtcttcatt ttccaggaac ttggtgatga tatcgtgggt gagttcattt accaggtgct 2640

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gcagcaccca gctggacagc ttcttacagt gctggatgtt aaacatgcct aaacgcttca 2760

tcataggcac cttcacggtg gtcacctggt ccacgtggaa gtcctcttcc tcggtgtcct 2820

tgacttcaaa gggtctctcc catttgcctg gagagagggg aaggtgggca tcaccagggg 2880

tgagtgaagg tttggaagag tgtagcagaa taagaaacca tgagtcccct ccctgagaag 2940

ccctgagccc ccttgacgac acacatccct cgaggctcag cttcatcatc tgtaaaaggt 3000

gctgaaactg accatttaaa t 3021

<210> 1391
<211> 1209
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1391
tctgtgaccc cggagaggtc agccccattg ctgaagacct tagtgatgcc cagttgaccc 60

aggacgctct tcagatcata ggttccagta atggacagtt tgggtaaatg taagctggca 120

gacctgtcgt gcagaaaaga aattcaaggc atggcacagc attcctcttg ttcttctggg 180

acccaccaca gtgcaagtgt tttcttttct gattatttct gccacttact cctgtgtcct 240

ccacccacac taagatggga actcggcttt ggtttgttct acttttagct cttctacatt 300

gagtcaaaga atgttaacat cgaatgaatc acaaaagctt gaaatgccac ctcctctgat 360

attctaggtg tcctggaagc ctgtctcatc ttgccctgta gtgttgggtc acctggcccc 420

cagcctgtaa catccccagg gccctacacc cagagaaaca cggggctggt ggcagtgccc 480

agtgacaacc gtttagtgga taagagaaga gtgaccacac caggctgagt gctcctctct 540

ggttttccat ggggagacaa tgccaccctg agcagggtct ggtgtgagcg ggcagcttgg 600

ctctgggctc tctgatccgt taccctctca gcctctttgt tctttctcaa cccctggagc 660

agagacctca ggaggtgctg gcatggaaca gagaaattcc agcctcgatt cctattatga 720

acccgacacc ttttgtattt tcatcttggt tttacagtgt acaaaacgaa ctagatcagc 780

agggcatggg cataatcacg aatgcacaca catacactaa tgtgtggctc atgtttaagt 840

atcacttact acaggacacc caatctaaca gcaccgataa agtgacagag aaacgcaagc 900

cttctgcgaa catggcctgg ctgttccaat tccgaacctt gcttttctgg gccttgccac 960

acaggctctt cccccgtccc cccagggaca ttctaccctt gaactccaca ctccactgct 1020

gcctttgcca ggaagcccat ctgttccttt ttggttctgc cagaacgtgt ggtggtgctg 1080

ctgtccctgc cctgggcact ggatattggg aagggacagt gtccacactg gagtgggaag 1140

tccccaggga cgagaccttt acctcctcac ccctgggtac tgttctcctc atggagcatg 1200

gatttaaat 1209

<210> 1392
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1392
ccagggattt acagatcaca tgcaggcagg gaccagctca actcttctat ttaaat 56

<210> 1393
<211> 1519
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1393
aatgttaaca tcgaatgaat cacaaaagct tgaaatgcca cctcctctga tattctaggt 60

gtcctggaag cctgtctcat cttgccctgt agtgttgggt cacctggccc ccagcctgta 120

acatccccag ggccctacac ccagagaaac acggggctgg tggcagtgcc cagtgacaac 180

cgtttagtgg ataagagaag agtgaccaca ccaggctgag tgctcctctc tggttttcca 240

tggggagaca atgccaccct gagcagggtc tggtgtgagc gggcagcttg gctctgggct 300

ctctgatccg ttaccctctc agcctctttg ttctttctca acccctggag cagagacctc 360

aggaggtgct ggcatggaac agagaaattc cagcctcgat tcctattatg aacccgacac 420

cttttgtatt ttcatcttgg ttttacagtg tacaaaacga actagatcag cagggcatgg 480

gcataatcac gaatgcacac acatacacta atgtgtggct catgtttaag tatcacttac 540

tacaggacac ccaatctaac agcaccgata aagtgacaga gaaacgcaag ccttctgcga 600

acatggcctg gctgttccaa ttccgaacct tgcttttctg ggccttgcca cacaggctct 660

tcccccgtcc ccccagggac attctaccct tgaactccac actccactgc tgcctttgcc 720

aggaagccca tctgttcctt tttggttctg ccagaacgtg tggtggtgct gctgtccctg 780

ccctgggcac tggatattgg gaagggacag tgtccacact ggagtgggaa gtccccaggg 840

acgagacctt tacctcctca cccctgggta ctgtcctcct catggagcat ggatggcgct 900

gcctgaactc agtggtggcc tcattctgga agccaagttt atacagagta gcagtgaccc 960

agggatgtgg ggttcaccct cctcagccct ctggccagtc ctgatgggcc tcagtcccaa 1020

catggctaag aggtgtgggc agcttcttgg tcaccctcag gttggggaat caccttctgt 1080

cttcattttc caggaacttg gtgatgatat cgtgggtgag ttcattttcc aggtgctgta 1140

gtttcccctc atcaggcagg aagaagatgg cggtggcatt gcccaggtat ttcatcagca 1200

gcacccagct ggacagcttc ttacagtgct ggatgttaaa catgcctaaa cgcttcatca 1260

taggcacctt cacggtggtc acctggtcca cgtggaagtc ctcttcctcg gtgtccttga 1320

cttcaaaggg tctctcccat ttgcctggag agaggggaag gtgggcatca ccaggggtga 1380

gtgaaggttt ggaagagtgt agcagaataa agaaaccatg agtcccctcc ctgagaagcc 1440

ctgagccccc ttgacgacac acatccctcg aggctcagct tcatcatctg taaaaggtgc 1500

tgaaactgac catttaaat 1519

<210> 1394
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1394
gagagaagca gagacacgtt gtaaggctga tcccaggcct cgagcaaggc tcacgtggac 60

acctcccagg aagcgctcac tccccctgga cggccctggc cctgcacatc ctctccctcc 120

ctgtcacata ggccttgctc ctcctcaagg ctttggctga tggggctggc tcccctctgt 180

ccatcttcct gacaagcgcc tctccccctg ctcaggtgca cccacaactc agaacaggga 240

agagcatcgt cactccacgt ctgcctccag ggctctctcc tttctagtac acggcttgaa 300

gctccttgag gacacggacc ctggcagtga ccttcacagt gcccagacca tttaaat 357

<210> 1395
<211> 2403
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1395
aattcgccct tgggcctagg caattggatc cgccggcaga gaaaacatcc cagggattta 60

cagatcacat gcaggcaggg accagctcaa cccttcttta atgtcatcca gggaggggggc 120

cagggatgga ggggaggggt tgaggagcga gaggcagtta tttttgggtg ggattcacca 180

cttttcccat gaagagggga gacttggtat tttgttcaat cattaagaag acaaagggtt 240

tgttgaactt gacctcgggg gggatagaca tgggtatggc ctctaaaaac atggccccag 300

cagcttcagt ccctttctcg tcgatggtca gcacagcctt atgcacggcc tggaggggag 360

agaagcagag acacgttgta aggctgatcc caggcctcga gcaaggctca cgtggacacc 420

tcccaggaag cgctcactcc ccctggacgg ccctggccct gcacatcctc tccctccctg 480

tcacataggc cttgctcctc ctcaaggctt tggctgatgg ggctggctcc cctctgtcca 540

tcttcctgac aagcgcctct ccccctgctc aggtgcaccc acaactcaga acagggaaga 600

gcatcgtcac tccacgtctg cctccagggc tctctccttt ctagtacacg gcttgaagct 660

ccttgaggac acggaccctg gcagtgacct tcacagtgcc cagaccccaa gataatgcag 720

ccattcatgg aactgcaggt tgttcattgg tcgcctttag ttttccaaaa taagtgtcac 780

tttagctgaa atcattcatt aattcagaca ccaaatctca cagatcgaag gagtcagaaa 840

ttcctttgaa acaacttagc ccaaaccttt ctgtgtcagt atggataaat caaggcccaa 900

tgtctagaag gtcttgggca aagttgaaat tcagggtcag tgacacaacc tcaagggagg 960

ccccgaaagt gccagctgca cagcagcccc tgcctggctt tgctgtttgc ccaccgtccc 1020

gtgtcagtga atcacgggca tcttcaggag ctcagcctgg gtcttcattt gtttccctcg 1080

gcccccttcct cagcctcagg acagtgctgc agcccccaca cattcttccc tacagatacc 1140

atggtgcaac aaggtcgtca gggtgatctc accttggaga gcttcagggg tgcctcctct 1200

gtgaccccgg agaggtcagc cccattgctg aagaccttag tgatgcccag ttgacccagg 1260

acgctcttca gatcataggt tccagtaatg gacagtttgg gtaaatgtaa gctggcagac 1320

ctgtcgtgca gaaaagaaat tcaaggcatg gcacagcatt cctcttgttc ttctgggacc 1380

caccacagtg caagtgtttt cttttctgat tatttctgcc acttactcct gtgtcctcca 1440

cccacactaa gatgggaact cggctttggt ttgttctact tttagctctt ctacattgag 1500

tcaaagaatg ttaacatcga atgaatcaca aaagcttgaa atgccacctc ctctgatatt 1560

ctaggtgtcc tggaagcctg tctcatcttg ccctgtagtg ttgggtcacc tggcccccag 1620

cctgtaacat ccccagggcc ctacacccag agaaacacgg ggctggtggc agtgcccagt 1680

gacaaccgtt tagtggataa gagaagagtg accacaccag gctgagtgct cctctctggt 1740

tttccatggg gagacaatgc caccctgagc agggtctggt gtgagcggca gctggctctg 1800

ggctctctga tccgttaccc tctcagcctc tttgttcttt ctcaacccct ggagcagaga 1860

cctcaggagg tgctggcatg gaacagagaa attccagcct cgattcctat tatgaacccg 1920

acacctttg tattttcatc ttggttttac agtgtacaaa acgaactaga tcagcagggc 1980

atgggcataa tcacgaatgc acacacatac actaatgtgt ggctcatgtt taagtatcac 2040

ttactacagg acacccaatc taacagcacc gataaagtga cagagaaacg caagccttct 2100

gcgaacatgg cctggctgtt ccaattccga accttgcttt tctgggcctt gccacacagg 2160

ctcttccccc gtccccccag ggacattcta cccttgaact ccacactcca ctgctgcctt 2220

tgccaggaag cccatctgtt ccttttttggt tctgccagaa cgtgtggtgg tgctgctgtc 2280

cctgccttgg gcactggata ttgggaaggg acagtgtcca cactggagtg ggaagttccc 2340

agggacgaga cctttacctc ctcaccctgg gtactgttct cctcatggag catggattta 2400

aat 2403

<210> 1396
<211> 105

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1396
aattcgccct tgggcctagg caattggatc cgccggcaga gaaaacatcc cagggattta 60

cagatcacat gcaggcaggg accagctcaa cccttctatt taaat 105

<210> 1397
<211> 382
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1397
cgcgtcgaca ttgattattg actagttatt aatagtaatc aattacgggg tcattagttc 60

atagcccata tatggagttc cgcgttacat aacttacggt aaatggcccg cctggctgac 120

cgcccaacga cccccgccca ttgacgtcaa taatgacgta tgttcccata gtaacgccaa 180

tagggacttt ccattgacgt caatgggtgg agtatttacg gtaaactgcc cacttggcag 240

tacatcaagt gtatcatatg ccaagtacgc cccctattga cgtcaatgac ggtaaatggc 300

ccgcctggca ttatgcccag tacatgacct tatgggactt tcctacttgg cagtacatct 360

acgtattagt catcgctatt ac 382

<210> 1398
<211> 303
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1398
cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc cccgcccatt 60

gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc attgacgtca 120

atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt atcatatgcc 180

aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt atgcccagta 240

catgacctta tgggactttc ctacttggca gtacatctag tattagtcat cgctattacc 300

atg 303

<210> 1399
<211> 260
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1399
ccacgttctg cttcactctc cccatctccc ccccctcccc acccccaatt ttgtatttat 60

ttatttttta attattttgt gcagcgatgg gggcgggggg ggggggcgcg cgccaggcgg 120

ggcggggcgg ggcgaggggc ggggcggggc gaggcggaga ggtgcggcgg cagccaatca 180

gagcggcgcg ctccgaaagt ttccttttat ggcgaggcgg cggcggcggc ggccctataa 240

aaagcgaagc gcgcggcggg 260

<210> 1400
<211> 588
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1400
gttgacattg attattgact agttattaat agtaatcaat tacggggtca ttagttcata 60

gcccatatat ggagttccgc gttacataac ttacggtaaa tggcccgcct ggctgaccgc 120

ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag 180

ggactttcca ttgacgtcaa tgggtggagt atttacggta aactgcccac ttggcagtac 240

atcaagtgta tcatatgcca agtacgcccc ctattgacgt caatgacggt aaatggcccg 300

cctggcatta tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg 360

tattagtcat cgctattacc atggtgatgc ggttttggca gtacatcaat gggcgtggat 420

agcggtttga ctcacgggga tttccaagtc tccaccccat tgacgtcaat gggagtttgt 480

tttggcacca aaatcaacgg gactttccaa aatgtcgtaa caactccgcc ccattgacgc 540

aaatgggcgg taggcgtgta cggtgggagg tctatataag cagagctc 588

<210> 1401
<211> 204
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1401
gtgatgcggt tttggcagta catcaatggg cgtggatagc ggtttgactc acggggattt 60

ccaagtctcc accccattga cgtcaatggg agtttgtttt ggcaccaaaa tcaacgggac 120

tttccaaaat gtcgtaacaa ctccgcccca ttgacgcaaa tgggcggtag gcgtgtacgg 180

tgggaggtct atataagcag agct 204

<210> 1402
<211> 219
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1402
aattcgaacg ctgacgtcat caacccgctc caaggaatcg cgggcccagt gtcactaggc 60

gggaacaccc agcgcgcgtg cgccctggca ggaagatggc tgtgagggac agggagtggc 120

gccctgcaat atttgcatgt cgctatgtgt tctgggaaat caccataaac gtgaaatgtc 180

tttggatttg ggaatcttat aagttctgta tgagaccac 219

<210> 1403
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1403
taatacgact cactata 17

<210> 1404
<211> 134
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1404
tcagatcgcc tggagacgcc atccacgctg ttttgacctc catagaagac accgggaccg 60

atccagcctc cgcggattcg aatcccggcc gggaacggtg cattggaacg cggattcccc 120

gtgccaagag tgac 134

<210> 1405
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1405
ctcctgggca acgtgctggt ctgtgtgctg gcccatcact ttggcaaaga att 53

<210> 1406
<211> 172
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1406
gaactgaaaa accagaaagt taactggtaa gtttagtctt tttgtctttt atttcaggtc 60

ccggatccgg tggtggtgca aatcaaagaa ctgctcctca gtggatgttg cctttacttc 120

taggcctgta cggaagtgtt acttctgctc taaaagctgc ggaattgtac cc 172

<210> 1407
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1407
gtaagtaccg cctatagagt ctataggccc ac 32

<210> 1408
<211> 347
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1408
aaaaaatgct ttcttctttt aatatacttt tttgtttatc ttatttctaa tactttccct 60

aatctctttc tttcagggca ataatgatac aatgtatcat gcctctttgc accattctaa 120

agaataacag tgataatttc tgggttaagg caatagcaat atttctgcat ataaatattt 180

ctgcatataa attgtaactg atgtaagagg tttcatattg ctaatagcag ctacaatcca 240

gctaccattc tgcttttatt ttatggttgg gataaggctg gattattctg agtccaagct 300

aggccctttt gctaatcatg ttcatacctc ttatcttcct cccacag 347

<210> 1409
<211> 201
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1409
gaactgaaaa accagaaagt taactggtaa gtttagtctt tttgtctttt atttcaggtc 60

ccggatccgg tggtggtgca aatcaaagaa ctgctcctca gtggatgttg cctttacttc 120

taggcctgta cggaagtgtt acttctgctc taaaagctgc ggaattgtac ccgcggccga 180

tccaccggta aacttaagct t 201

<210> 1410
<211> 127
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1410
gatcttttc cctctgccaa aaattatggg gacatcatga agcccttga gcatctgact 60

tctggctaat aaaggaaatt tattttcatt gcaatagtgt gttggaattt tttgtgtctc 120

tcactcg 127

<210> 1411
<211> 225

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1411
ctgtgccttc tagttgccag ccatctgttg tttgcccctc ccccgtgcct tccttgaccc 60

tggaaggtgc cactcccact gtcctttcct aataaaatga ggaaattgca tcgcattgtc 120

tgagtaggtg tcattctatt ctgggggggtg gggtggggca ggacagcaag ggggaggatt 180

gggaagacaa tagcaggcat gctggggatg cggtgggctc tatgg 225

<210> 1412
<211> 477
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1412
gggtggcatc cctgtgaccc ctccccagtg cctctcctgg ccctggaagt tgccactcca 60

gtgcccacca gccttgtcct aataaaatta agttgcatca ttttgtctga ctaggtgtcc 120

ttctataata ttatggggtg gagggggggtg gtatggagca aggggcaagt tgggaagaca 180

acctgtaggg cctgcggggt ctattgggaa ccaagctgga gtgcagtggc acaatcttgg 240

ctcactgcaa tctccgcctc ctgggttcaa gcgattctcc tgcctcagcc tcccgagttg 300

ttgggattcc aggcatgcat gaccaggctc agctaatttt tgtttttttg gtagagacgg 360

ggtttcacca tattggccag gctggtctcc aactcctaat ctcaggtgat ctacccacct 420

tggcctccca aattgctggg attacaggcg tgaaccactg ctcccttccc tgtcctt 477

<210> 1413
<211> 476
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1413
gggtggcatc cctgtgaccc ctccccagtg cctctcctgg ccctggaagt tgccactcca 60

gtgcccacca gccttgtcct aataaaatta agttgcatca ttttgtctga ctaggtgtcc 120

ttctataata ttatggggtg gaggggggtg gtatggagca aggggcaagt tgggaagaca 180

acctgtaggg cctgcggggt ctattgggaa ccaagctgga gtgcagtggc acaatcttgg 240

ctcactgcaa tctccgcctc ctgggttcaa gcgattctcc tgcctcagcc tcccgagttg 300

ttgggattcc aggcatgcat gaccaggctc agctaatttt tgtttttttg gtagagacgg 360

ggtttcacca tattggccag gctggtctcc aactcctaat ctcaggtgat ctacccacct 420

tggcctccca aattgctggg attacaggcg tgaaccactg ctcccttccc tgtcct 476

<210> 1414
<211> 1975
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1414
ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgtcg ggcgaccttt 60

ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gagtgtagcc atgctctagg 120

aagatcaatt caattcacgc gtcgacattg attattgact agttattaat agtaatcaat 180

tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 240

tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt 300

tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggagt atttacggta 360

aactgcccac ttggcagtac atcaagtgta tcatatgcca agtacgcccc ctattgacgt 420

caatgacggt aaatggcccg cctggcatta tgcccagtac atgaccttat gggactttcc 480

tacttggcag tacatctacg tattagtcat cgctattacc atgtcgaggc cacgttctgc 540

ttcactctcc ccatctcccc cccctcccca cccccaattt tgtatttatt tatttttaa 600

ttattttgtg cagcgatggg ggcgggggggg gggggcgcgc gccaggcggg gcggggcggg 660

gcgaggggcg gggcggggcg aggcggagag gtgcggcggc agccaatcag agcggcgcgc 720

tccgaaagtt tccttttatg gcgaggcggc ggcggcggcg gccctataaa aagcgaagcg 780

cgcggcgggc gggagcaagc ttgcctggag acgccatcca cgctgttttg acctccatag 840

aagacaccgg gaccgatcca gcctccgcgg attcgaatcc cggccgggaa cggtgcattg 900

gaacgcggat tccccgtgcc aagagtgacg taagtaccgc ctatagagtc tataggccca 960

caaaaaatgc tttcttcttt taatatactt ttttgtttat cttatttcta atactttccc 1020

taatctcttt ctttcagggc aataatgata caatgtatca tgcctctttg caccattcta 1080

aagaataaca gtgataattt ctgggttaag gcaatagcaa tatttctgca tataaatatt 1140

tctgcatata aattgtaact gatgtaagag gtttcatatt gctaatagca gctacaatcc 1200

agctaccatt ctgcttttat tttatggttg ggataaggct ggattattct gagtccaagc 1260

taggcccttt tgctaatcat gttcatacct cttatcttcc tcccacagct cctgggcaac 1320

gtgctggtct gtgtgctggc ccatcacttt ggcaaagaat tgggattcga acatcgaccg 1380

gtgaagcaaa gaaggggcag agggagcccg tgagctgagt gggccaggga ctgggagaag 1440

gagtgaggag gcagggccgg catgcctctg ctgctggcca gacccttaa ctcatttgtt 1500

cccgtctgca cctgtcacta gtaacagatg agttaagggg tttggccgtg tagtgctacc 1560

cagcgctggc tgcctcctca gcattgcaat tcctctccca tctgggcacc agtcagctac 1620

cctggtggga atctgggtag ccctcgagga cggggtgaac tacgcctgag gatccgatct 1680

ttttccctct gccaaaaatt atggggacat catgaagccc cttgagcatc tgacttctgg 1740

ctaataaagg aaatttattt tcattgcaat agtgtgttgg aatttttgt gtctctcact 1800

cggcctaggt agataagtag catggcgggt taatcattaa ctacaaggaa cccctagtga 1860

tggagttggc cactccctct ctgcgcgctc gctcgctcac tgaggccggg cgaccaaagg 1920

tcgcccgacg cccgggcttt gcccgggcgg cctcagtgag cgagcgagcg cgcag 1975

<210> 1415
<211> 1900
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1415
ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgtcg ggcgaccttt 60

ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gagtgtagcc atgctctagg 120

aagatcaatt caattcacgc gtatatctag actagttatt aatagtaatc aattacgggg 180

tcattagttc atagcccata tatggagttc cgcgttacat aacttacggt aaatggcccg 240

cctggctgac cgcccaacga cccccgccca ttgacgtcaa taatgacgta tgttcccata 300

gtaacgtcaa tagggacttt ccattgacgt caatgggtgg agtatttacg gtaaactgcc 360

cacttggcag tacatcaagt gtatcatatg ccaagtacgc cccctattga cgtcaatgac 420

ggtaaatggc ccgcctggca ttatgcccag tacatgacct tatgggactt tcctacttgg 480

cagtacatct acgtattagt catcgctatt accatggtga tgcggttttg gcagtacatc 540

aatgggcgtg gatagcggtt tgactcacgg ggatttccaa gtctccaccc cattgacgtc 600

aatgggagtt tgttttgcac caaaatcaac gggactttcc aaaatgtcgt aacaactccg 660

ccccattgac gcaaatgggc ggtaggcgtg tacggtggga ggtctatata agcagagctc 720

gtttagtgaa ccgtcagatc gcctggagac gccatccacg ctgttttgac ctccatagaa 780

gacaccggga ccgatccagc ctccgcggat tcgaatcccg gccgggaacg gtgcattgga 840

acgcggattc cccgtgccaa gagtgacgta agtaccgcct atagagtcta taggcccaca 900

aaaaatgctt tcttctttta atatactttt ttgtttatct tatttctaat actttcccta 960

atctctttct ttcagggcaa taatgataca atgtatcatg cctctttgca ccattctaaa 1020

gaataacagt gataatttct gggttaaggc aatagcaata tttctgcata taaatatttc 1080

tgcatataaa ttgtaactga tgtaagaggt ttcatattgc taatagcagc tacaatccag 1140

ctaccattct gcttttattt tatggttggg ataaggctgg attattctga gtccaagcta 1200

ggccctttg ctaatcatgt tcatacctct tatcttcctc ccacagctcc tgggcaacgt 1260

gctggtctgt gtgctggccc atcactttgg caaagaattg gaccggtgaa gcaaagaagg 1320

ggcagaggga gcccgtgagc tgagtgggcc agggactggg agaaggagtg aggaggcagg 1380

gccggcatgc ctctgctgct ggccagaccc cttaactcat ttgttcccgt ctgcacctgt 1440

cactagtaac agatgagtta aggggtttgg ccgtgtagtg ctacccagcg ctggctgcct 1500

cctcagcatt gcaattcctc tcccatctgg gcaccagtca gctaccctgg tgggaatctg 1560

ggtagccctc gaggacgggg tgaactacgc ctgaggatcc gatcttttc cctctgccaa 1620

aaattatggg gacatcatga agccccttga gcatctgact tctggctaat aaaggaaatt 1680

tattttcatt gcaatagtgt gttggaattt tttgtgtctc tcactcggcc taggtagata 1740

agtagcatgg cgggttaatc attaactaca aggaacccct agtgatggag ttggccactc 1800

cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc cgacgcccgg 1860

gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag 1900

<210> 1416
<211> 1881
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1416
ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgtcg ggcgaccttt 60

ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gagtgtagcc atgctctagg 120

aagatcaatt caattcacgc gtcgacattg attattgact agttattaat agtaatcaat 180

tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 240

tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt 300

tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggagt atttacggta 360

aactgcccac ttggcagtac atcaagtgta tcatatgcca agtacgcccc ctattgacgt 420

caatgacggt aaatggcccg cctggcatta tgcccagtac atgaccttat gggactttcc 480

tacttggcag tacatctacg tattagtcat cgctattacc atgtcgaggc cacgttctgc 540

ttcactctcc ccatctcccc cccctcccca cccccaattt tgtatttatt tatttttaa 600

ttattttgtg cagcgatggg ggcgggggggg gggggcgcgc gccaggcggg gcggggcggg 660

gcgaggggcg gggcggggcg aggcggagag gtgcggcggc agccaatcag agcggcgcgc 720

tccgaaagtt tccttttatg gcgaggcggc ggcggcggcg gccctataaa aagcgaagcg 780

cgcggcgggc gggagcaagc ttgcctggag acgccatcca cgctgttttg acctccatag 840

aagacaccgg gaccgatcca gcctccgcgg attcgaatcc cggccgggaa cggtgcattg 900

gaacgcggat tccccgtgcc aagagtgacg taagtaccgc ctatagagtc tataggccca 960

caaaaaatgc tttcttcttt taatatactt ttttgtttat cttatttcta atactttccc 1020

taatctcttt ctttcagggc aataatgata caatgtatca tgcctctttg caccattcta 1080

aagaataaca gtgataattt ctgggttaag gcaatagcaa tatttctgca tataaatatt 1140

tctgcatata aattgtaact gatgtaagag gtttcatatt gctaatagca gctacaatcc 1200

agctaccatt ctgcttttat tttatggttg ggataaggct ggattattct gagtccaagc 1260

taggcccttt tgctaatcat gttcatacct cttatcttcc tcccacagct cctgggcaac 1320

gtgctggtct gtgtgctggc ccatcacttt ggcaaagaat tgggattcga acatcgaccg 1380

gtaccgagct gtgctgggcg gggggcggcg ggccctcccg cagaacacca tgcgctcttc 1440

ggaaccctta actgatctgt taacctgtga cctggttaac agatgagtta agggttctgt 1500

ggagcgcctt gacagcagcc atgggagggc cgccccctac ctcagtgact cgaggacggg 1560

gtgaactacg cctgaggatc cgatcttttt ccctctgcca aaaattatgg ggacatcatg 1620

aagccccttg agcatctgac ttctggctaa taaaggaaat ttattttcat tgcaatagtg 1680

tgttggaatt ttttgtgtct ctcactcggc ctaggtagat aagtagcatg gcgggttaat 1740

cattaactac aaggaacccc tagtgatgga gttggccact ccctctctgc gcgctcgctc 1800

gctcactgag gccgggcgac caaaggtcgc ccgacgcccg ggctttgccc gggcggcctc 1860

agtgagcgag cgagcgcgca g 1881

<210> 1417
<211> 1805
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1417
ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgtcg ggcgaccttt 60

ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gagtgtagcc atgctctagg 120

aagatcaatt caattcacgc gtaccgagct ctagttatta atagtaatca attacggggt 180

cattagttca tagcccatat atggagttcc gcgttacata acttacggta aatggcccgc 240

ctggctgacc gcccaacgac ccccgcccat tgacgtcaat aatgacgtat gttcccatag 300

taacgtcaat agggactttc cattgacgtc aatgggtgga gtatttacgg taaactgccc 360

acttggcagt acatcaagtg tatcatatgc caagtacgcc ccctattgac gtcaatgacg 420

gtaaatggcc cgcctggcat tatgcccagt acatgacctt atgggacttt cctacttggc 480

agtacatcta cgtattagtc atcgctatta ccatggtgat gcggttttgg cagtacatca 540

atgggcgtgg atagcggttt gactcacggg gatttccaag tctccacccc attgacgtca 600

atgggagttt gttttgcacc aaaatcaacg ggactttcca aaatgtcgta acaactccgc 660

cccattgacg caaatgggcg gtaggcgtgt acggtgggag gtctatataa gcagagctcg 720

tttagtgaac cgtcagatcg cctggagacg ccatccacgc tgttttgacc tccatagaag 780

acaccgggac cgatccagcc tccgcggatt cgaatcccgg ccgggaacgg tgcattggaa 840

cgcggattcc ccgtgccaag agtgacgtaa gtaccgccta tagagtctat aggcccacaa 900

aaaatgcttt cttcttttaa tatacttttt tgtttatctt atttctaata ctttccctaa 960

tctctttctt tcagggcaat aatgatacaa tgtatcatgc ctctttgcac cattctaaag 1020

aataacagtg ataatttctg ggttaaggca atagcaatat ttctgcatat aaatatttct 1080

gcatataaat tgtaactgat gtaagaggtt tcatattgct aatagcagct acaatccagc 1140

taccattctg cttttatttt atggttggga taaggctgga ttattctgag tccaagctag 1200

gccctttttgc taatcatgtt catacctctt atcttcctcc cacagctcct gggcaacgtg 1260

ctggtctgtg tgctggccca tcactttggc aaagaattgg accggtaccg agctgtgctg 1320

ggcgggggggc ggcgggccct cccgcagaac accatgcgct cttcggaacc cttaactgat 1380

ctgttaacct gtgacctggt taacagatga gttaagggtt ctgtggagcg ccttgacagc 1440

agccatggga gggccgcccc ctacctcagt gactcgagga cggggtgaac tacgcctgag 1500

gatccgatct ttttccctct gccaaaaatt atggggacat catgaagccc cttgagcatc 1560

tgacttctgg ctaataaagg aaatttattt tcattgcaat agtgtgttgg aatttttgt 1620

gtctctcact cggcctaggt agataagtag catggcgggt taatcattaa ctacaaggaa 1680

cccctagtga tggagttggc cactccctct ctgcgcgctc gctcgctcac tgaggccggg 1740

cgaccaaagg tcgcccgacg cccgggcttt gcccgggcgg cctcagtgag cgagcgagcg 1800

cgcag 1805

<210> 1418
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1418

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445
```

```
Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Asp Gly Thr Leu Ala Val
            580                 585                 590

Pro Phe Lys Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670
```

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
675 680 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
690 695 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705 710 715 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
725 730 735

Arg Tyr Leu Thr Arg Asn Leu
740

<210> 1419
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1419

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Gln Ala Val Arg
            580                 585                 590

Thr Ser Leu Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735
```

Arg Tyr Leu Thr Arg Asn Leu
            740

<210> 1420
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1420

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  1421
<211>  534
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1421

Met Ala Glu Gly Gly Gly Gly Ala Met Gly Asp Ser Ser Gly Gly Ala
1               5                   10                  15


Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Gln Trp
            20                  25                  30
```

```
Met Gly Asn Thr Val Ile Thr Lys Thr Thr Arg Thr Trp Val Leu Pro
        35                  40                  45

Ser Tyr Asn Asn His Ile Tyr Lys Ala Ile Thr Ser Gly Thr Ser Gln
    50                  55                  60

Asp Ala Asn Val Gln Tyr Ala Gly Tyr Ser Thr Pro Trp Gly Tyr Phe
65                  70                  75                  80

Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg
                85                  90                  95

Leu Ile Asn Asn His Trp Gly Ile Arg Pro Lys Ser Leu Lys Phe Lys
            100                 105                 110

Ile Phe Asn Val Gln Val Lys Glu Val Thr Thr Gln Asp Gln Thr Lys
        115                 120                 125

Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Asp
    130                 135                 140

Glu His Gln Leu Pro Tyr Val Leu Gly Ser Ala Thr Glu Gly Thr Met
145                 150                 155                 160

Pro Pro Phe Pro Ser Asp Val Tyr Ala Leu Pro Gln Tyr Gly Tyr Cys
                165                 170                 175

Thr Met His Thr Asn Gln Asn Gly Ala Arg Phe Asn Asp Arg Ser Ala
            180                 185                 190

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
        195                 200                 205

Asn Phe Glu Phe Thr Phe Asp Phe Glu Glu Val Pro Phe His Ser Met
    210                 215                 220

Phe Ala His Ser Gln Asp Leu Asp Arg Leu Met Asn Pro Leu Val Asp
225                 230                 235                 240

Gln Tyr Leu Trp Asn Phe Asn Glu Val Asp Ser Ser Arg Asn Ala Gln
                245                 250                 255
```

```
Phe Lys Lys Ala Val Lys Gly Ala Tyr Gly Thr Met Gly Arg Asn Trp
            260                 265                 270

Leu Pro Gly Pro Lys Phe Leu Asp Gln Arg Val Arg Ala Tyr Thr Gly
        275                 280                 285

Gly Thr Asp Asn Tyr Ala Asn Trp Asn Ile Trp Ser Asn Gly Asn Lys
    290                 295                 300

Val Asn Leu Lys Asp Arg Gln Tyr Leu Leu Gln Pro Gly Pro Val Ser
305                 310                 315                 320

Ala Thr Tyr Thr Glu Gly Glu Ala Ser Ser Leu Pro Ala Gln Asn Ile
                325                 330                 335

Leu Gly Ile Ala Lys Asp Pro Tyr Arg Ser Gly Ser Thr Thr Ala Gly
            340                 345                 350

Ile Ser Asp Ile Met Val Thr Glu Glu Gln Glu Val Ala Pro Thr Asn
        355                 360                 365

Gly Val Gly Trp Lys Pro Tyr Gly Arg Thr Val Thr Asn Glu Gln Asn
    370                 375                 380

Thr Thr Thr Ala Pro Thr Ser Ser Asp Leu Asp Val Leu Gly Ala Leu
385                 390                 395                 400

Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Leu Gln Gly Pro Ile
                405                 410                 415

Gly Ala Lys Ile Pro Lys Thr Asp Gly Lys Phe His Pro Ser Pro Asn
            420                 425                 430

Leu Gly Gly Phe Gly Leu His Asn Pro Pro Pro Gln Val Phe Ile Lys
        435                 440                 445

Asn Thr Pro Val Pro Ala Asp Pro Pro Val Glu Tyr Val His Gln Lys
    450                 455                 460
```

```
Trp Asn Ser Tyr Ile Thr Gln Tyr Ser Thr Gly Gln Cys Thr Val Glu
465                 470                 475                 480


Met Val Trp Glu Leu Arg Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
                485                 490                 495


Ile Gln Phe Thr Ser Asn Phe Ser Asn Arg Thr Ser Ile Met Phe Ala
            500                 505                 510


Pro Asn Glu Thr Gly Gly Tyr Val Glu Asp Arg Leu Ile Gly Thr Arg
        515                 520                 525


Tyr Leu Thr Gln Asn Leu
    530


<210>  1422
<211>  554
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1422

Met Thr Ser Val Asn Ser Ala Glu Ala Ser Thr Gly Ala Gly Gly Gly
1               5                   10                  15


Gly Ser Asn Pro Val Lys Ser Met Trp Ser Glu Gly Ala Thr Phe Ser
            20                  25                  30


Ala Asn Ser Val Thr Cys Thr Phe Ser Arg Gln Phe Leu Ile Pro Tyr
        35                  40                  45


Asp Pro Glu His His Tyr Lys Val Phe Ser Pro Ala Ala Ser Ser Cys
    50                  55                  60


His Asn Ala Ser Gly Lys Glu Ala Lys Val Cys Thr Ile Ser Pro Ile
65                  70                  75                  80


Met Gly Tyr Ser Thr Pro Trp Arg Tyr Leu Asp Phe Asn Ala Leu Asn
                85                  90                  95
```

```
Leu Phe Phe Ser Pro Leu Glu Phe Gln His Leu Ile Glu Asn Tyr Gly
            100                 105                 110

Ser Ile Ala Pro Asp Ala Leu Thr Val Thr Ile Ser Glu Ile Ala Val
        115                 120                 125

Lys Asp Val Thr Asp Lys Thr Gly Gly Gly Val Gln Val Thr Asp Ser
    130                 135                 140

Thr Thr Gly Arg Leu Cys Met Leu Val Asp His Glu Tyr Lys Tyr Pro
145                 150                 155                 160

Tyr Val Leu Gly Gln Gly Gln Asp Thr Leu Ala Pro Glu Leu Pro Ile
                165                 170                 175

Trp Val Tyr Phe Pro Pro Gln Tyr Ala Tyr Leu Thr Val Gly Asp Val
            180                 185                 190

Asn Thr Gln Gly Ile Ser Gly Asp Ser Lys Lys Leu Ala Ser Glu Glu
        195                 200                 205

Ser Ala Phe Tyr Val Leu Glu His Ser Ser Phe Gln Leu Leu Gly Thr
    210                 215                 220

Gly Gly Thr Ala Thr Met Ser Tyr Lys Phe Pro Pro Val Pro Pro Glu
225                 230                 235                 240

Asn Leu Glu Gly Cys Ser Gln His Phe Tyr Glu Met Tyr Asn Pro Leu
                245                 250                 255

Tyr Gly Ser Arg Leu Gly Val Pro Asp Thr Leu Gly Gly Asp Pro Lys
            260                 265                 270

Phe Arg Ser Leu Thr His Glu Asp His Ala Ile Gln Pro Gln Asn Phe
        275                 280                 285

Met Pro Gly Pro Leu Val Asn Ser Val Ser Thr Lys Glu Gly Asp Ser
    290                 295                 300

Phe Asn Thr Gly Ala Gly Lys Ala Leu Thr Gly Leu Ser Thr Gly Thr
305                 310                 315                 320
```

```
Ser Gln Asn Thr Arg Ile Ser Leu Arg Pro Gly Pro Val Ser Gln Pro
                325                 330                 335

Tyr His His Trp Asp Thr Asp Lys Tyr Val Thr Gly Ile Asn Ala Ile
            340                 345                 350

Ser His Gly Gln Thr Thr Tyr Gly Asn Ala Glu Asp Lys Glu Tyr Gln
        355                 360                 365

Gln Gly Val Gly Arg Phe Pro Asn Glu Lys Glu Gln Leu Lys Gln Leu
    370                 375                 380

Gln Gly Leu Asn Met His Thr Tyr Phe Pro Asn Lys Gly Thr Gln Gln
385                 390                 395                 400

Tyr Thr Asp Gln Ile Glu Arg Pro Leu Met Val Gly Ser Val Trp Asn
                405                 410                 415

Arg Arg Ala Leu His Tyr Glu Ser Gln Leu Trp Ser Lys Ile Pro Asn
            420                 425                 430

Leu Asp Asp Ser Phe Lys Thr Gln Phe Ala Ala Leu Gly Gly Trp Gly
        435                 440                 445

Leu His Gln Pro Pro Pro Gln Ile Phe Leu Lys Ile Leu Pro Gln Ser
    450                 455                 460

Gly Pro Ile Gly Gly Ile Lys Ser Met Gly Ile Thr Thr Leu Val Gln
465                 470                 475                 480

Tyr Ala Val Gly Ile Met Thr Val Thr Met Thr Phe Lys Leu Gly Pro
                485                 490                 495

Arg Lys Ala Thr Gly Arg Trp Asn Pro Gln Pro Gly Val Tyr Pro Pro
            500                 505                 510

His Ala Ala Gly His Leu Pro Tyr Val Leu Tyr Asp Pro Thr Ala Thr
        515                 520                 525
```

Asp Ala Lys Gln His His Arg His Gly Tyr Glu Lys Pro Glu Glu Leu
530 535 540

Trp Thr Ala Lys Ser Arg Val His Pro Leu
545 550

<210> 1423
<211> 587
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1423

Met Ser Asp Gly Thr Ser Gln Pro Asp Gly Gly Asn Ala Val His Ser
1 5 10 15

Ala Ala Arg Val Glu Arg Ala Ala Asp Gly Pro Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Val Gly Val Ser Thr Gly Ser Tyr Asp
35 40 45

Asn Gln Thr His Tyr Arg Phe Leu Gly Asp Gly Trp Val Glu Ile Thr
50 55 60

Ala Leu Ala Thr Arg Leu Val His Leu Asn Met Pro Lys Ser Glu Asn
65 70 75 80

Tyr Cys Arg Ile Arg Val His Asn Thr Thr Asp Thr Ser Val Lys Gly
85 90 95

Asn Met Ala Lys Asp Asp Ala His Glu Gln Ile Trp Thr Pro Trp Ser
100 105 110

Leu Val Asp Ala Asn Ala Trp Gly Val Trp Leu Gln Pro Ser Asp Trp
115 120 125

Gln Tyr Ile Cys Asn Thr Met Ser Gln Leu Asn Leu Val Ser Leu Asp
130 135 140

```
Gln Glu Ile Phe Asn Val Val Leu Lys Thr Val Thr Glu Gln Asp Ser
145                 150                 155                 160

Gly Gly Gln Ala Ile Lys Ile Tyr Asn Asn Asp Leu Thr Ala Cys Met
                165                 170                 175

Met Val Ala Val Asp Ser Asn Asn Ile Leu Pro Tyr Thr Pro Ala Ala
            180                 185                 190

Asn Ser Met Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Ala
        195                 200                 205

Ser Pro Tyr Arg Tyr Tyr Phe Cys Val Asp Arg Asp Leu Ser Val Thr
    210                 215                 220

Tyr Glu Asn Gln Glu Gly Thr Ile Glu His Asn Val Met Gly Thr Pro
225                 230                 235                 240

Lys Gly Met Asn Ser Gln Phe Phe Thr Ile Glu Asn Thr Gln Gln Ile
                245                 250                 255

Thr Leu Leu Arg Thr Gly Asp Glu Phe Ala Thr Gly Thr Tyr Tyr Phe
            260                 265                 270

Asp Thr Asn Pro Val Lys Leu Thr His Thr Trp Gln Thr Asn Arg Gln
        275                 280                 285

Leu Gly Gln Pro Pro Leu Leu Ser Thr Phe Pro Glu Ala Asp Thr Asp
    290                 295                 300

Ala Gly Thr Leu Thr Ala Gln Gly Ser Arg His Gly Ala Thr Gln Met
305                 310                 315                 320

Glu Val Asn Trp Val Ser Glu Ala Ile Arg Thr Arg Pro Ala Gln Val
                325                 330                 335

Gly Phe Cys Gln Pro His Asn Asp Phe Glu Ala Ser Arg Ala Gly Pro
            340                 345                 350

Phe Ala Ala Pro Lys Val Pro Ala Asp Val Thr Gln Gly Met Asp Arg
        355                 360                 365
```

```
Glu Ala Asn Gly Ser Val Arg Tyr Ser Tyr Gly Lys Gln His Gly Glu
    370                 375                 380

Asn Trp Ala Ala His Gly Pro Ala Pro Glu Arg Tyr Thr Trp Asp Glu
385                 390                 395                 400

Thr Asn Phe Gly Ser Gly Arg Asp Thr Arg Asp Gly Phe Ile Gln Ser
                405                 410                 415

Ala Pro Leu Val Val Pro Pro Pro Leu Asn Gly Ile Leu Thr Asn Ala
            420                 425                 430

Asn Pro Ile Gly Thr Lys Asn Asp Ile His Phe Ser Asn Val Phe Asn
        435                 440                 445

Ser Tyr Gly Pro Leu Thr Thr Phe Ser His Pro Ser Pro Val Tyr Pro
    450                 455                 460

Gln Gly Gln Ile Trp Asp Lys Glu Leu Asp Leu Glu His Lys Pro Arg
465                 470                 475                 480

Leu His Ile Thr Ala Pro Phe Val Cys Lys Asn Asn Ala Pro Gly Gln
                485                 490                 495

Met Leu Val Arg Leu Gly Pro Asn Leu Thr Asp Gln Tyr Asp Pro Asn
            500                 505                 510

Gly Ala Thr Leu Ser Arg Ile Val Thr Tyr Gly Thr Phe Phe Trp Lys
        515                 520                 525

Gly Lys Leu Thr Met Arg Ala Lys Leu Arg Ala Asn Thr Thr Trp Asn
    530                 535                 540

Pro Val Tyr Gln Val Ser Val Glu Asp Asn Gly Asn Ser Tyr Met Ser
545                 550                 555                 560

Val Thr Lys Trp Leu Pro Thr Ala Thr Gly Asn Met Gln Ser Val Pro
                565                 570                 575
```

Leu Ile Thr Arg Pro Val Ala Arg Asn Thr Tyr
580 585

<210> 1424
<211> 584
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1424

Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg
1 5 10 15

Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly
20 25 30

Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln
35 40 45

Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn
50 55 60

Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys
65 70 75 80

Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met
85 90 95

Ala Leu Asp Asp Ile His Val Glu Ile Val Thr Pro Trp Ser Leu Val
100 105 110

Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu
115 120 125

Ile Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu
130 135 140

Ile Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro
145 150 155 160

```
Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala
                165                 170                 175

Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser
            180                 185                 190

Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp
        195                 200                 205

Arg Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly
    210                 215                 220

Thr Ser Gly Thr Pro Thr Asn Val Tyr His Gly Thr Asp Pro Asp Asp
225                 230                 235                 240

Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg
                245                 250                 255

Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro
            260                 265                 270

Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro
        275                 280                 285

Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly
    290                 295                 300

Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly
305                 310                 315                 320

Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val
                325                 330                 335

Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro
            340                 345                 350

Phe Lys Thr Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu
        355                 360                 365

Asn Gln Ala Ala Asp Gly Asp Pro Arg Tyr Ala Phe Gly Arg Gln His
    370                 375                 380
```

```
Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr
385                 390                 395                 400

Ile Ala His Gln Asp Thr Gly Arg Tyr Pro Glu Gly Asp Trp Ile Gln
                405                 410                 415

Asn Ile Asn Phe Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro
            420                 425                 430

Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe
        435                 440                 445

Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr
    450                 455                 460

Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro
465                 470                 475                 480

Arg Leu His Ile Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro Gly
                485                 490                 495

Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Gln Tyr Asp Pro
            500                 505                 510

Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp
        515                 520                 525

Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg Ala Ser His Thr
    530                 535                 540

Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val Asp Asn Gln Phe Asn
545                 550                 555                 560

Tyr Val Pro Asn Asn Ile Gly Ala Met Lys Ile Val Tyr Glu Lys Ser
                565                 570                 575

Gln Leu Ala Pro Arg Lys Leu Tyr
            580
```

<210> 1425
<211> 548
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1425

```
Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln Thr Glu Phe Lys
1               5                   10                  15


Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn Ser Ser Arg Leu
            20                  25                  30


Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Arg Arg Val Val Val
        35                  40                  45


Asn Asn Met Asp Lys Thr Ala Val Asn Gly Asn Met Ala Leu Asp Asp
    50                  55                  60


Ile His Ala Gln Ile Val Thr Pro Trp Ser Leu Val Asp Ala Asn Ala
65                  70                  75                  80


Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu Ile Val Asn Thr
                85                  90                  95


Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu Ile Phe Asn Val
            100                 105                 110


Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro Thr Lys Val
        115                 120                 125


Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala Leu Asp Ser Asn
    130                 135                 140


Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu Thr Leu Gly
145                 150                 155                 160


Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg Tyr Tyr Phe
                165                 170                 175
```

```
Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr Ser Gly Thr
            180                 185                 190

Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp Val Gln Phe Tyr
        195                 200                 205

Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg Thr Gly Asp Glu
    210                 215                 220

Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro Cys Arg Leu Thr
225                 230                 235                 240

His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro Pro Phe Leu Asn
                245                 250                 255

Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly Asp Ile Gly Val
            260                 265                 270

Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly Asn Thr Asn Tyr
        275                 280                 285

Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val Gly Tyr Ser Ala
    290                 295                 300

Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro Phe Lys Thr Pro
305                 310                 315                 320

Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala
                325                 330                 335

Asp Gly Asn Pro Arg Tyr Ala Phe Gly Arg Gln His Gly Gln Lys Thr
            340                 345                 350

Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr Ile Ala His Gln
        355                 360                 365

Asp Thr Gly Arg Tyr Pro Glu Gly Asp Trp Ile Gln Asn Ile Asn Phe
    370                 375                 380

Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro Thr Asp Pro Ile
385                 390                 395                 400
```

```
Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe Asn Thr Tyr Gly
                405                 410                 415

Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr Pro Asn Gly Gln
            420                 425                 430

Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro Arg Leu His Val
        435                 440                 445

Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro Gly Gln Leu Phe Val
    450                 455                 460

Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr Asp Pro Asp Ala Ser Ala
465                 470                 475                 480

Asn Met Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp Trp Lys Gly Lys
                485                 490                 495

Leu Val Phe Lys Ala Lys Leu Arg Ala Ser His Thr Trp Asn Pro Ile
            500                 505                 510

Gln Gln Met Ser Ile Asn Val Asp Asn Gln Phe Asn Tyr Val Pro Ser
        515                 520                 525

Asn Ile Gly Gly Met Lys Ile Val Tyr Glu Lys Ser Gln Leu Ala Pro
    530                 535                 540

Arg Lys Leu Tyr
545
```

<210> 1426
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1426

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 1427
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1427

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1428
<211> 736

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1428

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Glu Pro Asp Ser Ser Ser Gly Thr
145 150 155 160

Gly Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro
180 185 190

```
Pro Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn
                485                 490                 495

Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala
            580                 585                 590

Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  1429
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1429

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Val Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asp Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asn Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210>  1430
<211>  737
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1430

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575
```

```
Arg Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Glu Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 1431
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1431

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Val Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asp Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asn Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1432
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1432

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Val Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asp Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1433
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1433

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asp Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asn Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

```
Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1434
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1434

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Val Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210>  1435
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1435

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Val Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asn Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575
```

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1436
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1436
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

aacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag 360

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcaaaaaag agactcaatt ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

atccaagtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtgct cggctcggcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggctgtg ggccggtcgt ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgaat tcagctacaa cttcgaggac 1260

gtgcccttcc acagcagcta cgcgcacagc cagagcctgg accggctgat gaaccctctc 1320

atcgaccagt acttgtacta cctgtcccgg actcaaagca cgggcggtac tgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aacaacatgt cggctcaggc caagaactgg 1440

ctacccggtc cctgctaccg gcagcaacgc gtctccacga cactgtcgca gaacaacaac 1500

agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

aatcctggcg ttgccatggc tacccacaag gacgacgaag agcgattttt tccatccagc 1620

ggagtcttaa tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtg 1680

atgctaacca gcgaggaaga aataaagacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaatagt 1800

caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caagctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 1437
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1437

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320
```

```
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540
```

```
Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 1438
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1438

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Ser Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
```

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
               405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
               485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
               565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

```
Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 1439
<211> 4472
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1439

```
ctccatcact aggggtaacc gcgaagcgcc tcccacgctg ccgcgtcagc gctgacgtaa       60

attacgtcat aggggagtgg tcctgtatta gctgtcacgt gagtgctttt gcgacatttt      120

gcgacaccac gtggccattc atggtatata tggccgagtg agcgagcagg atctccattt      180

tgaccgcgaa atttgaacga gcagcagcca tgccgggctt ctacgagatc gtgcttaagg      240

tgccgagcga cctggacgag cacctgccgg gcatttctga ctcgtttgtg aactgggtgg      300
```

cagagaagga atgggagctg cccccggatt ctgacatgga tcggaatctg attgagcagg 360

caccctgac cgtggccgag aagctacagc gcgacttcct ggtccaatgg cgccgcgtga 420

gtaaggcccc ggaggccctc ttctttgttc agttcgagaa gggcgagtcc tacttccacc 480

tccatattct ggtagagacc acgggggtca aatccatggt gctgggccgc ttcctgagtc 540

agattcggga caagctggtg cagaccatct accgcgggat cgagccgacc ctgcccaact 600

ggttcgcggt gacaaagacg cgtaatggcg ccggaggggg gaacaaggtg gtggacgagt 660

gctacatccc caactacctg ctgcccaaga ctcagcccga gctgcagtgg gcgtggacta 720

acatggagga gtatataagc gcgtgcttga acctggccga gcgcaaacgg ctcgtggcgc 780

agcacctgac ccacgtcagc cagacccagg agcagaacaa ggagaatctg aacccgaatt 840

ctgacgcgcc tgtcatccgg tcaaaaacct ccgcgcgcta catggagctg gtcgggtggc 900

tggtggaccg gggcatcacc tccgagaagc agtggatcca ggaggaccag gcctcgtaca 960

tctccttcaa cgccgcctcc aactcgcggt ctcagatcaa ggccgcgctg gacaatgccg 1020

gcaagatcat ggcgctgacc aaatccgcgc ccgactacct ggtaggcccc gctctgcccg 1080

cggacattaa atccaaccgc atctaccgca tcctggagct gaatggctac gaccctgcct 1140

acgccggttc cgtctttctc ggctgggccc agaaaaagtt tggcaaaagg aacaccatct 1200

ggctgtttgg gccggccacc acgggcaaga ccaacatcgc ggaagccatc gcccacgccg 1260

tgcccttcta cggctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg 1320

acaagatggt gatctggtgg gaggagggca agatgacggc caaggtcgtg gagtccgcca 1380

aggccattct cggcggcagc aaggtgcgcg tggaccaaaa gtgcaagtcg tccgcccaga 1440

tcgatcccac ccccgtgatc gtcacctcca acaccaacat gtgcgccgtg attgacggga 1500

acagcaccac cttcgagcac cagcagccgt tgcaggaccg gatgttcaaa tttgaactta 1560

cccgccgtct ggagcacgac tttggcaagg tgacaaagca ggaagtcaaa gagttcttcc 1620

gctgggcgca ggatcacgtg accgaggtgg cgcatgagtt ctacgtcaga aagggtggag 1680

ctaacaaaag acccgccccc gatgacgcgg atataagcga gcccaagcgg gcctgcccct 1740

cagtcgcgga tccatcgacg tcagacgcgg aaggagctcc ggtggacttt gccgacaggt 1800

accaaaacaa atgttctcgt cacgcgggca tgcttcagat gctgtttccc tgcaaaacat 1860

gcgagagaat gaatcagaat ttcaacattt gcttcacgca cgggaccaga gactgttcag 1920

aatgtttccc tggcgtgtca gaatctcaac cggtcgtcag aaaaaagacg tatcggaaac 1980

tctgtgcgat tcatcatctg ctggggcggg cacccgagat tgcttgctcg gcctgcgacc 2040

tggtcaacgt ggacctggat gactgtgttt ctgagcaata aatgacttaa accaggtatg 2100

gctgccgatg gttatcttcc agattggctc gaggacaacc tctctgaggg cattcgcgag 2160

tggtgggacc tgaaacctgg agccccgaaa cccaaagcca accagcaaaa gcaggacaac 2220

ggccggggtc tggtgcttcc tggctacaag tacctcggac ccttcaacgg actcgacaag 2280

ggggagcccg tcaacgcggc ggacgcagcg gccctcgagc acgacaaggc ctacgaccag 2340

cagctccaag cgggtgacaa tccgtacctg cggtataatc acgccgacgc cgagtttcag 2400

gagcgtctgc aagaagatac gtcttttggg ggcaacctcg ggcgcgcagt cttccaggcc 2460

aaaaagcggg ttctcgaacc tctgggcctg gttgaatcgc cggttaagac ggctcctgga 2520

aagaagagac cggtagagcc atcaccccag cgctctccag actcctctac gggcatcggc 2580

aagaaaggcc agcagcccgc aaaaaagaga ctcaattttg ggcagactgg cgactcagag 2640

tcagtccccg accctcaacc aatcggagaa ccaccagcag gcccctctgg tctgggatct 2700

ggtacaatgg ctgcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 2760

gtgggtagtt cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 2820

accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta caagcaaatc 2880

tccaacggga cctcgggagg aagcaccaac gacaacacct acttcggcta cagcaccccc 2940

tgggggtatt ttgacttcaa cagattccac tgccactttt caccacgtga ctggcagcga 3000

ctcatcaaca acaactgggg attccggccc aagaggctca acttcaagct cttcaacatc 3060

caagtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa ccttaccagc 3120

acgattcagg tctttacgga ctcggaatac cagctcccgt acgtgctcgg ctcggcgcac 3180

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cgggtacctg 3240

actctgaaca atggcagtca ggctgtgggc cggtcgtcct tctactgcct ggagtacttt 3300

ccttctcaaa tgctgagaac gggcaacaac tttgaattca gctacaactt cgaggacgtg 3360

cccttccaca gcagctacgc gcacagccag agcctggacc ggctgatgaa ccctctcatc 3420

gaccagtact tgtactacct gtcccggact caaagcacgg gcggtactgc aggaactcag 3480

cagttgctat tttctcaggc cgggcctaac aacatgtcgg ctcaggccaa gaactggcta 3540

cccggtccct gctaccggca gcaacgcgtc tccacgacac tgtcgcagaa caacaacagc 3600

aactttgcct ggacgggtgc caccaagtat catctgaatg gcagagactc tctggtgaat 3660

cctggcgttg ccatggctac ccacaaggac gacgaagagc gatttttttcc atccagcgga 3720

gtcttaatgt ttgggaaaca gggagctgga aaagacaacg tggactatag cagcgtgatg 3780

ctaaccagcg aggaagaaat aaagaccacc aacccagtgg ccacagaaca gtacggcgtg 3840

gtggccgata acctgcaaca gcaaaacgcc gctcctattg taggggccgt caatagtcaa 3900

ggagccttac ctggcatggt gtggcagaac cgggacgtgt acctgcaggg tcccatctgg 3960

gccaagattc ctcatacgga cggcaacttt catccctcgc cgctgatggg aggctttgga 4020

ctgaagcatc cgcctcctca gatcctgatt aaaaacacac ctgttcccgc ggatcctccg 4080

accaccttca atcaggccaa gctggcttct ttcatcacgc agtacagtac cggccaggtc 4140

agcgtggaga tcgagtggga gctgcagaag gagaacagca aacgctggaa cccagagatt 4200

cagtacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa tactgagggt 4260

acttattccg agcctcgccc cattggcacc cgttacctca cccgtaatct gtaattacat 4320

gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctcctgt ccttcttatc 4380

ttatcggtta ccatagaaac tggttactta ttaactgctt ggtgcgcttc gcgataaaag 4440

acttacgtca tcgggttacc cctagtgatg ga 4472

<210> 1440
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1440

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480
```

```
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
               485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
               565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
               645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685
```

```
Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 1441
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1441

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Arg Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Arg Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Arg Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Arg Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Arg Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540
```

```
Phe Gly Arg Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 1442
<211> 738

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1442

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Arg Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Ser Pro Val Arg Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Arg Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

```
Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Arg Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Arg Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
```

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Arg Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620
```

```
Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 1443
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1443

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Arg Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Arg Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Arg Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Arg Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Arg Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480
```

```
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Arg Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Arg Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685
```

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 1444
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1444

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Arg Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Arg Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Arg Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Arg Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Arg Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Arg Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540
```

```
Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Arg Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 1445
<211> 738

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1445

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Arg Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Ser Pro Val Arg Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

```
Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Arg Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Arg Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
```

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Arg Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Arg Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620
```

```
Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Arg Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 1446
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1446

```
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

aacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag      360
```

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcaaaaaag agactcaatt ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag cagccccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

atccaagtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtgct cggctcggcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggctgtg ggccggtcgt ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgaat tcagctacaa cttcgaggac 1260

gtgcccttcc acagcagcta cgcgcacagc cagagcctgg accggctgat gaaccctctc 1320

atcgaccagt acttgtacta cctgtcccgg actcaaagca cgggcggtac tgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aacaacatgt cggctcaggc caagaactgg 1440

ctacccggtc cctgctaccg gcagcaacgc gtctccacga cactgtcgca gaacaacaac 1500

agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

aatcctggcg ttgccatggc tacccacaag gacgacgaag agcgattttt tccatccagc 1620

ggagtcttaa tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtg 1680

atgctaacca gcgaggaaga aataaagacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaatagt 1800

caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caagctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctg 2214

<210> 1447
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1447
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaggcaggac 120

aacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacag ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag 360

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttag gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcaagaaag agactcaatt ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag cagccccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaggcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

atccaagtca aggaggtcac gcagaatgaa ggcaccagga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtgct cggctcggcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggctgtg ggccggtcgt ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgaat tcagctacaa cttcgaggac 1260

gtgcccttcc acagcagcta cgcgcacagc cagagcctgg accggctgat gaaccctctc 1320

atcgaccagt acttgtacta cctgtcccgg actcaaagca cgggcggtac tgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aacaacatgt cggctcaggc caagaactgg 1440

ctacccggtc cctgctaccg gcagcaacgc gtctccacga cactgtcgca gaacaacaac 1500

agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

aatcctggcg ttgccatggc tacccacagg gacgacgaag agcgattttt tccatccagc 1620

ggagtcttaa tgtttgggag acagggagct ggaagagaca acgtggacta tagcagcgtg 1680

atgctaacca gcgaggaaga aataaggacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaatagt 1800

caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caagctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 1448
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1448
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaggcaggac 120

aacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aaggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacag ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag 360

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttag gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagagag gccagcagcc cgcaagaaag agactcaatt ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag cagccccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaggcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

atccaagtca aggaggtcac gcagaatgaa ggcaccagga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtgct cggctcggcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggctgtg ggccggtcgt ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgaat tcagctacaa cttcgaggac 1260

gtgcccttcc acagcagcta cgcgcacagc cagagcctgg accggctgat gaaccctctc 1320

atcgaccagt acttgtacta cctgtcccgg actcaaagca cgggcggtac tgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aacaacatgt cggctcaggc caagaactgg 1440

ctacccggtc cctgctaccg gcagcaacgc gtctccacga cactgtcgca gaacaacaac 1500

agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

aatcctggcg ttgccatggc tacccacagg gacgacgaag agcgattttt tccatccagc 1620

ggagtcttaa tgtttgggaa acagggagct ggaagagaca acgtggacta tagcagcgtg 1680

atgctaacca gcgaggaaga aataaggacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaatagt 1800

caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caagctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 1449
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1449
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gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaggcaggac 120

aacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacag ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag 360

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttag gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagagag gccagcagcc cgcaaaaaag agactcaatt ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag cagcccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaggcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

atccaagtca aggaggtcac gcagaatgaa ggcaccagga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtgct cggctcggcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggctgtg ggccggtcgt ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgaat tcagctacaa cttcgaggac 1260

gtgcccttcc acagcagcta cgcgcacagc cagagcctgg accggctgat gaaccctctc 1320

atcgaccagt acttgtacta cctgtcccgg actcaaagca cgggcggtac tgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aacaacatgt cggctcaggc caagaactgg 1440

ctacccggtc cctgctaccg gcagcaacgc gtctccacga cactgtcgca gaacaacaac 1500

agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

aatcctggcg ttgccatggc tacccacagg gacgacgaag agcgattttt tccatccagc 1620

ggagtcttaa tgtttgggag acagggagct ggaagagaca acgtggacta tagcagcgtg 1680

atgctaacca gcgaggaaga aataaggacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaatagt 1800

caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caagctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 1450
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaggcaggac 120

aacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacag ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag 360

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttag gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagagag gccagcagcc cgcaaaaaag agactcaatt ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag cagccccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaggcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

atccaagtca aggaggtcac gcagaatgaa ggcaccagga ccatcgccaa taaccttacc 1020

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caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

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tttccttctc aaatgctgag aacgggcaac aactttgaat tcagctacaa cttcgaggac 1260

gtgcccttcc acagcagcta cgcgcacagc cagagcctgg accggctgat gaaccctctc 1320

atcgaccagt acttgtacta cctgtcccgg actcaaagca cgggcggtac tgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aacaacatgt cggctcaggc caagaactgg 1440

ctacccggtc cctgctaccg gcagcaacgc gtctccacga cactgtcgca gaacaacaac 1500

agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

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ggagtcttaa tgtttgggaa acagggagct ggaagagaca acgtggacta tagcagcgtg 1680

atgctaacca gcgaggaaga aataaggacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaatagt 1800

caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caggctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 1451
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1451
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gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaggcaggac 120

aacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacag ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag 360

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttag gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcaaaaaag agactcaatt ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag cagccccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaggcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

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caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggctgtg ggccggtcgt ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgaat tcagctacaa cttcgaggac 1260

gtgcccttcc acagcagcta cgcgcacagc cagagcctgg accggctgat gaaccctctc 1320

atcgaccagt acttgtacta cctgtcccgg actcaaagca cgggcggtac tgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aacaacatgt cggctcaggc caagaactgg 1440

ctacccggtc cctgctaccg gcagcaacgc gtctccacga cactgtcgca gaacaacaac 1500

agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

aatcctggcg ttgccatggc tacccacagg gacgacgaag agcgattttt tccatccagc 1620

ggagtcttaa tgtttgggag acagggagct ggaagagaca acgtggacta tagcagcgtg 1680

atgctaacca gcgaggaaga aataaggacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaatagt 1800

caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caggctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 1452
<211> 744

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1452

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

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Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
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Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Gln Arg Gly Glu Ser Gly
            580                 585                 590

His Gly Tyr Phe Ala Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly
        595                 600                 605

Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly
    610                 615                 620
```

```
Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser
625                 630                 635                 640


Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
                645                 650                 655


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala
            660                 665                 670


Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
        675                 680                 685


Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
    690                 695                 700


Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val Asn Val Asp
705                 710                 715                 720


Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly
                725                 730                 735


Thr Arg Tyr Leu Thr Arg Asn Leu
            740
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<210> 1453
<211> 8359
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1453

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ttgtgacgtg gcgcggggcg tgggaacggg gcgggtgacg tagtagctct agaggtcctg      120

tattagaggt cacgtgagtg ttttgcgaca ttttgcgaca ccatgtggtc acgctgggta      180

tttaagcccg agtgagcacg cagggtctcc attttgaagc gggaggtttg aacgcgcagc      240

cgccatgccg gggttttacg agattgtgat taaggtcccc agcgaccttg acgagcatct      300

gcccggcatt tctgacagct ttgtgaactg ggtggccgag aaggaatggg agttgccgcc      360
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agattctgac atggatctga atctgattga gcaggcaccc ctgaccgtgg ccgagaagct 420

gcagcgcgac tttctgacgg aatggcgccg tgtgagtaag gcaccggagg ccctttttctt 480

tgtgcaattt gagaagggag agagctactt ccacatgcac gtgctcgtgg aaaccaccgg 540

ggtgaaatcc atggttttgg gacgtttcct gagtcagatt cgcgaaaaac tgattcagag 600

aatttaccgc gggatcgagc cgactttgcc aaactggttc gcggtcacaa agaccagaaa 660

tggcgccgga ggcgggaaca aggtggtgga tgagtgctac atccccaatt acttgctccc 720

caaaacccag cctgagctcc agtgggcgtg gactaatatg gaacagtatt taagcgcctg 780

tttgaatctc acggagcgta aacggttggt ggcgcagcat ctgacgcacg tgtcgcagac 840

gcaggagcag aacaaagaga atcagaatcc caattctgat gcgccggtga tcagatcaaa 900

aacttcagcc aggtacatgg agctggtcgg gtggctcgtg gacaaggga ttacctcgga 960

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taaaattttg gaactaaacg ggtacgatcc ccaatatgcg gcttccgtct ttctgggatg 1200

ggccacgaaa aagttcggca agaggaacac catctggctg tttgggcctg caactaccgg 1260

gaagaccaac atcgcggagg ccatagccca cactgtgccc ttctacgggt gcgtaaactg 1320

gaccaatgag aactttccct tcaacgactg tgtcgacaag atggtgatct ggtgggagga 1380

ggggaagatg accgccaagg tcgtggagtc ggccaaagcc attctcggag gaagcaaggt 1440

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ctccaacacc aacatgtgcg ccgtgattga cgggaactca acgaccttcg aacaccagca 1560

gccgttgcaa gaccggatgt tcaaatttga actcacccgc cgtctggatc atgactttgg 1620

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cgcagatata agtgagccca aacgggtgcg cgagtcagtt gcgcagccat cgacgtcaga 1800

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catgaatctg atgctgtttc cctgcagaca atgcgagaga atgaatcaga attcaaatat 1920

ctgcttcact cacggacaga aagactgttt agagtgcttt cccgtgtcag aatctcaacc 1980

cgtttctgtc gtcaaaaagg cgtatcagaa actgtgctac attcatcata tcatgggaaa 2040

ggtgccagac gcttgcactg cctgcgatct ggtcaatgtg gatttggatg actgcatctt 2100

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aggacactct ctctgaagga ataagacagt ggtggaagct caaacctggc ccaccaccac 2220

caaagcccgc agagcggcat aaggacgaca gcaggggtct tgtgcttcct gggtacaagt 2280

acctcggacc cttcaacgga ctcgacaagg gagagccggt caacgaggca gacgccgcgg 2340

ccctcgagca cgacaaagcc tacgaccggc agctcgacag cggagacaac ccgtacctca 2400

agtacaacca cgccgacgcg gagtttcagg agcgccttaa agaagatacg tcttttgggg 2460

gcaacctcgg acgagcagtc ttccaggcga aaaagagggt tcttgaacct ctgggcctgg 2520

ttgaggaacc tgttaagacg gctccgggaa aaaagaggcc ggtagagcac tctcctgtgg 2580

agccagactc ctcctcggga accggaaagg cgggccagca gcctgcaaga aaaagattga 2640

attttggtca gactggagac gcagactcag tacctgaccc ccagcctctc ggacagccac 2700

cagcagcccc ctctggtctg ggaactaata cgatggctac aggcagtggc gcaccaatgg 2760

cagacaataa cgagggcgcc gacggagtgg gtaattcctc gggaaattgg cattgcgatt 2820

ccacatggat gggcgacaga gtcatcacca ccagcacccg aacctgggcc ctgcccacct 2880

acaacaacca cctctacaaa caaatttcca gccaatcagg agcctcgaac gacaatcact 2940

actttggcta cagcacccct tgggggtatt ttgacttcaa cagattccac tgccactttt 3000

caccacgtga ctggcaaaga ctcatcaaca acaactgggg attccgaccc aagagactca 3060

acttcaagct ctttaacatt caagtcaaag aggtcacgca gaatgacggt acgacgacga 3120

ttgccaataa ccttaccagc acggttcagg tgtttactga ctcggagtac cagctcccgt 3180

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gctacacttt tgaggacgtt cctttccaca gcagctacgc tcacagccag agtctggacc 3420

gtctcatgaa tcctctcatc gaccagtacc tgtattactt gagcagaaca aacactccaa 3480

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tggacattga aaaggtcatg attacagacg aagaggaaat caggacaacc aatcccgtgg 3840

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gcatggtctg gcaggacaga gatgtgtacc ttcaggggcc catctgggca aagattccac 4020

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cggcaaagtt tgcttccttc atcacacagt actccacggg acaggtcagc gtggagatcg 4200

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actacaacaa gtctgttaat gtggacttta ctgtggacac taatggcgtg tattcagagc 4320

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ccgtttaatt cgtttcagtt gaactttggt ctctgcgtat ttctttctta tctagtttcc 4440

atgctctaga ggtcctgtat tagaggtcac gtgagtgttt tgcgacattt tgcgacacca 4500

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ggcggagcct atggaaaaac gccagcaacg cggccttttt acggttcctg gccttttgct 8160

ggccttttgc tcacatgttc tttcctgcgt tatcccctga ttctgtggat aaccgtatta 8220

ccgcctttga gtgagctgat accgctcgcc gcagccgaac gaccgagcgc agcgagtcag 8280

tgagcgagga agcggaagag cgcccaatac gcaaaccgcc tctccccgcg cgttggccga 8340

ttcattaatg cagaattcc 8359

<210> 1454
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1454

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

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Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

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Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

```
Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1455
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1455

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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420
```

ggaaagaaga gaccggtaga gcaatcaccc caggaaccag actcctcttc gggcatcggc 480

aagaaaggcc agcagcccgc gaagaagaga ctcaactttg ggcagacagg cgactcagag 540

tcagtgcccg accctcaacc actcggagaa ccccccgcag ccccctctgg tgtgggatct 600

aatacaatgg cagcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaacg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctcccc acctacaaca accacctcta caagcaaatc 780

tccagccaat cgggagcaag caccaacgac aacacctact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgacgaa tgatggcacc acgaccatcg ccaataacct taccagcacg 1020

gttcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctgc ctccgttccc ggcggacgtc ttcatgattc ctcagtacgg gtacctgact 1140

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cagtacctgt actacctgtc tcggactcag accacgagtg gtaccgcagg aaatcggacg 1380

ttgcaatttt ctcaggccgg gcctagtagc atggcgaatc aggccaaaaa ctggctaccc 1440

gggccctgct accggcagca acgcgtctcc aagacagcga atcaaaataa caacagcaac 1500

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ggtcccgcta tggcaaccca caaggacgac gaagacaaat tttttccgat gagcggagtc 1620

ttaatatttg ggaaacaggg agctggaaat agcaacgtgg accttgacaa cgttatgata 1680

accagtgagg aagaaattaa aaccaccaac ccagtggcca cagaacagta cggcacggtg 1740

gccactaacc tgcaatcgtc aaacaccgct cctgctacag ggaccgtcaa cagtcaagga 1800

gccttacctg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc tatctgggcc 1860

aagattcctc acacggacgg acactttcat ccctcgccgc tgatgggagg ctttggactg 1920

aaacacccgc ctcctcagat cctgattaag aatacacctg ttcccgcgaa tcctccaact 1980

accttcagtc cagctaagtt tgcgtcgttc atcacgcagt acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc agagattcaa 2100

tacacttcca actacaacaa atctacaaat gtggactttg ctgttgacac aaatggcgtt 2160

tattctgagc ctcgccccat cggcacccgt tacctcaccc gtaatctg 2208

<210> 1456
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1456

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

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Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe
    450                 455                 460

Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ala Gly Asn Asp Asn Val Asp Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575
```

Glu Tyr Gly Val Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro
580 585 590

Gln Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 1457
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1457
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcaatcaccc caggaaccag actcctctac gggcatcggc 480

aagaaaggcc agcagcccgc gaaaaagaga ctcaactttg ggcagactgg cgactcagag 540

tcagtgcccg accctcaacc actcggagaa ccccccgcag ccccctctgg tgtgggatct 600

aatacaatgg ctgcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctcccc acctacaaca accacctcta caagcaaatc 780

tccaacagcc aatcgggagg aagcaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgac gaatgatggc accacgacca tcgccaataa ccttaccagc 1020

acggttcagg tctttacgga ctcggaatac cagctcccgt acgtcctcgg ctctgcgcac 1080

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gaccagtacc tgtactacct gtctcggact cagaccacgg gaggtaccgc aggaaatcgg 1380

acgttgcaat tttctcaggc cgggcctagt agcatggcga atcaggccaa aaactggcta 1440

cccgggccct gctaccggca gcaacgcgtc tccaagacaa cgaatcaaaa taacaacagc 1500

aactttgcct ggaccggtgc caccaagtat catctgaatg gcagagactc tctggtaaat 1560

cccggtgtcg ctatggcaac ccacaaggac gacgaagacc gatttttcc gtccagcgga 1620

gtcttaatat ttgggaaaca gggagctgga aatgacaacg tggaccttga caacgttatg 1680

ataaccagtg aggaagaaat taaaaccacc aacccagtgg ccacagaaga gtacggcgtg 1740

gtggccacta acctgcaatc ggcaaacacc gctcctcaaa cagggaccgt caacagtcaa 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcctatctgg 1860

gccaagattc ctcacacgga cggaaacttt catccctcgc cgctgatggg aggctttgga 1920

ctgaaacacc cgcctcctca gatcctgatt aagaatacac ctgttcccgc gaatcctcca 1980

actaccttca gtccagctaa gtttgcgtcg ttcatcacgc agtacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaaa gaaaacagca aacgctggaa cccagagatt 2100

caatacactt ccaactacaa caaatctaca aatgtggact ttgctgttga cacagaaggc 2160

gtttattctg agcctcgccc catcggcacc cgttacctca cccgtaatct g 2211

<210> 1458
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1458

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Arg Glu Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320
```

```
Ile Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Gly Thr Gln Thr Leu Gln
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Asn Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Ile Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Val Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala
            580                 585                 590

Pro Gln Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 1459
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1459
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcagtcacca cagcgtgagc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccaaaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

tctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aagaggtcac gacgaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccgtcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aactttcaat tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagacta cgggaggcac agcgggaacc 1380

cagacgttgc agttttctca ggccgggcct agcagcatgg cgaatcaggc caaaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga caacgaatca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagg accgcttctt cccatccagc 1620

ggcgtcctca tatttggcaa gcagggagct ggaaatgaca acgtggacta tagcaacgtg 1680

atgataacca gcgaggaaga aatcaagacc accaaccccg tggccacaga agagtatggc 1740

gtggtggcta ctaacctaca gtcggcaaac accgctcctc aaacggggac cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacaacgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctg 2214

<210> 1460
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1460

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Arg Glu Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270
```

```
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Gly Thr Gln Thr Leu Gln
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480
```

```
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 1461
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1461
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcagtcacca cagcgtgagc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

tctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aactttcaat tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagacta cgggaggcac agcgggaacc 1380

cagacgttgc agttttctca ggccgggcct agcaacatgg cgaatcaggc caaaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga caacgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tatttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga agagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctcctc aaatagggac cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacaacgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctg 2214

<210> 1462
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1462

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220
```

```
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430
```

```
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655
```

```
Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 1463
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1463

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atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc      480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca      540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tggtgtggga      600
```

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aactttgagt tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc caaaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacaacgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctg 2214

<210> 1464
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1464

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175
```

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
```

```
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 1465
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1465
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctc cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacttcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtcct cggctctgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggccgtg ggccgttcct ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgagt tcagctacac gtttgaggac 1260

gtgccttttc acagcagcta cgcgcacagc caaagcctgg accggctgat gaaccccctc 1320

atcgaccagt acctgtacta cctgtctcgg actcagtcca cgggaggtac cgcaggaact 1380

cagcagttgc tattttctca ggccgggcct agtaacatgt cggctcaggc caaaaactgg 1440

ctacccgggc cctgctaccg gcagcaacgc gtctccacga cactgtcgca aaataacaac 1500

agcaactttg cctggaccgg tgccaccaag tatcatctga atggcagaga ctctctggta 1560

aatcccggtg tcgctatggc aacccacaag gacgacgaag agcgattttt tccgtccagc 1620

ggagtcttaa tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtt 1680

atgctaacca gtgaggaaga aattaaaacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac accgctccta ttgtaggggc cgtcaacagt 1800

caaggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatc 1860

tgggccaaga ttcctcacac ggacggaaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaaac acccgcctcc tcagatcctg attaagaata cacctgttcc cgcggatcct 1980

ccaactacct tcagtcaagc taagctggcg tcgttcatca cgcagtacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaagaaaaca gcaaacgctg gaacccagag 2100

attcaataca cttccaacta ctacaaatct acaaatgtgg actttgctgt taacacagaa 2160

ggcacttatt ctgagcctcg ccccatcggc acccgttacc tcacccgtaa tctg 2214

<210> 1466
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1466

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Thr Thr Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Ala Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560
```

```
Met Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Val Val Ser Ser Asn Leu Gln Ser Ala Asn Thr Ala Pro
            580                 585                 590

Gln Thr Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Asp Lys Ser Thr Asn Val Asp Phe Ala Val Asp Ser Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 1467
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1467
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtcattt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccaaaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

attaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc aaagtgcagg tagtaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagaagctgc ggttcaagct cttcaacatc 960

caggtcaagg aggtcacgac gaatgacggc gttacgacca tcgctaataa ccttaccagc 1020

acggttcagg tattctcgga ctcggaatac cagctgccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg 1140

actctcaaca atggcagtca gtctgtggga cgttcctcct tctactgcct ggagtacttc 1200

ccctctcaga tgctgagaac gggcaacaac tttgagttca gctacacctt cgaggacgtg 1260

cctttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcccctcatc 1320

gaccagtact tgtactacct ggccagaaca cagagtacca caggaggcac agctggcaat 1380

cgggaactgc agttttacca ggccgggcct tcaactatgg ccgaacaagc caagaattgg 1440

ttacctggac cttgctaccg gcaacaaaga gtctccaaaa cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggcagaaa ctcgttggtt 1560

aatcccggcg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc 1620

ggagtcctga tttttggaaa aactggagca gctaacaaaa ctacattgga aaatgtgtta 1680

atgacaaatg aagaagaaat taaaactact aatcctgtag ccacggaaga atacggggta 1740

gtcagcagca acttacaatc ggctaatact gcaccccaga cacaaactgt caacagccag 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga tggcaacttt cacccgtctc ctttgatggg cggctttgga 1920

cttaaacatc cgcctcctca gatcctgatc aagaacactc ccgttcccgc taatcctccg 1980

gaggtgttta ctcctgccaa gtttgcttcg ttcatcacac agtacagcac cggacaagtc 2040

agcgtggaaa tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatt 2100

cagtacacct ccaactatga taagtcgact aatgtggact ttgccgttga cagcgagggt 2160

gtttactctg agcctcgccc tattggcact cgttacctca cccgtaatct g 2211

<210> 1468
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1468

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
               85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
               165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
               245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Gln Thr Thr Ser Gly Thr Ala Gln Asn Arg Glu Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ala Gly Ala Ser Asn Val Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala Thr
            580                 585                 590

Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Ala Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1469
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1469
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctcttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagtcaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcag ccccctctgg tgtgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtcaat caggggccag caacgacaac cactacttcg gctacagcac cccctggggg 840

tattttgatt tcaacagatt ccactgccat ttctcaccac gtgactggca gcgactcatc 900

aacaacaatt ggggattccg gcccaagaga ctcaacttca agctcttcaa catccaagtc 960

aaggaggtca cgacgaatga tggcaccacg accatcgcta ataaccttac cagcacggtt 1020

caagtcttca cggactcgga gtaccagttg ccgtacgtcc tcggctctgc gcaccagggc 1080

tgcctccctc cgttcccggc ggacgtgttc atgattccgc agtacggcta cctaacgctc 1140

aacaatggca gccaggcagt gggacggtca tccttttact gcctggaata tttcccatcg 1200

cagatgctga gaacgggcaa taactttacc ttcagctaca ccttcgagga cgtgcctttc 1260

cacagcagct acgcgcacag ccagagcctg gaccggctga tgaatcctct catcgaccag 1320

tacctgtatt acctgagcag aactcagact acgtccggaa ctgcccaaaa cagggagttg 1380

cagtttagcc aggcgggtcc atctagcatg gctaatcagg ccaaaaactg gctacctgga 1440

ccctgttacc ggcagcagcg cgtttctaaa acagcaaatg acaacaacaa cagcaacttt 1500

gcctggactg gtgctacaaa atatcacctt aatgggcgtg attctttagt caaccctggc 1560

cctgctatgg cctcacacaa agacgacgaa gacaagttct ttcccatgag cggtgtcttg 1620

atttttggaa agcagggcgc cggagcttca aacgttgatt tggacaatgt catgatcaca 1680

gacgaagagg aaatcaaaac cactaacccc gtggccaccg aacaatatgg gactgtggca 1740

accaatctcc agagcagcaa cacagcccct gcgaccggaa ctgtgaattc tcagggagcc 1800

ttacctggaa tggtgtggca agacagagac gtatacctgc agggtcctat ttgggccaaa 1860

attcctcaca cggatggaca ctttcacccg tctcctctca tgggcggctt tggacttaag 1920

cacccgcctc ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccgacaacg 1980

ttttcgcctg caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg 2040

gagattgaat gggagctgca gaaagaaaac agcaaacgct ggaatcccga aatacagtat 2100

acatctaact ataataaatc tgccaacgtt gatttcactg tggacaccaa tggagtttat 2160

agtgagcctc gccccattgg cacccgttac ctcacccgta acctg 2205

<210> 1470
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1470

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Gln Thr Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480
```

```
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Ala Ser Asn Val Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala Thr
            580                 585                 590

Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685
```

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1471
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1471
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg atctgaaacc tggagcccct caacccaaag cgaaccaaca acaccaggac 120

gacggtcggg gtcttgtgct tccgggttac aaatacctcg gacccttaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga gggtccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga acagtctcct caggaaccgg actcatcatc tggtattggc 480

aaatcgggcc aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg agactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag ccccctcagg tgtgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcaacttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atgatccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttcaca ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgagcag aacgcaaaca acctctggaa caacccaaca atcacggctg 1380

caatttagcc aggctgggcc ttcgtctatg gctcagcagg ccaaaaattg gctacctggg 1440

ccctgctacc ggcaacagag agtttcaaag actgctaacg acaacaacaa cagtaacttt 1500

gcttggacag gggccaccaa atatcatctc aatggccgcg actcgctggt gaatccagga 1560

ccagctatgg ccagtcacaa ggacgatgaa gaaaaatttt tccctatgca cggcgttcta 1620

atatttggca aacaagggac aggggcaagt aacgtagatt tagataatgt aatgattacg 1680

gatgaagaag agattcgtac caccaatcct gtggcaacag agcagtatgg aactgtggca 1740

actaacttgc agagctcaaa tacagctccc gcgactggaa ctgtcaatag tcaggggggcc 1800

ttacctggca tggtgtggca agatcgtgac gtgtaccttc aaggacctat ctgggcaaag 1860

attcctcaca cggatggaca ctttcatcct tctcctctga tgggaggctt tggactgaaa 1920

catccgcctc ctcaaatctt gatcaaaaat actccggtac cggcaaatcc tccgacgact 1980

ttcagcccgg ccaagtttgc ttcatttatc actcagtact ccactggaca ggtcagcgtg 2040

gaaattgagt gggagctaca gaaagaaaac agcaaacgtt ggaatccaga gattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tagacactaa tggtgtttat 2160

agtgaacctc gccctattgg aacccggtat ctcacacgaa acttg 2205

<210> 1472
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1472

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445
```

```
Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1473
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1473

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1474
<211> 736

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1474

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

```
Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1475
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1475

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1476
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1476

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575
```

```
Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  1477
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1477

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445
```

```
Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1478
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1478

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1479
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1479

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  1480
<211>  2211
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polynucleotide

<400>  1480
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaga gaccggtaga gcaatcaccc caggaaccag actcctcttc gggcatcggc      480

aagaaaggcc agcagcccgc gaaaaagaga ctcaactttg ggcagacagg cgactcagag      540
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tcagtgcccg accctcaacc actcggagaa ccccccgcag ccccctctgg tgtgggatct 600

aatacaatgg ctgcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaacg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctcccc acctacaaca accacctcta caagcaaatc 780

tccagccaat cgggagcaag caccaacgac aacacctact tcggctacag cacccctgg 840

gggtattttg actttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgacgaa tgatggcacc acgaccatcg ccaataacct taccagcacg 1020

gttcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctgc ctccgttccc ggcggacgtc ttcatgattc ctcagtacgg gtacctgact 1140

ctgaacaatg gcagtcaggc cgtgggccgt tcctccttct actgcctgga gtactttcct 1200

tctcaaatgc tgagaacggg caacaacttt gagttcagct acacgtttga ggacgtgcct 1260

tttcacagca gctacgcgca cagccaaagc ctggaccggc tgatgaaccc cctcatcgac 1320

cagtacctgt actacctgtc tcggactcag accacgagtg gtaccgcagg aaatcggacg 1380

ttgcaatttt ctcaggccgg gcctagtagc atggcgaatc aggccaaaaa ctggctaccc 1440

gggccctgct accggcagca acgcgtctcc aagacagcga atcaaaataa caacagcaac 1500

tttgcctgga ccggtgccac caagtatcat ctgaatggca gagactctct ggtaaatccc 1560

ggtcccgcta tggcaaccca caaggacgac gaagacaaat tttttccgat gagcggagtc 1620

ttaatatttg ggaaacaggg agctggaaat agcaacgtgg accttgacaa cgttatgata 1680

accagtgagg aagaaattaa aaccaccaac ccagtggcca cagaacagta cggcacggtg 1740

gccactaacc tgcaatcgtc aaacaccgct cctgctacag ggaccgtcaa cagtcaagga 1800

gccttacctg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc tatctgggcc 1860

aagattcctc acacggacgg acactttcat ccctcgccgc tgatgggagg ctttggactg 1920

aaacacccgc ctcctcagat cctgattaag aatacacctg ttcccgcgaa tcctccaact 1980

accttcagtc cagctaagtt tgcgtcgttc atcacgcagt acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc agagattcaa 2100

tacacttcca actacaacaa atctacaaat gtggactttg ctgttgacac aaatggcgtt 2160

tattctgagc ctcgccccat cggcacccgt tacctcaccc gtaatctgta a 2211

<210> 1481
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1481

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

```
Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
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Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590
```

```
Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 1482
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1482
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cgcgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgag tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa caggcaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc atgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacacac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catctgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ccgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 1483
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1483
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cgcgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgag tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa caggcaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc atgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catctgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ccgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 1484
<211> 2202
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1484
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tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg acttgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgaac acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc cgagtttcag 300

gagcgtcttc aagaagatac gtcttttggg ggcaacctcg gacgagcagt cttccaggcc 360

aaaaagagga tccttgagcc tctgggtctg gttgaggaag cggctaagac ggctcctgga 420

aaaaagagac ctgtagagca atctccagca gaaccggact cctcttcggg catcggcaaa 480

tcaggccagc agcccgctag aaaaagactg aattttggtc agactggcga cacagagtca 540

gtcccagacc ctcaaccact cggacaacct cccgcagccc cctctggtgt gggatctact 600

acaatggctt caggcggtgg cgcaccaatg gcagacaata acgagggtgc cgatggagtg 660

ggtaattcct caggaaattg gcattgcgat tcccaatggc tgggcgacag agtcatcacc 720

accagcaccc gcacctgggc cctgcccacc tacaacaatc acctctacaa gcaaatctcc 780

agccaatcag gagccaccaa cgacaaccac tactttggct acagcacccc ctgggggtat 840

tttgacttca acagattcca ctgccacttt tcaccacgtg actggcaaag actcatcaac 900

aacaactggg gattccgacc caagagactc aacttcaagc tctttaacat tcaagtcaaa 960

gaggtcacgc agaatgacgg tacgacgacg attgccaata accttaccag cacggttcag 1020

gtgtttactg actccgagta ccagctcccg tacgtcctcg gctcggcgca tcagggatgc 1080

ctcccgccgt tcccagcaga cgtcttcatg gtcccacagt atggatacct caccctgaac 1140

aacgggagtc aggcggtagg acgctcttcc ttttactgcc tggagtactt tccttctcag 1200

atgctgcgta ctggaaacaa ctttcagttt agctacactt ttgaagacgt gcctttccac 1260

agcagctacg ctcacagcca aagtctggac cgtctcatga atcctctgat cgaccagtac 1320

ctgtactatc tgaacaggac acaaacagcc agtggaactc agcagtctcg gctactgttt 1380

agccaagctg gacccaccag tatgtctctt caagctaaaa actggctgcc tggaccttgc 1440

tacagacagc agcgtctgtc aaagcaggca aacgacaaca acaacagcaa ctttccctgg 1500

actggtgcca ccaaatatca tctgaatggc cgggactcat tggtgaaccc gggccctgct 1560

atggccagtc acaaggatga caaagaaaag tttttcccca tgcatggaac cctgatattt 1620

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gaagaaatcc gcaccaccaa tcccgtggct acggagcagt acgggactgt gtcaaataat 1740

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ggtatggtgt ggcaggatcg agacgtgtac ctgcagggac ccatttgggc caagattcct 1860

cacaccgatg gacactttca tccttctcca ctgatgggag gttttgggct caaacacccg 1920

cctcctcaga tcatgatcaa aaacactccc gttccagcca atcctcccac aaactttagt 1980

gcggcaaagt ttgcttcctt catcacacag tactccacgg ggcaggtcag cgtggagatc 2040

gagtgggagc tgcagaagga gaacagcaaa cgctggaatc ccgaaattca gtacacttcc 2100

aactacaaca aatctgttaa tgtggacttt actgtggaca ctaatggtgt gtattcagag 2160

cctcgcccca ttggcaccag atacctgact cgtaatctgt aa 2202

<210> 1485
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1485
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catctgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ccgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 1486
<211> 2211

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1486
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

aagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggagagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ccgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 1487
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1487
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

aacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacacac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catctgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ccgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 1488
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1488
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aaccagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agctcaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aaacacccgc ctcctcagat cctcatcaaa aacacacctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagc 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ccgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 1489
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1489
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcagtcgccc caagaaccag actcctcatc gggcatcggc 480

aaatcaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatt 720

accaccagca cccgaacctg ggccctgccc acctataaca accacctcta caaacaaatc 780

tccagcgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg attttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaaca 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt accttcagct acacattcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccaaagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacttgt attacctaaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcttcaca caaagacgac gaagacaagt tctttccaat gagcggtgtc 1620

atgatttttg gcaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc aatttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagt 2040

gtggaaattg aatgggagtt gcagaaagaa aacagcaagc gttggaatcc cgaagtgcag 2100

tacacatcta attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1490
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1490
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcaccc caagaaccag actcctcctc gggcattggc 480

aaatcaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tttgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagc 2040

gtggaaattg aatgggagtt gcagaaagaa aacagtaagc gctggaatcc cgaagtgcag 2100

tacacatcta attatgcaaa atctgccaac gttgacttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1491
<211> 2970
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1491
agatgaccgc caaggtcgta gagtccgcca aggccattct gggcggcagc aaggtgcgcg 60

tggaccaaaa atgcaaggcc tctgcgcaga tcgaccccac ccccgtgatc gtcacctcca 120

acaccaacat gtgcgccgtg attgacggga acagcaccac cttcgagcac cagcagcccc 180

tgcaggaccg gatgttcaag tttgaactca cccgccgcct cgactacgac tttggcaagg 240

tcaccaagca ggaagtcaag gacttttcc ggtgggcggc tgatcacgtg actgacgtgg 300

ctcatgagtt ttacgtcaca aagggtggag ctaagaaaag gcccgccccc tctgacgagg 360

atataagcga gcccaagcgg ccgcgcgtgt catttgcgca gccggagacg tcagacgcgg 420

aagctcccgg agacttcgcc gacaggtacc aaaacaaatg ttctcgtcac gcgggtatgc 480

tgcagatgct ctttccctgc aagacgtgcg agagaatgaa tcagaattcc aacgtctgct 540

tcacgcacgg tcagaaagat tgcggggagt gctttcccgg gtcagaatct caaccggttt 600

ctgtcgtcag aaaaacgtat cagaaactgt gcatccttca tcagctccgg ggggcacccg 660

agatcgcctg ctctgcttgc gaccaactca accccgattt ggacgattgc caatttgagc 720

aataaatgac tgaaatcagg tatggctgct gacggttatc ttccagattg gctcgaggac 780

aacctctctg aaggcattcg cgagtggtgg gcgctgaaac ctggagctcc acaacccaag 840

gccaaccaac agcatcagga caacggcagg ggtcttgtgc ttcctgggta caagtacctc 900

ggacccttca acggactcga caagggagag ccggtcaacg aggcagacgc cgcggccctc 960

gagcacgaca aggcctacga caagcagctc gagcaggggg acaacccgta tctcaagtac 1020

aaccacggcg acgccgagtt ccagcagcgc ttggcgaccg acacctcttt tgggggcaac 1080

ctcgggcgag cagtcttcca ggccaaaaag aggattctcg agcctctggg tctggttgaa 1140

gagggcgtta aaacggctcc tggaaagaaa cgcccattag aaaagactcc aaatcggccg 1200

accaacccgg actctgggaa ggccccggcc aagaaaaagc aaaaagacgg cgaaccagcc 1260

gactctgcta gaaggacact cgactttgaa gactctggag caggagacgg acccccctgag 1320

ggatcatctt ccggagaaat gtctcatgat gctgagatgc gtgcggcgcc aggcggaaat 1380

gctgtcgagg cgggacaagg tgccgatgga gtgggtaatg cctccggtga ttggcattgc 1440

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ggattctcca ccccctgggg atactttgac tttaaccgct tccactgcca cttttcccca 1620

cgcgactggc agcgactcat caacaacaac tggggactca ggccgaaatc gatgcgtgtt 1680

aaaatcttca acatacaggt caaggaggtc acgacgtcaa acggcgagac tacggtcgct 1740

aataacctta ccagcacggt tcagatcttt gcggattcga cgtatgaact cccatacgtg 1800

atggacgccg gtcaggaggg gagctttcct ccgtttccca acgacgtctt tatggttccc 1860

caatacggat actgcggagt tgtcactgga aaaaaccaga accagacaga cagaaatgcc 1920

ttttactgcc tggaatactt tccatcccaa atgctaagaa ctggcaacaa ttttgaagtc 1980

agttaccaat ttgaaaaagt tcctttccat tcaatgtacg cgcacagcca gagcctggac 2040

agaatgatga atcctttact ggatcagtac ctgtggcatc tgcaatcgac cactaccgga 2100

aattccctta atcaaggaac agctaccacc acgtacggga aaattaccac tggagacttt 2160

gcctactaca ggaaaaactg gttgcctgga gcctgcatta aacaacaaaa attttcaaag 2220

aatgccaatc aaaactacaa gattcccgcc agcgggggag acgccctttt aaagtatgac 2280

acgcatacca ctctaaatgg gcgatggagt aacatggctc ctggacctcc aatggcaacc 2340

gcaggtgccg gggactcgga ttttagcaac agccagctga tctttgccgg acccaatccg 2400

agcggtaaca cgaccacatc ttcaaacaat ttgttgttta cctcagaaga ggagattgcc 2460

acaacaaacc cacgagacac ggacatgttt ggacagattg cagataataa tcaaaatgcc 2520

accaccgccc ctcacatcgc taacctggac gctatgggaa ttgttcccgg aatggtctgg 2580

caaaacagag acatctacta ccagggccct atttgggcca aggtccctca cacggacgga 2640

cactttcacc cttcgccgct gatgggagga tttggactga aacacccgcc tccacagatt 2700

ttcatcaaaa acacccccgt acccgccaat cccaatacta cctttagcgc tgcaaggatt 2760

aattcttttc tgacgcagta cagcaccgga caagttgccg ttcagatcga ctgggaaatt 2820

cagaaggagc attccaaacg ctggaatccc gaagttcaat ttacttcaaa ctacggcact 2880

caaaattcta tgctgtgggc tcccgacaat gctggcaact accacgaact ccgggctatt 2940

gggtcccgtt tcctcaccca ccacttgtaa 2970

<210> 1492
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1492

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Ser Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Gly Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly His Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr His Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1493
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1493

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Ser Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Gly Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly His Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr His Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1494
<211> 733

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1494

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
115 120 125

Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro
130 135 140

Val Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145 150 155 160

Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr Gly
165 170 175

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro Ala
180 185 190

```
Ala Pro Ser Gly Val Gly Ser Thr Thr Met Ala Ser Gly Gly Gly Ala
        195                 200                 205

Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser
    210                 215                 220

Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255

Lys Gln Ile Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Tyr Phe
            260                 265                 270

Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
        275                 280                 285

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
    290                 295                 300

Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys
305                 310                 315                 320

Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu Thr
                325                 330                 335

Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val
            340                 345                 350

Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
        355                 360                 365

Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln
    370                 375                 380

Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
385                 390                 395                 400
```

```
Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp
                405                 410                 415

Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
            420                 425                 430

Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln
        435                 440                 445

Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460

Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480

Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn Ser
                485                 490                 495

Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp Lys
        515                 520                 525

Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu Gly
    530                 535                 540

Thr Asn Ala Asn Asn Ala Asp Leu Glu Asn Val Met Ile Thr Asp Glu
545                 550                 555                 560

Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Thr
                565                 570                 575

Val Ser Asn Asn Leu Gln Asn Ser Asn Ala Gly Pro Thr Thr Gly Thr
            580                 585                 590

Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg Asp
        595                 600                 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
    610                 615                 620
```

```
His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640


Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro
                645                 650                 655


Thr Asn Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670


Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
        675                 680                 685


Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys
    690                 695                 700


Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu
705                 710                 715                 720


Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730


<210>  1495
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1495

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210>  1496
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1496

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Lys Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575
```

```
Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210>  1497
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1497

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr His Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1498
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1498

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Leu Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1499
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1499

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Gly Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1500
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1500

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Leu Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Lys Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720
```

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1501
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1501

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Ala Thr Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Glu Lys Thr Pro Asn Arg Pro Thr Asn Pro Asp Ser Gly Lys
145 150 155 160

```
Ala Pro Ala Lys Lys Lys Gln Lys Asp Gly Glu Pro Ala Asp Ser Ala
                165                 170                 175

Arg Arg Thr Leu Asp Phe Glu Asp Ser Gly Ala Gly Asp Gly Pro Pro
            180                 185                 190

Glu Gly Ser Ser Ser Gly Glu Met Ser His Asp Ala Glu Met Arg Ala
        195                 200                 205

Ala Pro Gly Gly Asn Ala Val Glu Ala Gly Gln Gly Ala Asp Gly Val
    210                 215                 220

Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Ser Glu Gly
225                 230                 235                 240

Arg Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Thr Tyr Asn
                245                 250                 255

Asn His Leu Tyr Leu Arg Ile Gly Thr Thr Ala Asn Ser Asn Thr Tyr
            260                 265                 270

Asn Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Leu Arg Pro Lys Ser Met Arg Val Lys Ile Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Ile Phe Ala Asp Ser Thr Tyr Glu Leu Pro Tyr
            340                 345                 350

Val Met Asp Ala Gly Gln Glu Gly Ser Phe Pro Pro Phe Pro Asn Asp
        355                 360                 365
```

```
Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Val Val Thr Gly Lys
    370                 375                 380

Asn Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Val Ser Tyr Gln
                405                 410                 415

Phe Glu Lys Val Pro Phe His Ser Met Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Met Met Asn Pro Leu Leu Asp Gln Tyr Leu Trp His Leu Gln
        435                 440                 445

Ser Thr Thr Thr Gly Asn Ser Leu Asn Gln Gly Thr Ala Thr Thr Thr
    450                 455                 460

Tyr Gly Lys Ile Thr Thr Gly Asp Phe Ala Tyr Tyr Arg Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Ala Cys Ile Lys Gln Gln Lys Phe Ser Lys Asn Ala Asn
                485                 490                 495

Gln Asn Tyr Lys Ile Pro Ala Ser Gly Gly Asp Ala Leu Leu Lys Tyr
            500                 505                 510

Asp Thr His Thr Thr Leu Asn Gly Arg Trp Ser Asn Met Ala Pro Gly
        515                 520                 525

Pro Pro Met Ala Thr Ala Gly Ala Gly Asp Ser Asp Phe Ser Asn Ser
    530                 535                 540

Gln Leu Ile Phe Ala Gly Pro Asn Pro Ser Gly Asn Thr Thr Thr Ser
545                 550                 555                 560

Ser Asn Asn Leu Leu Phe Thr Ser Glu Glu Glu Ile Ala Thr Thr Asn
                565                 570                 575

Pro Arg Asp Thr Asp Met Phe Gly Gln Ile Ala Asp Asn Asn Gln Asn
            580                 585                 590
```

```
Ala Thr Thr Ala Pro His Ile Ala Asn Leu Asp Ala Met Gly Ile Val
        595                 600                 605

Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile
    610                 615                 620

Trp Ala Lys Val Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
625                 630                 635                 640

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Phe Ile Lys
                645                 650                 655

Asn Thr Pro Val Pro Ala Asn Pro Asn Thr Thr Phe Ser Ala Ala Arg
            660                 665                 670

Ile Asn Ser Phe Leu Thr Gln Tyr Ser Thr Gly Gln Val Ala Val Gln
        675                 680                 685

Ile Asp Trp Glu Ile Gln Lys Glu His Ser Lys Arg Trp Asn Pro Glu
    690                 695                 700

Val Gln Phe Thr Ser Asn Tyr Gly Thr Gln Asn Ser Met Leu Trp Ala
705                 710                 715                 720

Pro Asp Asn Ala Gly Asn Tyr His Glu Leu Arg Ala Ile Gly Ser Arg
                725                 730                 735

Phe Leu Thr His His Leu
            740
```

<210> 1502
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1502
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa ggcggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcag ccccctcagg tctgggacct 600

aatacaatgg cttcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggca cctcgggagg aagcaccaac gacaacacct attttggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcactttt caccacgtga ctggcaacga 900

ctcatcaaca acaattgggg attccggccc aaaagactca acttcaagct gttcaacatc 960

caggtcaagg aagtcacgac gaacgaaggc accaagacca tcgccaataa tctcaccagc 1020

accgtgcagg tctttacgga ctcggagtac cagttaccgt acgtgctagg atccgctcac 1080

cagggatgtc tgcctccgtt cccggcggac gtcttcatgg ttcctcagta cggctattta 1140

actttaaaca atggaagcca agccctggga cgttcctcct tctactgtct ggagtatttc 1200

ccatcgcaga tgctgagaac cggcaacaac tttcagttca gctacacctt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agcctggaca ggctgatgaa tcccctcatc 1320

gaccagtacc tgtactacct ggtcagaacg caaacgactg gaactggagg gacgcagact 1380

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ggaccttgct accggcagca gcgcgtctcc acgacaacca accagaacaa caacagcaac 1500

tttgcctgga cgggagctgc caagtttaag ctgaacggcc gagactctct aatgaatccg 1560

ggcgtggcaa tggcttccca caaggatgac gacgaccgct tcttcccttc gagcggggtc 1620

ctgatttttg gcaagcaagg agccgggaac gatggagtgg attacagcca agtgctgatt 1680

acagatgagg aagaaatcaa ggctaccaac cccgtggcca cagaagaata tggagcagtg 1740

gccatcaaca accaggccgc caatacgcag gcgcagaccg gactcgtgca caaccagggg 1800

gtgattcccg gcatggtgtg gcagaataga gacgtgtacc tgcagggtcc catctgggcc 1860

aaaattcctc acacggacgg caactttcac ccgtctcccc tgatgggcgg ctttggactg 1920

aagcacccgc ctcctcaaat tctcatcaag aacacaccgg ttccagcgga cccgccgctt 1980

accttcaacc aggccaagct gaactctttc atcacgcagt acagcaccgg acaggtcagc 2040

gtggaaatcg agtgggagct gcagaaagaa aacagcaaac gctggaatcc agagattcaa 2100

tacacttcca actactacaa atctacaaat gtggactttg ctgtcaacac ggagggggtt 2160

tatagcgagc ctcgccccat tggcacccgt tacctcaccc gcaacctgta a 2211

<210> 1503
<211> 2592
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1503
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gatggaagtg 420

cagctccaag ccagtggtgg cggactggtg caggcaggag gcagcttgag gctcagctgt 480

gccgccagcg gcttcaagat cacccactac accatgggct ggttccggca ggcccctggc 540

aaggagaggg agttcgtgag caggattacc tggggtggtg acaacacctt ctacagcaac 600

agcgtgaagg gcaggttcac catcagcagg gacaacgcca agaacaccgt gtacctgcag 660

atgaacagcc tgaagcccga ggacaccgcc gactactact gtgcagccgg cagtaccagc 720

accgctaccc ccctgagggt ggactactgg ggcaaaggca ctcaggtgac agtgtcttca 780

ggagggggtg gcagcgctcc tggaaagaaa cgtccggtag agcagtcgcc acaagagcca 840

gactcctcct cgggcatcgg caagacaggc cagcagcccg ctaaaaagag actcaatttt 900

ggtcagactg gcgactcaga gtcagtcccc gatccacaac ctctcggaga acctccagca 960

gccccctcag gtctgggacc taatacaatg gcttcaggcg gtggcgctcc aatggcagac 1020

aataacgaag gcgccgacgg agtgggtaat tcctcgggaa attggcattg cgattccaca 1080

tggctggggg acagagtcat caccaccagc acccgaacct gggccctgcc cacctacaac 1140

aaccacctct acaagcaaat ctccaacggc acctcgggag gaagcaccaa cgacaacacc 1200

tattttggct acagcacccc ctgggggtat tttgacttca acagattcca ctgtcacttt 1260

tcaccacgtg actggcaacg actcatcaac aacaattggg gattccggcc caaaagactc 1320

aacttcaagc tgttcaacat ccaggtcaag gaagtcacga cgaacgaagg caccaagacc 1380

atcgccaata atctcaccag caccgtgcag gtctttacgg actcggagta ccagttaccg 1440

tacgtgctag gatccgctca ccagggatgt ctgcctccgt tcccggcgga cgtcttcatg 1500

gttcctcagt acggctattt aactttaaac aatggaagcc aagccctggg acgttcctcc 1560

ttctactgtc tggagtattt cccatcgcag atgctgagaa ccggcaacaa ctttcagttc 1620

agctacacct tcgaggacgt gcctttccac agcagctacg cgcacagcca gagcctggac 1680

aggctgatga atcccctcat cgaccagtac ctgtactacc tggtcagaac gcaaacgact 1740

ggaactggag ggacgcagac tctggcattc agccaagcgg gtcctagctc aatggccaac 1800

caggctagaa attgggtgcc cggaccttgc taccggcagc agcgcgtctc cacgacaacc 1860

aaccagaaca acaacagcaa ctttgcctgg acgggagctg ccaagtttaa gctgaacggc 1920

cgagactctc taatgaatcc gggcgtggca atggcttccc acaaggatga cgacgaccgc 1980

ttcttccctt cgagcggggt cctgattttt ggcaagcaag gagccgggaa cgatggagtg 2040

gattacagcc aagtgctgat tacagatgag gaagaaatca aggctaccaa ccccgtggcc 2100

acagaagaat atggagcagt ggccatcaac aaccaggccg ccaatacgca ggcgcagacc 2160

ggactcgtgc acaaccaggg ggtgattccc ggcatggtgt ggcagaatag agacgtgtac 2220

ctgcagggtc ccatctgggc caaaattcct cacacggacg gcaactttca cccgtctccc 2280

ctgatgggcg gctttggact gaagcacccg cctcctcaaa ttctcatcaa gaacacaccg 2340

gttccagcgg acccgccgct taccttcaac caggccaagc tgaactcttt catcacgcag 2400

tacagcaccg gacaggtcag cgtggaaatc gagtgggagc tgcagaaaga aaacagcaaa 2460

cgctggaatc cagagattca atacacttcc aactactaca aatctacaaa tgtggacttt 2520

gctgtcaaca cggaggggt ttatagcgag cctcgcccca ttggcacccg ttacctcacc 2580

cgcaacctgt aa 2592

<210> 1504
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gatggaggtg 420

cagctgcagg cttctggagg aggactggtg caggctggag ggagtctgag gctgtcttgc 480

agtgcctcag tgaggacttt ctccatctac gccatgggct ggtttaggca ggctcccggg 540

aaggagcgcg aattcgtggc cggaatcaac cggtctggcg acgtgaccaa gtacgctgat 600

ttcgtgaaag gccggtttag catttccaga gacaacgcca agaatatggt gtatctgcag 660

atgaactccc tgaaacctga agacacagct ctgtactatt gtgccgctac ttgggcctac 720

gataccgtgg gggctctgac atcaggatat aatttttggg gccaggggac ccaggtgaca 780

gtgagctccg gaggaggagg aagcgctcct ggaaagaaac gtccggtaga gcagtcgcca 840

caagagccag actcctcctc gggcatcggc aagacaggcc agcagcccgc taaaaagaga 900

ctcaattttg gtcagactgg cgactcagag tcagtccccg atccacaacc tctcggagaa 960

cctccagcag ccccctcagg tctgggacct aatacaatgg cttcaggcgg tggcgctcca 1020

atggcagaca ataacgaagg cgccgacgga gtgggtaatt cctcgggaaa ttggcattgc 1080

gattccacat ggctggggga cagagtcatc accaccagca cccgaacctg ggccctgccc 1140

acctacaaca accacctcta caagcaaatc tccaacggca cctcgggagg aagcaccaac 1200

gacaacacct attttggcta cagcaccccc tgggggtatt ttgacttcaa cagattccac 1260

tgtcactttt caccacgtga ctggcaacga ctcatcaaca acaattgggg attccggccc 1320

aaaagactca acttcaagct gttcaacatc caggtcaagg aagtcacgac gaacgaaggc 1380

accaagacca tcgccaataa tctcaccagc accgtgcagg tctttacgga ctcggagtac 1440

cagttaccgt acgtgctagg atccgctcac cagggatgtc tgcctccgtt cccggcggac 1500

gtcttcatgg ttcctcagta cggctattta actttaaaca atggaagcca agccctggga 1560

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acgacaacca accagaacaa caacagcaac tttgcctgga cgggagctgc caagtttaag 1920

ctgaacggcc gagactctct aatgaatccg ggcgtggcaa tggcttccca caaggatgac 1980

gacgaccgct tcttcccttc gagcggggtc ctgatttttg gcaagcaagg agccgggaac 2040

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cccgtggcca cagaagaata tggagcagtg gccatcaaca accaggccgc caatacgcag 2160

gcgcagaccg gactcgtgca caaccagggg gtgattcccg gcatggtgtg gcagaataga 2220

gacgtgtacc tgcagggtcc catctgggcc aaaattcctc acacggacgg caactttcac 2280

ccgtctcccc tgatgggcgg ctttggactg aagcacccgc ctcctcaaat tctcatcaag 2340

aacacaccgg ttccagcgga cccgccgctt accttcaacc aggccaagct gaactctttc 2400

atcacgcagt acagcaccgg acaggtcagc gtggaaatcg agtgggagct gcagaaagaa 2460

aacagcaaac gctggaatcc agagattcaa tacacttcca actactacaa atctacaaat 2520

gtggactttg ctgtcaacac ggaggggggtt tatagcgagc ctcgccccat tggcacccgt 2580

tacctcaccc gcaacctgta a 2601

<210> 1505
<211> 2367

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gatgccaagc 420

agtgtaatcg atgcgctgca gtacaagctg gagggcacca cgaggctgac caggaagagg 480

ggtctgaagc tggccacggc cctcagcctt agcaataagt tcgtagaggg cagccccagc 540

ggcggcggcg gcagcggcgg cggcggcagc gctcctggaa agaaacgtcc ggtagagcag 600

tcgccacaag agccagactc ctcctcgggc atcggcaaga caggccagca gcccgctaaa 660

aagagactca attttggtca gactggcgac tcagagtcag tccccgatcc acaacctctc 720

ggagaacctc cagcagcccc ctcaggtctg ggacctaata caatggcttc aggcggtggc 780

gctccaatgg cagacaataa cgaaggcgcc gacggagtgg gtaattcctc gggaaattgg 840

cattgcgatt ccacatggct gggggacaga gtcatcacca ccagcacccg aacctgggcc 900

ctgcccacct acaacaacca cctctacaag caaatctcca acggcacctc gggaggaagc 960

accaacgaca acacctattt tggctacagc acccccctggg ggtattttga cttcaacaga 1020

ttccactgtc acttttcacc acgtgactgg caacgactca tcaacaacaa ttggggattc 1080

cggcccaaaa gactcaactt caagctgttc aacatccagg tcaaggaagt cacgacgaac 1140

gaaggcacca agaccatcgc caataatctc accagcaccg tgcaggtctt tacggactcg 1200

gagtaccagt taccgtacgt gctaggatcc gctcaccagg gatgtctgcc tccgttcccg 1260

gcggacgtct tcatggttcc tcagtacggc tatttaactt taaacaatgg aagccaagcc 1320

ctgggacgtt cctccttcta ctgtctggag tatttcccat cgcagatgct gagaaccggc 1380

aacaactttc agttcagcta caccttcgag gacgtgcctt tccacagcag ctacgcgcac 1440

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agctcaatgg ccaaccaggc tagaaattgg gtgcccggac cttgctaccg gcagcagcgc 1620

gtctccacga caaccaacca gaacaacaac agcaactttg cctggacggg agctgccaag 1680

tttaagctga acggccgaga ctctctaatg aatccgggcg tggcaatggc ttcccacaag 1740

gatgacgacg accgcttctt cccttcgagc ggggtcctga tttttggcaa gcaaggagcc 1800

gggaacgatg gagtggatta cagccaagtg ctgattacag atgaggaaga aatcaaggct 1860

accaaccccg tggccacaga agaatatgga gcagtggcca tcaacaacca ggccgccaat 1920

acgcaggcgc agaccggact cgtgcacaac caggggggtga ttcccggcat ggtgtggcag 1980

aatagagacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 2040

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atcaagaaca caccggttcc agcggacccg ccgcttacct tcaaccaggc caagctgaac 2160

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acccgttacc tcacccgcaa cctgtaa 2367

<210> 1506
<211> 2328
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1506
ctggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gatgtatacc 420

atctggatgc ccgagaaccc caggcccggt acccccctgcg acatcttcac caacagcagg 480

ggcaagcgag ccagcaacgg cggcggcggc ggcagcggcg gcggcggcag cgctcctgga 540

aagaaacgtc cggtagagca gtcgccacaa gagccagact cctcctcggg catcggcaag 600

acaggccagc agcccgctaa aaagagactc aattttggtc agactggcga ctcagagtca 660

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acaatggctt caggcggtgg cgctccaatg gcagacaata acgaaggcgc cgacggagtg 780

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aacggcacct cgggaggaag caccaacgac aacacctatt ttggctacag cacccccctgg 960

gggtattttg acttcaacag attccactgt cacttttcac cacgtgactg gcaacgactc 1020

atcaacaaca attggggatt ccggcccaaa agactcaact tcaagctgtt caacatccag 1080

gtcaaggaag tcacgacgaa cgaaggcacc aagaccatcg ccaataatct caccagcacc 1140

gtgcaggtct ttacggactc ggagtaccag ttaccgtacg tgctaggatc cgctcaccag 1200

ggatgtctgc ctccgttccc ggcggacgtc ttcatggttc ctcagtacgg ctatttaact 1260

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cagtacctgt actacctggt cagaacgcaa acgactggaa ctggagggac gcagactctg 1500

gcattcagcc aagcgggtcc tagctcaatg gccaaccagg ctagaaattg ggtgcccgga 1560

ccttgctacc ggcagcagcg cgtctccacg acaaccaacc agaacaacaa cagcaacttt 1620

gcctggacgg gagctgccaa gtttaagctg aacggccgag actctctaat gaatccgggc 1680

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atttttggca agcaaggagc cgggaacgat ggagtggatt acagccaagt gctgattaca 1800

gatgaggaag aaatcaaggc taccaacccc gtggccacag aagaatatgg agcagtggcc 1860

atcaacaacc aggccgccaa tacgcaggcg cagaccggac tcgtgcacaa ccaggggggtg 1920

attcccggca tggtgtggca gaatagagac gtgtacctgc agggtcccat ctgggccaaa 1980

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acttccaact actacaaatc tacaaatgtg gactttgctg tcaacacgga gggggtttat 2280

agcgagcctc gccccattgg cacccgttac ctcacccgca acctgtaa 2328

<210> 1507
<211> 2298
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1507
ctggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gatgaccttc 420

ttctacggcg gcagcagggg caagaggaac aacttcaaga ccgaggagta cggcggcggc 480

ggcagcggcg gcggcggcag cgctcctgga aagaaacgtc cggtagagca gtcgccacaa 540

gagccagact cctcctcggg catcggcaag acaggccagc agcccgctaa aaagagactc 600

aattttggtc agactggcga ctcagagtca gtccccgatc cacaacctct cggagaacct 660

ccagcagccc cctcaggtct gggacctaat acaatggctt caggcggtgg cgctccaatg 720

gcagacaata acgaaggcgc cgacggagtg ggtaattcct cgggaaattg gcattgcgat 780

tccacatggc tgggggacag agtcatcacc accagcaccc gaacctgggc cctgcccacc 840

tacaacaacc acctctacaa gcaaatctcc aacggcacct cgggaggaag caccaacgac 900

aacacctatt ttggctacag caccccctgg gggtattttg acttcaacag attccactgt 960

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acgactggaa ctggagggac gcagactctg gcattcagcc aagcgggtcc tagctcaatg 1500

gccaaccagg ctagaaattg ggtgcccgga ccttgctacc ggcagcagcg cgtctccacg 1560

acaaccaacc agaacaacaa cagcaacttt gcctggacgg gagctgccaa gtttaagctg 1620

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gtggccacag aagaatatgg agcagtggcc atcaacaacc aggccgccaa tacgcaggcg 1860

cagaccggac tcgtgcacaa ccaggggggtg attcccggca tggtgtggca gaatagagac 1920

gtgtacctgc agggtcccat ctgggccaaa attcctcaca cggacggcaa ctttcacccg 1980

tctcccctga tgggcggctt tggactgaag cacccgcctc ctcaaattct catcaagaac 2040

acaccggttc cagcggaccc gccgcttacc ttcaaccagg ccaagctgaa ctctttcatc 2100

acgcagtaca gcaccggaca ggtcagcgtg gaaatcgagt gggagctgca gaaagaaaac 2160

agcaaacgct ggaatccaga gattcaatac acttccaact actacaaatc tacaaatgtg 2220

gactttgctg tcaacacgga gggggtttat agcgagcctc gccccattgg cacccgttac 2280

ctcacccgca acctgtaa 2298

<210> 1508
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1508
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa ggcggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca actacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacgatt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacga agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccataaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 1509
<211> 2277
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1509
ctggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gatgaacaac 420

cagaagatcg tgaacctgaa ggagaaggtg gcccagctgg aggccggcgg cggcggcagc 480

gctcctggaa agaagaggcc tgtagagcag tctcctcagg aaccggactc ctccgcgggt 540

attggcaaat cgggtgcaca gcccgctaaa aagagactca atttcggtca gactggcgac 600

acagagtcag tcccagaccc tcaaccaatc ggagaacctc ccgcagcccc ctcaggtgtg 660

ggatctctta caatggcttc aggtggtggc gcaccagtgg cagacaataa cgaaggtgcc 720

gatggagtgg gtagttcctc gggaaattgg cattgcgatt cccaatggct gggggacaga 780

gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaatca cctctacaag 840

caaatctcca acagcacatc tggaggatct tcaaatgaca acgcctactt cggctacagc 900

acccccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc acgtgactgg 960

cagcgactca tcaacaacaa ctggggattc cggcctaagc gactcaactt caagctcttc 1020

aacattcagg tcaaagaggt tacggacaac aatggagtca agaccatcgc caataacctt 1080

accagcacgg tccaggtctt cacggactca gactatcagc tcccgtacgt gctcgggtcg 1140

gctcacgagg gctgcctccc gccgttccca gcggacgttt tcatgattcc tcagtacggg 1200

tatctgacgc ttaatgatgg aagccaggcc gtgggtcgtt cgtcctttta ctgcctggaa 1260

tatttcccgt cgcaaatgct aagaacgggt aacaacttcc agttcaacta cgagtttgag 1320

aacgtacctt tccatagcag ctacgctcac agccaaagcc tggaccgact aatgaatcca 1380

ctcatcgacc aatacttgta ctatctctca aagactatta acgattctgg acagaatcaa 1440

caaacgctaa aattcagtgt ggccggaccc agcaacatgg ctgtccaggg aagaaactac 1500

atacctggac ccagctaccg acaacaacgt gtctcaacca ctgtgactca aaacaacaac 1560

agcgaatttg cttggcctgg agcttcttct tgggctctca atggacgtaa tagcttgatg 1620

aatcctggac ctgctatggc cagccacaaa gaaggagagg accgtttctt tcctttgtct 1680

ggatctttaa tttttggcaa acaaggaact ggaagagaca acgtggatgc ggacgaagtc 1740

atgataacca acgaagaaga aattaaaact actaacccgg tagcaacgga gtcctatgga 1800

caagtggcca taaaccacca gagtgcccaa gcacaggcgc agaccggctg ggttcaaaac 1860

caaggaatac ttccgggtat ggtttggcag gacagagatg tgtacctgca aggacccatt 1920

tgggccaaaa ttcctcacac ggacggcaac tttcaccctt ctccgctgat gggagggttt 1980

ggaatgaagc acccgcctcc tcagatcctc atcaaaaaca cacctgtacc tgcggatcct 2040

ccaacggcct tcaacaagga caagctgaac tctttcatca cccagtattc tactggccaa 2100

gtcagcgtgg agatcgagtg ggagctgcag aaggaaaaca gcaagcgctg gaacccggag 2160

atccagtaca cttccaacta ttacaagtct aataatgttg aatttgctgt taatactgaa 2220

ggtgtatata gtgaaccccg ccccattggc accagatacc tgactcgtaa tctgtaa 2277

<210> 1510
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1510
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gatgtatacc 420

atctggatgc ccgagaaccc caggcccggt acccccctgcg acatcttcac caacagcagg 480

ggcaagcgag ccagcaacgg cggcggcggc ggcagcgctc ctggaaagaa gaggcctgta 540

gagcagtctc ctcaggaacc ggactcctcc gcgggtattg gcaaatcggg tgcacagccc 600

gctaaaaaga gactcaattt cggtcagact ggcgacacag agtcagtccc agaccctcaa 660

ccaatcggag aacctcccgc agccccctca ggtgtgggat ctcttacaat ggcttcaggt 720

ggtggcgcac cagtggcaga caataacgaa ggtgccgatg gagtgggtag ttcctcggga 780

aattggcatt gcgattccca atggctgggg gacagagtca tcaccaccag cacccgaacc 840

tgggccctgc ccacctacaa caatcacctc tacaagcaaa tctccaacag cacatctgga 900

ggatcttcaa atgacaacgc ctacttcggc tacagcaccc cctgggggta ttttgacttc 960

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 1020

ggattccggc ctaagcgact caacttcaag ctcttcaaca ttcaggtcaa agaggttacg 1080

gacaacaatg gagtcaagac catcgccaat aaccttacca gcacggtcca ggtcttcacg 1140

gactcagact atcagctccc gtacgtgctc gggtcggctc acgagggctg cctcccgccg 1200

ttcccagcgg acgttttcat gattcctcag tacgggtatc tgacgcttaa tgatggaagc 1260

caggccgtgg gtcgttcgtc cttttactgc ctggaatatt tcccgtcgca aatgctaaga 1320

acgggtaaca acttccagtt caactacgag tttgagaacg tacctttcca tagcagctac 1380

gctcacagcc aaagcctgga ccgactaatg aatccactca tcgaccaata cttgtactat 1440

ctctcaaaga ctattaacga ttctggacag aatcaacaaa cgctaaaatt cagtgtggcc 1500

ggacccagca acatggctgt ccagggaaga aactacatac ctggacccag ctaccgacaa 1560

caacgtgtct caaccactgt gactcaaaac aacaacagcg aatttgcttg gcctggagct 1620

tcttcttggg ctctcaatgg acgtaatagc ttgatgaatc ctggacctgc tatggccagc 1680

cacaaagaag gagaggaccg tttctttcct ttgtctggat ctttaatttt tggcaaacaa 1740

ggaactggaa gagacaacgt ggatgcggac gaagtcatga taaccaacga agaagaaatt 1800

aaaactacta acccggtagc aacggagtcc tatggacaag tggccataaa ccaccagagt 1860

gcccaagcac aggcgcagac cggctgggtt caaaaccaag gaatacttcc gggtatggtt 1920

tggcaggaca gagatgtgta cctgcaagga cccatttggg ccaaaattcc tcacacggac 1980

ggcaactttc acccttctcc gctgatggga gggtttggaa tgaagcaccc gcctcctcag 2040

atcctcatca aaaacacacc tgtacctgcg gatcctccaa cggccttcaa caaggacaag 2100

ctgaactctt tcatcaccca gtattctact ggccaagtca gcgtggagat cgagtgggag 2160

ctgcagaagg aaaacagcaa gcgctggaac ccggagatcc agtacacttc caactattac 2220

aagtctaata atgttgaatt tgctgttaat actgaaggtg tatatagtga accccgcccc 2280

attggcacca gatacctgac tcgtaatctg taa 2313

<210> 1511
<211> 2283
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1511
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gatgaccttc 420

ttctacggcg gcagcagggg caagaggaac aacttcaaga ccgaggagta cggcggcggc 480

ggcagcgctc ctggaaagaa gaggcctgta gagcagtctc ctcaggaacc ggactcctcc 540

gcgggtattg gcaaatcggg tgcacagccc gctaaaaaga gactcaattt cggtcagact 600

ggcgacacag agtcagtccc agaccctcaa ccaatcggag aacctcccgc agccccctca 660

ggtgtgggat ctcttacaat ggcttcaggt ggtggcgcac cagtggcaga caataacgaa 720

ggtgccgatg gagtgggtag ttcctcggga aattggcatt gcgattccca atggctgggg 780

gacagagtca tcaccaccag cacccgaacc tgggccctgc ccacctacaa caatcacctc 840

tacaagcaaa tctccaacag cacatctgga ggatcttcaa atgacaacgc ctacttcggc 900

tacagcaccc cctgggggta ttttgacttc aacagattcc actgccactt ctcaccacgt 960

gactggcagc gactcatcaa caacaactgg ggattccggc ctaagcgact caacttcaag 1020

ctcttcaaca ttcaggtcaa agaggttacg gacaacaatg gagtcaagac catcgccaat 1080

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tacgggtatc tgacgcttaa tgatggaagc caggccgtgg gtcgttcgtc cttttactgc 1260

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tttgagaacg tacctttcca tagcagctac gctcacagcc aaagcctgga ccgactaatg 1380

aatccactca tcgaccaata cttgtactat ctctcaaaga ctattaacga ttctggacag 1440

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aactacatac ctggacccag ctaccgacaa caacgtgtct caaccactgt gactcaaaac 1560

aacaacagcg aatttgcttg gcctggagct tcttcttggg ctctcaatgg acgtaatagc 1620

ttgatgaatc ctggacctgc tatggccagc cacaaagaag gagaggaccg tttctttcct 1680

ttgtctggat ctttaatttt tggcaaacaa ggaactggaa gagacaacgt ggatgcggac 1740

gaagtcatga taaccaacga agaagaaatt aaaactacta acccggtagc aacggagtcc 1800

tatggacaag tggccataaa ccaccagagt gcccaagcac aggcgcagac cggctgggtt 1860

caaaaccaag gaatacttcc gggtatggtt tggcaggaca gagatgtgta cctgcaagga 1920

cccatttggg ccaaaattcc tcacacggac ggcaactttc acccttctcc gctgatggga 1980

gggtttggaa tgaagcaccc gcctcctcag atcctcatca aaaacacacc tgtacctgcg 2040

gatcctccaa cggccttcaa caaggacaag ctgaactctt tcatcaccca gtattctact 2100

ggccaagtca gcgtggagat cgagtgggag ctgcagaagg aaaacagcaa gcgctggaac 2160

ccggagatcc agtacacttc caactattac aagtctaata atgttgaatt tgctgttaat 2220

actgaaggtg tatatagtga accccgcccc attggcacca gatacctgac tcgtaatctg 2280

taa 2283

<210> 1512
<211> 2283
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1512
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gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gatggcagct 420

gcggccgccg cggctgcagc ggctgcagcc gccgcagctg cggctgcagc gggcggcggc 480

ggcagcgctc ctggaaagaa gaggcctgta gagcagtctc ctcaggaacc ggactcctcc 540

gcgggtattg gcaaatcggg tgcacagccc gctaaaaaga gactcaattt cggtcagact 600

ggcgacacag agtcagtccc agaccctcaa ccaatcggag aacctcccgc agccccctca 660

ggtgtgggat ctcttacaat ggcttcaggt ggtggcgcac cagtggcaga caataacgaa 720

ggtgccgatg gagtgggtag ttcctcggga aattggcatt gcgattccca atggctgggg 780

gacagagtca tcaccaccag cacccgaacc tgggccctgc ccacctacaa caatcacctc 840

tacaagcaaa tctccaacag cacatctgga ggatcttcaa atgacaacgc ctacttcggc 900

tacagcaccc cctgggggta ttttgacttc aacagattcc actgccactt ctcaccacgt 960

gactggcagc gactcatcaa caacaactgg ggattccggc ctaagcgact caacttcaag 1020

ctcttcaaca ttcaggtcaa agaggttacg gacaacaatg gagtcaagac catcgccaat 1080

aaccttacca gcacggtcca ggtcttcacg gactcagact atcagctccc gtacgtgctc 1140

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tacgggtatc tgacgcttaa tgatggaagc caggccgtgg gtcgttcgtc cttttactgc 1260

ctggaatatt tcccgtcgca aatgctaaga acgggtaaca acttccagtt caactacgag 1320

tttgagaacg tacctttcca tagcagctac gctcacagcc aaagcctgga ccgactaatg 1380

aatccactca tcgaccaata cttgtactat ctctcaaaga ctattaacga ttctggacag 1440

aatcaacaaa cgctaaaatt cagtgtggcc ggacccagca acatggctgt ccagggaaga 1500

aactacatac ctggacccag ctaccgacaa caacgtgtct caaccactgt gactcaaaac 1560

aacaacagcg aatttgcttg gcctggagct tcttcttggg ctctcaatgg acgtaatagc 1620

ttgatgaatc ctggacctgc tatggccagc cacaaagaag gagaggaccg tttctttcct 1680

ttgtctggat ctttaatttt tggcaaacaa ggaactggaa gagacaacgt ggatgcggac 1740

gaagtcatga taaccaacga agaagaaatt aaaactacta acccggtagc aacggagtcc 1800

tatggacaag tggccataaa ccaccagagt gcccaagcac aggcgcagac cggctgggtt 1860

caaaaccaag gaatacttcc gggtatggtt tggcaggaca gagatgtgta cctgcaagga 1920

cccatttggg ccaaaattcc tcacacggac ggcaactttc acccttctcc gctgatggga 1980

gggtttggaa tgaagcaccc gcctcctcag atcctcatca aaaacacacc tgtacctgcg 2040

gatcctccaa cggccttcaa caaggacaag ctgaactctt tcatcaccca gtattctact 2100

ggccaagtca gcgtggagat cgagtgggag ctgcagaagg aaaacagcaa gcgctggaac 2160

ccggagatcc agtacacttc caactattac aagtctaata atgttgaatt tgctgttaat 2220

actgaaggtg tatatagtga accccgcccc attggcacca gatacctgac tcgtaatctg 2280

taa 2283

<210> 1513
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1513

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Met Glu Val Gln Leu Gln Ala Ser Gly Gly Gly Leu Val Gln Ala Gly
1               5                  10                  15


Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Ile Thr His
            20                  25                  30


Tyr Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe
        35                  40                  45


Val Ser Arg Ile Thr Trp Gly Gly Asp Asn Thr Phe Tyr Ser Asn Ser
    50                  55                  60


Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val
65                  70                  75                  80


Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Asp Tyr Tyr
                85                  90                  95


Cys Ala Ala Gly Ser Thr Ser Thr Ala Thr Pro Leu Arg Val Asp Tyr
            100                 105                 110


Trp Gly Lys Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125


Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp
    130                 135                 140


Ser Ser Ser Gly Ile Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg
145                 150                 155                 160


Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln
                165                 170                 175


Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr
            180                 185                 190
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Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro
225                 230                 235                 240

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly
                245                 250                 255

Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn
    290                 295                 300

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Glu Gly
305                 310                 315                 320

Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
                325                 330                 335

Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly
            340                 345                 350

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe
    370                 375                 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn
385                 390                 395                 400

Phe Gln Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr
                405                 410                 415
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Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln
            420                 425                 430

Tyr Leu Tyr Tyr Leu Val Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr
        435                 440                 445

Gln Thr Leu Ala Phe Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln
    450                 455                 460

Ala Arg Asn Trp Val Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser
465                 470                 475                 480

Thr Thr Thr Asn Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala
                485                 490                 495

Ala Lys Phe Lys Leu Asn Gly Arg Asp Ser Leu Met Asn Pro Gly Val
            500                 505                 510

Ala Met Ala Ser His Lys Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser
        515                 520                 525

Gly Val Leu Ile Phe Gly Lys Gln Gly Ala Gly Asn Asp Gly Val Asp
    530                 535                 540

Tyr Ser Gln Val Leu Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn
545                 550                 555                 560

Pro Val Ala Thr Glu Glu Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala
                565                 570                 575

Ala Asn Thr Gln Ala Gln Thr Gly Leu Val His Asn Gln Gly Val Ile
            580                 585                 590

Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile
        595                 600                 605

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu
    610                 615                 620
```

```
Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys
625                 630                 635                 640


Asn Thr Pro Val Pro Ala Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys
                645                 650                 655


Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu
            660                 665                 670


Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
        675                 680                 685


Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala
    690                 695                 700


Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg
705                 710                 715                 720


Tyr Leu Thr Arg Asn Leu
                725
```

<210> 1514
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1514

```
Met Glu Val Gln Leu Gln Ala Ser Gly Gly Gly Leu Val Gln Ala Gly
1               5                   10                  15


Gly Ser Leu Arg Leu Ser Cys Ser Ala Ser Val Arg Thr Phe Ser Ile
            20                  25                  30


Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe
        35                  40                  45


Val Ala Gly Ile Asn Arg Ser Gly Asp Val Thr Lys Tyr Ala Asp Phe
    50                  55                  60
```

```
Val Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Met Val
65                  70                  75                  80

Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Leu Tyr Tyr
                85                  90                  95

Cys Ala Ala Thr Trp Ala Tyr Asp Thr Val Gly Ala Leu Thr Ser Gly
            100                 105                 110

Tyr Asn Phe Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly
        115                 120                 125

Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln
    130                 135                 140

Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly Gln Gln Pro Ala
145                 150                 155                 160

Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro
                165                 170                 175

Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser Gly Leu Gly
            180                 185                 190

Pro Asn Thr Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn
        195                 200                 205

Glu Gly Ala Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp
    210                 215                 220

Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp
225                 230                 235                 240

Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Gly
                245                 250                 255

Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly Tyr Ser Thr
            260                 265                 270

Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro
        275                 280                 285
```

```
Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys
    290                 295                 300

Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr
305                 310                 315                 320

Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln
                325                 330                 335

Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala
            340                 345                 350

His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro
        355                 360                 365

Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Leu Gly Arg
    370                 375                 380

Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His
                405                 410                 415

Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Tyr Tyr Leu Val Arg Thr Gln Thr Thr Gly Thr
        435                 440                 445

Gly Gly Thr Gln Thr Leu Ala Phe Ser Gln Ala Gly Pro Ser Ser Met
    450                 455                 460

Ala Asn Gln Ala Arg Asn Trp Val Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Val Ser Thr Thr Thr Asn Gln Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495
```

```
Thr Gly Ala Ala Lys Phe Lys Leu Asn Gly Arg Asp Ser Leu Met Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Ser His Lys Asp Asp Asp Asp Arg Phe Phe
        515                 520                 525

Pro Ser Ser Gly Val Leu Ile Phe Gly Lys Gln Gly Ala Gly Asn Asp
    530                 535                 540

Gly Val Asp Tyr Ser Gln Val Leu Ile Thr Asp Glu Glu Glu Ile Lys
545                 550                 555                 560

Ala Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Ala Val Ala Ile Asn
                565                 570                 575

Asn Gln Ala Ala Asn Thr Gln Ala Gln Thr Gly Leu Val His Asn Gln
            580                 585                 590

Gly Val Ile Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625                 630                 635                 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Leu Thr Phe Asn
                645                 650                 655

Gln Ala Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr Asn Val
    690                 695                 700

Asp Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile
705                 710                 715                 720
```

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 1515
<211> 651
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1515

Met Pro Ser Ser Val Ile Asp Ala Leu Gln Tyr Lys Leu Glu Gly Thr
1 5 10 15

Thr Arg Leu Thr Arg Lys Arg Gly Leu Lys Leu Ala Thr Ala Leu Ser
20 25 30

Leu Ser Asn Lys Phe Val Glu Gly Ser Pro Ser Gly Gly Gly Gly Ser
35 40 45

Gly Gly Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser
50 55 60

Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly Gln Gln
65 70 75 80

Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser
85 90 95

Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser Gly
100 105 110

Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp
115 120 125

Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His
130 135 140

Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
145 150 155 160

```
Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
                165                 170                 175

Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly Tyr
            180                 185                 190

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        195                 200                 205

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    210                 215                 220

Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
225                 230                 235                 240

Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr
                245                 250                 255

Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            260                 265                 270

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        275                 280                 285

Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Leu
    290                 295                 300

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
305                 310                 315                 320

Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp Val Pro
                325                 330                 335

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            340                 345                 350

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val Arg Thr Gln Thr Thr
        355                 360                 365
```

```
Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser Gln Ala Gly Pro Ser
    370                 375                 380

Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro Gly Pro Cys Tyr Arg
385                 390                 395                 400

Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn Asn Asn Ser Asn Phe
                405                 410                 415

Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn Gly Arg Asp Ser Leu
            420                 425                 430

Met Asn Pro Gly Val Ala Met Ala Ser His Lys Asp Asp Asp Asp Arg
        435                 440                 445

Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly Lys Gln Gly Ala Gly
    450                 455                 460

Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile Thr Asp Glu Glu Glu
465                 470                 475                 480

Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Ala Val Ala
                485                 490                 495

Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln Thr Gly Leu Val His
            500                 505                 510

Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
        515                 520                 525

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    530                 535                 540

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
545                 550                 555                 560

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Leu Thr
                565                 570                 575

Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            580                 585                 590
```

```
Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        595                 600                 605


Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr
    610                 615                 620


Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg
625                 630                 635                 640


Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                645                 650


<210>  1516
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1516

Met Tyr Thr Ile Trp Met Pro Glu Asn Pro Arg Pro Gly Thr Pro Cys
1               5                   10                  15


Asp Ile Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Asn Gly Gly Gly
            20                  25                  30


Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro Val
        35                  40                  45


Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Thr
    50                  55                  60


Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp
65                  70                  75                  80


Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala
                85                  90                  95


Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly Ala Pro
            100                 105                 110
```

```
Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser Gly
        115                 120                 125

Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr
    130                 135                 140

Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys
145                 150                 155                 160

Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr
                165                 170                 175

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
            180                 185                 190

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
        195                 200                 205

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
    210                 215                 220

Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu
225                 230                 235                 240

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
                245                 250                 255

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
            260                 265                 270

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
        275                 280                 285

Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
    290                 295                 300

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
305                 310                 315                 320
```

```
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
                325                 330                 335

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val Arg Thr
            340                 345                 350

Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser Gln Ala
        355                 360                 365

Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro Gly Pro
    370                 375                 380

Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn Asn Asn
385                 390                 395                 400

Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn Gly Arg
                405                 410                 415

Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys Asp Asp
            420                 425                 430

Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly Lys Gln
        435                 440                 445

Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile Thr Asp
    450                 455                 460

Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly
465                 470                 475                 480

Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln Thr Gly
                485                 490                 495

Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln Asn Arg
            500                 505                 510

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
        515                 520                 525

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
    530                 535                 540
```

```
Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro
545                 550                 555                 560


Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr Gln Tyr
                565                 570                 575


Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
            580                 585                 590


Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr
        595                 600                 605


Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr Ser
    610                 615                 620


Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
625                 630                 635


<210>  1517
<211>  628
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1517

Met Thr Phe Phe Tyr Gly Gly Ser Arg Gly Lys Arg Asn Asn Phe Lys
1               5                   10                  15


Thr Glu Glu Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro
            20                  25                  30


Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser
        35                  40                  45


Ser Gly Ile Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn
    50                  55                  60


Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu
65                  70                  75                  80
```

```
Gly Glu Pro Pro Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala
                85                  90                  95

Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly
            100                 105                 110

Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly
        115                 120                 125

Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr
    130                 135                 140

Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser
145                 150                 155                 160

Thr Asn Asp Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe
                165                 170                 175

Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg
            180                 185                 190

Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys
        195                 200                 205

Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys
    210                 215                 220

Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser
225                 230                 235                 240

Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu
                245                 250                 255

Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu
            260                 265                 270

Thr Leu Asn Asn Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys
        275                 280                 285
```

```
Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln
    290                 295                 300

Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His
305                 310                 315                 320

Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu
                325                 330                 335

Tyr Tyr Leu Val Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr
            340                 345                 350

Leu Ala Phe Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg
        355                 360                 365

Asn Trp Val Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr
    370                 375                 380

Thr Asn Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys
385                 390                 395                 400

Phe Lys Leu Asn Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met
                405                 410                 415

Ala Ser His Lys Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val
            420                 425                 430

Leu Ile Phe Gly Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser
        435                 440                 445

Gln Val Leu Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val
    450                 455                 460

Ala Thr Glu Glu Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn
465                 470                 475                 480

Thr Gln Ala Gln Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly
                485                 490                 495

Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
            500                 505                 510
```

Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly
515 520 525

Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr
530 535 540

Pro Val Pro Ala Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn
545 550 555 560

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu
565 570 575

Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
580 585 590

Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn
595 600 605

Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu
610 615 620

Thr Arg Asn Leu
625

<210> 1518
<211> 621
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1518

Met Asn Asn Gln Lys Ile Val Asn Leu Lys Glu Lys Val Ala Gln Leu
1 5 10 15

Glu Ala Gly Gly Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro Val Glu
20 25 30

Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys Ser Gly
35 40 45

```
Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Thr
    50                  55                  60

Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Ala Pro
65                  70                  75                  80

Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly Ala Pro Val
                85                  90                  95

Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn
            100                 105                 110

Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr Thr Ser
        115                 120                 125

Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln
    130                 135                 140

Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe
145                 150                 155                 160

Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
                165                 170                 175

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
            180                 185                 190

Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys
        195                 200                 205

Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu Thr
    210                 215                 220

Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr Val
225                 230                 235                 240

Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
                245                 250                 255
```

```
Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln
            260                 265                 270

Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
        275                 280                 285

Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Asn Tyr Glu Phe Glu Asn
    290                 295                 300

Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
305                 310                 315                 320

Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile
                325                 330                 335

Asn Asp Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala Gly
            340                 345                 350

Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser
        355                 360                 365

Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn Ser
    370                 375                 380

Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn
385                 390                 395                 400

Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly Glu
                405                 410                 415

Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly
            420                 425                 430

Thr Gly Arg Asp Asn Val Asp Ala Asp Glu Val Met Ile Thr Asn Glu
        435                 440                 445

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln
    450                 455                 460

Val Ala Ile Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp
465                 470                 475                 480
```

```
Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg Asp
                485                 490                 495


Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
            500                 505                 510


Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys His Pro
        515                 520                 525


Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
    530                 535                 540


Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser
545                 550                 555                 560


Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
                565                 570                 575


Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
            580                 585                 590


Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu
        595                 600                 605


Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
    610                 615                 620


<210>  1519
<211>  633
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1519

Met Tyr Thr Ile Trp Met Pro Glu Asn Pro Arg Pro Gly Thr Pro Cys
1               5                   10                  15


Asp Ile Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Asn Gly Gly Gly
            20                  25                  30
```

```
Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln
        35                  40                  45

Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys Ser Gly Ala Gln Pro Ala
    50                  55                  60

Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Thr Glu Ser Val Pro
65                  70                  75                  80

Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Ala Pro Ser Gly Val Gly
                85                  90                  95

Ser Leu Thr Met Ala Ser Gly Gly Gly Ala Pro Val Ala Asp Asn Asn
            100                 105                 110

Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp
        115                 120                 125

Ser Gln Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp
    130                 135                 140

Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser
145                 150                 155                 160

Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr
                165                 170                 175

Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro
            180                 185                 190

Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys
        195                 200                 205

Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp
    210                 215                 220

Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln
225                 230                 235                 240
```

```
Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala
                245                 250                 255

His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro
            260                 265                 270

Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg
        275                 280                 285

Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
    290                 295                 300

Gly Asn Asn Phe Gln Phe Asn Tyr Glu Phe Glu Asn Val Pro Phe His
305                 310                 315                 320

Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
                325                 330                 335

Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Asp Ser Gly
            340                 345                 350

Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met
        355                 360                 365

Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln
    370                 375                 380

Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp
385                 390                 395                 400

Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn
                405                 410                 415

Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe
            420                 425                 430

Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp
        435                 440                 445

Asn Val Asp Ala Asp Glu Val Met Ile Thr Asn Glu Glu Glu Ile Lys
    450                 455                 460
```

```
Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Ile Asn
465                 470                 475                 480

His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln
                485                 490                 495

Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln
            500                 505                 510

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
        515                 520                 525

Ser Pro Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile
    530                 535                 540

Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn
545                 550                 555                 560

Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
                565                 570                 575

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
            580                 585                 590

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val
        595                 600                 605

Glu Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile
    610                 615                 620

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
625                 630
```

<210> 1520
<211> 623
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1520

```
Met Thr Phe Phe Tyr Gly Gly Ser Arg Gly Lys Arg Asn Asn Phe Lys
1               5                  10                  15

Thr Glu Glu Tyr Gly Gly Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro
            20                  25                  30

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys
        35                  40                  45

Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly
    50                  55                  60

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala
65                  70                  75                  80

Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly Ala
                85                  90                  95

Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser
            100                 105                 110

Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr
        115                 120                 125

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
    130                 135                 140

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala
145                 150                 155                 160

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
                165                 170                 175

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
            180                 185                 190

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
        195                 200                 205
```

```
Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
    210                 215                 220

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
225                 230                 235                 240

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
                245                 250                 255

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly
            260                 265                 270

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
        275                 280                 285

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Asn Tyr Glu Phe
    290                 295                 300

Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
305                 310                 315                 320

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
                325                 330                 335

Thr Ile Asn Asp Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val
            340                 345                 350

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly
        355                 360                 365

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn
    370                 375                 380

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly
385                 390                 395                 400

Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu
                405                 410                 415

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys
            420                 425                 430
```

```
Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Glu Val Met Ile Thr
        435                 440                 445

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr
    450                 455                 460

Gly Gln Val Ala Ile Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr
465                 470                 475                 480

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
                485                 490                 495

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
            500                 505                 510

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys
        515                 520                 525

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
    530                 535                 540

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln
545                 550                 555                 560

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
                565                 570                 575

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
            580                 585                 590

Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr
        595                 600                 605

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
    610                 615                 620
```

<210> 1521
<211> 623
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1521

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Met Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
1               5                  10                  15


Ala Ala Ala Ala Gly Gly Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro
            20                  25                  30


Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys
        35                  40                  45


Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly
    50                  55                  60


Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala
65                  70                  75                  80


Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly Ala
                85                  90                  95


Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser
            100                 105                 110


Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr
        115                 120                 125


Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
    130                 135                 140


Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala
145                 150                 155                 160


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
                165                 170                 175


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
            180                 185                 190
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
        195                 200                 205

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
    210                 215                 220

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
225                 230                 235                 240

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
                245                 250                 255

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly
            260                 265                 270

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
        275                 280                 285

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Asn Tyr Glu Phe
    290                 295                 300

Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
305                 310                 315                 320

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
                325                 330                 335

Thr Ile Asn Asp Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val
            340                 345                 350

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly
        355                 360                 365

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn
    370                 375                 380

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly
385                 390                 395                 400

Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu
                405                 410                 415
```

```
Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys
            420                 425                 430

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Glu Val Met Ile Thr
        435                 440                 445

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr
    450                 455                 460

Gly Gln Val Ala Ile Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr
465                 470                 475                 480

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
                485                 490                 495

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
            500                 505                 510

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys
        515                 520                 525

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
    530                 535                 540

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln
545                 550                 555                 560

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
                565                 570                 575

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
            580                 585                 590

Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr
        595                 600                 605

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
    610                 615                 620
```

<210> 1522
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1522
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgtcgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaattttg gccagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggca cctcgggagg aagcaccaac gacaacacct attttggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcca aaaagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa ccttaccagc 1020

acgattcagg tatttacgga ctcggaatac cagctgccat acgtcctcgg ctccgcgcac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctt 1140

acactgaaca atggaagtca agccgtaggc cgttcctcct tctactgcct ggaatatttt 1200

ccttctcaaa tgctgagaac gggcaacaac tttgagttca gctaccagtt tgaggacgtg 1260

ccttttcaca gcagctacgc gcacagccaa agcctggacc ggctgatgaa ccccctcatc 1320

gaccagtacc tgtactacct gtctcggact cagtccacgg gaggtaccgc aagaactcag 1380

cagttgctat tttctcaggc cgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactctgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccatctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctacagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccgccc cattggcacc cgttacctca cccgtaatct gtaa 2214

<210> 1523
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1523
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg acggcgctaa gacggctcct 420

ggaaagaaga gaccagtaga gcagtcaccc caagaaccag actcctcctc gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaattttg gccagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaggac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa tcgagtggga gctgcagaaa gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca aatgtggact ttgctgtcaa cacggagggg 2160

gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaa 2214

<210> 1524
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (715)..(715)
<223> n is a, c, g, or t

<400> 1524
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagagg ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagantcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atattttcca 1200

tctcaaatgc tgcgaactgg aaacaatttt gaattcagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcaca cagccagagc ttggaccgac tgatgaatcc tctcatcgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac gaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

accttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct acagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca attactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccgccccat tggcacgcgt ttcctcaccc gtaatctgta a 2211

<210> 1525
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1525
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagagg ctcaattttg gccagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgtactagg atccgctcac 1080

cagggatgtc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatatttt 1200

ccatctcaga tgctgagaac gggcaataac tttaccttca gctacacctt cgaggacgtg 1260

cctttccaca gcagctatgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctaatggg aggatttgga 1920

ctgaagcacc cacctcctca gatcctgatc aagaacacgc cggtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgtactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

caatacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccgccc cattggcacc cgttacctca cccgtaatct gtaa 2214

<210> 1526
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1526

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Val Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Arg Thr Gln Gln Leu Leu Phe
    450                 455                 460

Ser Gln Ala Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Ser Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540
```

```
Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560


Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590


Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu
```

<210> 1527
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1527

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Asp Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605
```

```
Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 1528
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (239)..(239)
<223> Xaa can be any naturally occurring amino acid

<400> 1528

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Xaa Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445
```

```
Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Thr Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Phe Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1529
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1529

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
               325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
               405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
               485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525
```

```
Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Tyr Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 1530
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1530
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt cgacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag gttccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaaa agactcaact tcaagctgtt caacatccag 960

gtcaaggaag tcacgacgaa cgaaggcacc aagaccatcg ccaataatct caccagcacc 1020

gtgcaggtct ttacggactc ggagtaccag ttaccgtacg tgctaggatc cgctcaccag 1080

ggatgtctgc ctccgttccc ggcggacgtc ttcatggttc ctcagtacgg ctatttaact 1140

ttaaacaatg gaagccaagc cctgggacgt tcctccttct actgtctgga gtatttccca 1200

tcgcagatgc tgagaacggg caacaacttt acctttagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggacaggc tgatgaatcc cctcatcgac 1320

cagtacctgt actacctggt cagaacgcaa acgactggaa ctggagggac gcagactctg 1380

gcattcagcc aagcgggtcc tagctcaatg gccaaccagg ctagaaattg ggtgcccgga 1440

ccttgctacc ggcagcagcg cgtctccacg acaaccaacc agaacaacaa cagcaacttt 1500

gcctggacgg gagctgccaa gtttaagctg aacggccgag actctctaat gaatccgggc 1560

gtggcaatgg cttcccacaa ggatgacgac gaccgcttct tcccttcgag cggggtcctg 1620

atttttggca agcaaggagc cgggaacgat ggagtggatt acagccaagt gctgattaca 1680

gatgaggaag aaatcaaggc taccaacccc gtggccacag aagaatatgg agcagtggcc 1740

atcaacaacc aggccgccaa tacgcaggcg cagaccggac tcgtgcacaa ccaggggtg 1800

attcccggca tggtgtggca gaatagagac gtgtacctgc agggtcccat ctgggccaaa 1860

attcctcaca cggacggcaa ctttcacccg tctcccctga tgggcggctt tggactgaag 1920

cacccgcctc ctcaaattct catcaagaac acaccggttc cagcggaccc gccgcttacc 1980

ttcaaccagg ccaagctgaa ctctttcatc acgcagtaca gcaccggaca ggtcagcgtg 2040

gaaatcgagt gggagctgca gaaagaaaac agcaaacgct ggaatccaga gattcaatac 2100

acttccaact actacaaatc tacaaatgtg gactttgctg tcaacacgga gggggtttat 2160

agcgagcctc gccccattgg cacccgttac ctcacccgca acctgtaa 2208

<210> 1531
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (337)..(337)
<223> n is a, c, g, or t

<400> 1531
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcgaccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcnacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccagtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccatttct caccacgtga ctggcagcga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacgacca tcgctaataa ccttaccagc 1020

acggttcaag tcttctcgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cggctattta 1140

actttaaaca atggaagcca agccctggga cgttcctcct tctactgtct ggagtatttc 1200

ccatcgcaga tgctgagaac cggcaacaac tttcagttca gctacacctt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agcctggaca ggctgatgaa tcccctcatc 1320

gaccagtacc tgtactacct ggtcagaacg caaacgactg gaactggagg gacgcagact 1380

ctggcattca gccaagcggg tcctagctca atggccaacc aggctagaaa ttgggtgccc 1440

ggaccttgct accggcagca gcgcgtctcc acgacaacca accagaacaa caacagcaac 1500

tttgcctgga cgggagctgc caagtttaag ctgaacggcc gagactctct aatgaatccg 1560

ggcgtggcaa tggcttccca caaggatgac gacgaccgct tcttcccttc gagcggggtc 1620

ctgatttttg gcaagcaagg agccgggaac gatggagtgg attacagcca agtgctgatt 1680

acagatgagg aagaaatcaa ggctaccaac cccgtagcca cagaagaata tggagcagtg 1740

gccatcaaca accaggccgc caatacgcag gcgcagaccg gactcgtgca caaccagggg 1800

gtgattcccg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1532
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (335)..(335)
<223> n is a, c, g, or t

<400> 1532
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agccccgaag cccaaagcca accagcaaaa gcaggacgac 120

ggccggggtc tggtgcttcc tggctacaag tacctcggac ccttcaacgg actcgacaag 180

ggggagcccg tcaacgcggc ggacgcagcg gccctcgagc acgacaaggc ctacgaccag 240

cagctcaaag cgggtgacaa tccgtacctg cggtataacc acgccgacgc cgagtttcag 300

gagcgtctgc aagaagatac gtctttgggg ggcancctcg ggcgagcagt cttccaggcc 360

aagaagcggg ttctcgaacc tctcggtctg gttgaggaag gcgctaagac ggctcctgga 420

aagaaacgtc cggtagagcc atcaccccag cgttctccag actcctctac gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaattttg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttaa accaggccaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa cccagagatt 2100

cagtacactt caaactacta caaatctaca aatgtggact ttgctgtcaa tacagaggga 2160

acttatagtg aaccccgccc cattggcacc agatttctga ctcgtaatct gtaa 2214

<210> 1533
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (338)..(338)
<223> n is a, c, g, or t

<400> 1533
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gccccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcg aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcancc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccagtaga gcagtcaccc caagaaccag actcctcctc gggcatcggc 480

aggaaaggcc aacagcccgc cagaaaaaga ctcaattttg gccagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg cttcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcact aagaccatcg ccaataacct taccagcacg 1020

attcaggtat ttacggactc ggaataccag ctgccgtacg tcctcggctc cgcgcaccag 1080

ggctgcctgc ctccgttccc ggcggacgtc ttcatgattc cccagtacgg ctaccttaca 1140

ctgaacaatg gaagtcaagc cgtaggccgt tcctccttct actgcctgga atattttcca 1200

tctcaaatgc tgcgaactgg caacaacttc cagtttacct acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcag tccacaggag gaactcaagg tacccagcaa 1380

ttgttatttt ctcaagctgg gcctgcaaac atgtcggctc aggctaagaa ctggctacct 1440

ggaccttgct accggcagca gcgagtctct acgacactgt cgcaaaacaa caacagcaac 1500

tttgcttgga ctggtgccac caaatatcac ctgaacggaa gagactcttt ggtaaatccc 1560

ggtgtcgcca tggcaaccca caaggacgac gaggaacgct tcttcccgtc gagtggagtc 1620

ctgatgtttg gaaaacaggg tgctggaaga gacaatgtgg actacagcag cgttatgcta 1680

accagcgaag aagaaattaa aaccactaac cctgtagcca cagaacaata cggtgtggtg 1740

gttgataact tgcagcaaac caatacgggg cctattgtgg gaaatgtcaa cagccaagga 1800

gccttacctg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 1534
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1534

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

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Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
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Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val Arg
        435                 440                 445

Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro Gly
465                 470                 475                 480
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Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn Asn
                485                 490                 495

Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu Tyr
                565                 570                 575

Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln Thr
            580                 585                 590

Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
                645                 650                 655

Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
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Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1535
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (113)..(113)
<223> Xaa can be any naturally occurring amino acid

<400> 1535

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Thr Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Xaa Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335
```

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Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540
```

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Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1536
<211> 737
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (112)..(112)
<223> Xaa can be any naturally occurring amino acid

<400> 1536

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1   5   10   15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20   25   30

Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro Val
    50   55   60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65   70   75   80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala Asp
                85   90   95

Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly Xaa
            100   105   110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115   120   125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro
    130   135   140

Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile Gly
145   150   155   160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605
```

```
Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Leu Asn Gln Ala Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Phe Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 1537
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (113)..(113)
<223> Xaa can be any naturally occurring amino acid

<400> 1537

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15
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```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Xaa Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Arg Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445
```

```
Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Val Val Val Asp Asn Leu Gln Gln Thr Asn Thr Gly Pro Ile
            580                 585                 590

Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1538
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1538

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gagtggtggg ccctgaagcc cggcgccccc cagcccaagg ccaaccagca gcaccaggac      120

aacgcccgcg gcctggtgct gcccggctac aagtacctgg gccccggcaa cggcctggac      180

aagggcgagc ccgtgaacgc cgccgacgcc gccgccctgg agcacgacaa ggcctacgac      240

cagcagctga aggccggcga caacccctac ctgaagtaca accacgccga cgccgagttc      300

caggagcgcc tgaaggagga caccagcttc ggcggcaacc tgggccgcgc cgtgttccag      360

gccaagaagc gcctgctgga gcccctgggc ctggtggagg aggccgccaa gaccgccccc      420

ggcaagaagc gccccgtgga gcagagcccc caggagcccg acagcagcgc cggcatcggc      480

aagagcggcg cccagcccgc caagaagcgc ctgaacttcg gccagaccgg cgacaccgag      540

agcgtgcccg acccccagcc catcggcgag ccccccgccg cccccagcgg cgtgggcagc      600

ctgaccatgg ccagcggcgg cggcgccccc gtggccgaca acaacgaggg cgccgacggc      660

gtgggcagca gcagcggcaa ctggcactgc gacagccagt ggctgggcga ccgcgtgatc      720

accaccagca cccgcacctg ggccctgccc acctacaaca accacctgta caagcagatc      780
```

agcaacagca ccagcggcgg cagcagcaac gacaacgcct acttcggcta cagcaccccc 840

tggggctact tcgacttcaa ccgcttccac tgccacttca gcccccgcga ctggcagcgc 900

ctgatcaaca acaactgggg cttccgcccc aagcgcctga acttcaagct gttcaacatc 960

caggtgaagg aggtgaccga caacaacggc gtgaagacca tcgccaacaa cctgaccagc 1020

accgtgcagg tgttcaccga cagcgactac cagctgccct acgtgctggg cagcgcccac 1080

gagggctgcc tgcccccctt ccccgccgac gtgttcatga tcccccagta cggctacctg 1140

accctgaacg acggcagcca ggccgtgggc cgcagcagct tctactgcct ggagtacttc 1200

cccagccaga tgctgcgcac cggcaacaac ttccagttca gctacgagtt cgagaacgtg 1260

cccttccaca gcagctacgc ccacagccag agcctggacc gcctgatgaa ccccctgatc 1320

gaccagtacc tgtactacct gagcaagacc atcaacggca gcggccagaa ccagcagacc 1380

ctgaagttca gcgtggccgg ccccagcaac atggccgtgc agggccgcaa ctacatcccc 1440

ggccccagct accgccagca gcgcgtgagc accaccgtga cccagaacaa caacagcgag 1500

ttcgcctggc ccggcgccag cagctgggcc ctgaacggcc gcaacagcct gatgaacccc 1560

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ctgatcttcg gcaagcaggg caccggccgc gacaacgtgg acgccgacaa ggtgatgatc 1680

accaacgagg aggagatcaa gaccaccaac cccgtggcca ccgagagcta cggccaggtg 1740

gccaccaacc accagagcgc ccaggcccag gcccagaccg gctgggtgca gaaccagggc 1800

atcctgcccg gcatggtgtg gcaggaccgc gacgtgtacc tgcagggccc catctgggcc 1860

aagatccccc acaccgacgg caacttccac cccagccccc tgatgggcgg cttcggcatg 1920

aagcaccccc ccccccagat cctgatcaag aacacccccg tgcccgccga ccccccccacc 1980

gccttcaaca aggacaagct gaacagcttc atcacccagt acagcaccgg ccaggtgagc 2040

gtggagatcg agtgggagct gcagaaggag aacagcaagc gctggaaccc cgagatccag 2100

tacaccagca actactacaa gagcaacaac gtggagttcg ccgtgaacac cgagggcgtg 2160

tacagcgagc cccgccccat cggcacccgc tacctgaccc gcaacctgta a 2211

<210> 1539
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1539
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt taacattcaa 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc agagattcaa 2100

tacacttcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1540
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1540
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa agccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtttg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1541
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1541
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa tacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctccgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

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aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcctc acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagtcaa 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacca ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1542
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1542
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct taccagcacg 1020

attcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1543
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1543
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

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ttccacagca gctacgcgca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1544
<211> 2244
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (2241)..(2241)
<223> n is a, c, g, or t

<400> 1544
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc cgccgttccc agcggacgtt ttcatgattc ctcagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

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ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcaccaga tacctgactc gtaatctgta attgcttgtt 2220

aatcaataaa ccgtttaatt nttt 2244

<210> 1545
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1545
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattccc aatggctggg ggacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaatcacct ctacaagcaa 780

atctccaaca gcacatctgg aggatcttca aatgacaacg cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caaccgcttc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa actcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcctca gtacggctac 1140

ctaacgctca acaatggcag ccaggcagtg ggacggtcat ccttttactg cctggaatat 1200

ttcccatcgc agatgctgag aacgggcaac aactttacct tcagctacac ctttgaggac 1260

gttcctttcc acagcagcta cgctcacagc cagagtctgg accgtctcat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacaagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggacttaagc acccgcctcc tcagatcctc atcaaaaaca cgcctgttcc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaacccca ccccattggc acccgttacc tcacccgtcc cctgtaa 2217

<210> 1546
<211> 2214

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1546
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa agcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcaccc atgcaagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa ccttaccagc 1020

acgattcagg tctttacgga ttcggaatac cagctcccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcagta cggctaccta 1140

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cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1547
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1547
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc cgccgttccc agcggacgtt ttcatgattc ctcagtacgg gtatctgacg 1140

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1548
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1548
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac atgggccttg cccacctata acaaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccatttct caccacgtga ctggcagcga 900

ctcatcaaca acaatttggg atcccggccc aagagactca acttcaagct cttcatcatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacgacca tcgctaataa ccttaccagc 1020

acggttcaag tcttctcgga ctcggagtac cagttgccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcagta cggctaccta 1140

acgctcaaca atggcagcca ggcagtggga cggtcatcct tttactgcct ggaatatttc 1200

ccatcgcaga tgctgagaac gggcaataac tttaccttca gctacacctt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agcctggacc ggctgatgaa tcctctcatc 1320

gaccagtacc tgtattacct gaacagaact cagaatcagt ccggaagtgc ccaaaacaag 1380

gacttgctgt ttagccgggg gtctccagct ggcatgtctg ttcagcccaa aaactggcta 1440

cctggaccct gttaccggca gcagcgcgtt tctaaaacaa aaacagacaa caacaacagc 1500

aactttacct ggactggtgc ttcaaaatat aaccttaatg ggcgtgaatc tataatcaac 1560

cctggcactg ctatggcctc acacaaagac gacaaagaca agttctttcc catgagcggt 1620

gtcatgattt ttggaaagga gagcgccgga gcttcaaaca ctgcattgga caatgtcatg 1680

atcacagacg aagaggaaat caaagccact aaccccgtgg ccaccgaaag atttgggact 1740

gtggcagtca atctccagag cagcagcaca gaccctgcga ccggagatgt gcatgttatg 1800

ggagccttac ctggaatggt gtggcaagac agagacgtat acctgcaggg tcctatttgg 1860

gccaaaattc ctcacacgga tggacacttt cacccgtctc ctctcatggg cggctttgga 1920

cttaagcacc cgcctcctca gatcctcatc aaaaacacgc ctgttcctgc gaatcctccg 1980

gcagagtttt cggctacaaa gtttgcttca ttcatcaccc agtattccac aggacaagtg 2040

agcgtggaga ttgaatggga gctgcagaaa gaaaacagca aacgctggaa tcccgaagtg 2100

cagtatacat ctaactatgc aaaatctgcc aacgttgatt tcactgtgga caacaatgga 2160

ctttatactg agcctcgccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1549
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1549
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaactttg ggcagactgg cgactcagag 540

tcagtgcccg accctcaacc aatcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tcgcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggacgttcct 1260

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cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgatc cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1550
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1550
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca agagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa agcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct taccagcacg 1020

attcaggtct ttacggattc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tcgcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccga gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1551
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1551
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcacca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga caggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagaacag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtagacaa caatggactt 2160

tatactgtgc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1552
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1552
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacgc ggcggacgcg gcggccctcg aacacgacaa ggcttacgac 240

cagcagctca aggcgggtga caacccctac ctgcggtata accacgccga cgccgagttc 300

caggagcggc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caagaaccgg actcctcctc gggtattggc 480

aaaacaggtg agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctataaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt tcacggactc agagtatcag ctgccgtacg tgctcgggtc ggctcaccag 1080

ggctgcctcc ctccgttccc agcggacgtg ttcatgattc ctcagtacgg gtatctgaca 1140

ctcaacaacg gcagtcaggc agtgggacgg tcatccttct actgcctgga atattttcca 1200

tcgcagatgc tgagaaccgg caacaacttt ccgttcagtt acaccttcga ggacgtgcct 1260

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1553
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1553
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga acagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

gactgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1554
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1554
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcacca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga ctgagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatactc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1555
<211> 2211

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1555
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtactt caacgggggc cagtaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tcgcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct 1260

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ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg gacaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1556
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1556
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctgcggtata accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct taccagcacg 1020

attcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaaca 1140

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tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcact ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aggagcgttt ttttccagta ccgggatcct 1620

gattttggca aacaaaatgc tgccagagac aatgcggatt acagcgatgt catgctcacc 1680

agcgaggaag aaatcaaaac cactaaccct gtggctacag aggaatacgg tatcgtggca 1740

gataacttgc agcagcaaaa cacggctcct caaattggaa ctgtcaacag ccagggggcc 1800

ttacccggta tggtctggca gaaccgggac gtgtacctgc agggtcccat ctgggccaag 1860

attcctcaca cggacggcaa cttccacccg tctccgctga tgggcggctt tggcctgaaa 1920

catcctccgc ctcagatcct gatcaagaac acgcctgtac ctgcggatcc tccgaccacc 1980

ttcaaccagt caaagctgaa ctctttcatc acgcaataca gcaccggaca ggtcagcgtg 2040

gaaattgaat gggagctgca gaaggaaaac agcaagcgct ggaaccccga gatccagtac 2100

acctccaact actacaaatc tacaagtgtg gactttgctg ttaatacaga aggcgtgtac 2160

tctgaacccc accccattgg cacccgttac ctcacccgtc ccctgtaa 2208

<210> 1557
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1557
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccctac ctcaagtata accacgccga cgccgagttt 300

caggagcgtc ttcaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaagc gggttctcga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccttgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgta 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1558
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1558
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc cgccgttccc agcggacgtt ttcatgattc ctcagtacgg ctacctaaca 1140

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac aaaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatt 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1559
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1559
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gatgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1560
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1560
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca ccagaacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccgaccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaacgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctccgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acgctcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcact cgttacctca cccgtcccct gtaa 2214

<210> 1561
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1561
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccctac ctcaagtata accacgccga cgccgagttt 300

caggagcgtc ttcaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaagc gggttctcga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccttgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

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ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg acaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gatgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1562
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1562
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacc 1020

atccaggtct ttacggactc ggaataccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggacgttcct 1260

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cagtacctgt actacttgtc tcggactcaa acaacaggag gcaaggcaaa tacgcagact 1380

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1563
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1563
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1564
<211> 2211

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1564
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1565
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1565
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccttgccc acctataaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaacctg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1566
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1566
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc ctcgggcatc 480

ggcaagacag gccagcagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg tggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcacccgaac atgggccttg cccacctata acaaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttccccagta cggctaccta 1140

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ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc tcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

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aactttgcct ggactgctgg gaccaaatac catctgaaag gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca aacgctggaa cccagagatt 2100

caatacactt ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1567
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (676)..(676)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (697)..(697)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (715)..(715)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (748)..(748)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (750)..(750)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (757)..(757)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (763)..(763)
<223> n is a, c, g, or t

<400> 1567
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcangaaa ttggcattgc gattccncat ggctgggcga cagantcatc 720

accaccagca cccgaacctg ggccctgncn acctacnaca acnacctcta caagcaaatc 780

tccaacagca catctggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

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ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

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ggggccttac ccggtatggt ttggcagaac cgggacgtgt acctgcaggg tcctatctgg 1860

gccaagattc ctcacacgga cggaaacttt catccctcgc cgctgatggg aggctttgga 1920

ctgaaacacc cgcctcctca gatcctgatt aagaatacac ctgttcccgc ggatcctcca 1980

actaccttca gtcaagctaa gctggcgtcg ttcatcacgc aatacagcac aggacaagtg 2040

agtgtggaaa ttgaatggga gctgcagaaa gaaaacagca agcgctggaa tcccgaagtg 2100

cagtacacat ccaattatgc aaaatctgcc aacgttgatt ttactgtgga caacaatgga 2160

ctttatactg agcctcgccc cattggcacc cgttacctta cccgtcccct gtaa 2214

<210> 1568
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1568
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtgtggga 600

tctcttacaa tggcttcagg tggtggcgca ccagtggcag acaataacga aggtgccgat 660

ggagtgggta gttcctcggg aaattggcat tgcgattccc aatggctggg ggacagagtc 720

atcaccacca gcacccgaac atgggccttg cccacctata acaaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgga caatgatgga gtcaagacca tcgccaataa ccttaccagc 1020

acgattcagg tctttacgga ctcggaatac cagttgccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccgcagta cggctaccta 1140

acgctcaaca atggcagcca ggcagtggga cggtcatcct tttactgcct ggaatatttc 1200

ccatcgcaga tgctgagaac gggcaacaac tttaccttca gctacacttt tgaggacgtt 1260

cctttccaca gcagctacgc tcacagccag agtctggacc gtctcatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcacgcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccggacaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1569
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1569
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcacaaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1570
<211> 2211

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1570
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc ttcaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1571
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1571
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattccc aatggctggg ggacagagtc 720

atcaccacca gcaccagaac ctgggccctg cccacctaca acaatcacct ctacaagcaa 780

atctccaaca gcacatctgg aggatcttca aatgacaacg cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caaccgcttc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

attcaggtca aagaggttac ggacaacaat ggagtcaaga ccatcgccaa taaccttacc 1020

agcacggtcc aggtctttac ggactcggag taccagttgc cgtacgtcct cggctctgcg 1080

caccagggct gcctccctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatat 1200

ttcccttctc agatgctgag aacgggcaac aactttacct tcagctacac ctttgaggac 1260

gttcctttcc acagcagcta cgctcacagc cagagtctgg accgtctcat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacaagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggcaaaga ttccacacac ggacggacat tttcacccct ctcccctcat gggtggattc 1920

ggacttaaac accctcctcc acagattctc atcaagaaca ccccggtacc tgcgaatcct 1980

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gtgcagtaca catccaatta tgcaaaatct gccaacgttg attttactgt ggacaacaat 2160

ggactttata ctgagcctcg ccccattggc acccgttacc ttacccgtcc cctgtaa 2217

<210> 1572
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1572
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gagtggtggg cgctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aaggggctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaactttg ggcagactgg cgactcagag 540

tcagtgcccg atcctcaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct taccagcacg 1020

attcaggtct ttacggattc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcattattc cgcagtacgg ctacctaacg 1140

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ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

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ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgccag tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1573
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1573
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gagtggtggg cgctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga gggttcttga acctttggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtgcccg accctcaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

attcaggtct ttacggattc ggaataccag ctcccgtacg tcctcggctc tgcccaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tcgcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggacgttcct 1260

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cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc acgcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1574
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1574
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc ccgtcaacga ggcggacgcg gcggccctcg aacacgacaa ggcttacgac 240

cagcagctca aggccggtga caacccctac ctgcggtaca accacgccga cgccgagttc 300

caggagcggc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcaggtg cacagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctataaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagtaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa cgatggagtc aagaccatcg ccaataacct taccagcacc 1020

attcaggtgt ttacggactc ggaataccag ctgccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1575
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1575
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa agcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttgggt ctggttgagg aaggggctaa gacggctcct 420

ggaaagaaaa ggccggtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aagacaggtg cacagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtg cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctataaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagtaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

atccaggtct ttacggactc ggagtaccag ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1576
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1576
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact ttggctacag cacccttgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1577
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1577
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca ccagaacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

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tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccgaccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaacgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctccgcccac 1080

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cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1578
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1578
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggaa cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcggagtac cagttgccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca acggtagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1579
<211> 2211

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1579
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

agggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1580
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1580
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaattttg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acttacaaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt taacattcaa 960

gtcaaagagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acacctttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctggaac caaataccat ctgaatggaa gaaattcatt gtctaatcct 1560

ggcatcgcta tggcgacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacatgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1581
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1581
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaggaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cggctcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaaactctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcctcaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

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<210> 1582
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1582

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

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Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
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Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
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Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1583
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1583

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560
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```
Thr Ser Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1584
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1584

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Asn Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655
```

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660   665   670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675   680   685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Thr
    690   695   700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705   710   715   720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725   730   735

Leu

<210> 1585
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1585

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
               85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
               165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
               245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1586
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1586

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590
```

```
Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210>  1587
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1587

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30
```

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460
```

```
Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1588
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1588

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp
            260                 265                 270

Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560
```

```
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Pro Leu
```

<210> 1589
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1589

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Gln Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415
```

```
Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620
```

```
His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 1590
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1590

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1591
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1591

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Leu Gly Ser Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Ile Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575
```

```
Arg Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 1592
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1592

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Asp Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1593
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1593

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Glu Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Phe Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1594
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1594

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Asn Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Val Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1595
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1595

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Glu Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Pro Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1596
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1596

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Asp Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560
```

```
Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1597
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1597

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255

Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser Gln
    450                 455                 460

Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn Asn
                485                 490                 495

Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys Asp
        515                 520                 525

Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Ile Leu Thr
545                 550                 555                 560

Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
                565                 570                 575

Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln Ile
            580                 585                 590

Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
                645                 650                 655
```

Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr
705 710 715 720

Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1598
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1598

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525
```

```
Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1599
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1599

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Arg Ser Val Phe Phe Gln Tyr Arg Asp Pro Asp Phe Gly Lys
    530                 535                 540

Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu Thr
545                 550                 555                 560

Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
                565                 570                 575

Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln Ile
            580                 585                 590

Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
        595                 600                 605
```

```
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
                645                 650                 655

Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1600
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1600

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1601
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1601

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575
```

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
580 585 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1602
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1602

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445
```

```
Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1603
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1603

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
               325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
               405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
               485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525
```

```
Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 1604
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1604

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Asp
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1605
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1605

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Lys Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1606
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1606

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Gly Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560
```

```
Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1607
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1607

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1608
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1608

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Gln
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525
```

```
Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Leu Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1609
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1609

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160


Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175
```

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
               405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Val
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Ala Thr Gly Gln
               485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Lys Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
               565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605
```

```
Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 1610
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (226)..(226)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (233)..(233)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (239)..(239)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (250)..(250)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (253)..(253)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (255)..(255)
<223> Xaa can be any naturally occurring amino acid

<400> 1610

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Xaa Asn Trp His Cys Asp Ser Xaa Trp Leu Gly Asp Arg Xaa Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Xaa Thr Tyr Xaa Asn Xaa Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
```

```
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560
```

```
Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 1611
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1611

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180   185   190

Pro Ala Gly Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly

```
        195                 200                 205

Gly Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asp Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415
```

```
Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn His Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
```

625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 1612
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1612

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
```

```
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1613
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1613

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
```

```
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575
```

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
580 585 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1614
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1614

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
```

```
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp
            260                 265                 270

Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
```

```
Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asn Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
```

660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr
690 695 700

Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn
705 710 715 720

Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Pro Leu

<210> 1615
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1615

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp
            260                 265                 270

Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
```

```
        515                 520                 525

His Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asn Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn
705                 710                 715                 720

Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735
```

Pro Leu

<210> 1616
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1616

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Ile Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
```

```
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590
```

```
Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210>  1617
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1617

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460
```

```
Gln Gly Gly Pro Asn Thr Met Ala Asn His Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1618
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1618

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asp Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
```

```
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210>  1619
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide
```

<400> 1619

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
```

```
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1620
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1620

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
```

```
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn His Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
```

725 730 735

<210> 1621
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1621

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
```

595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 1622
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1622

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asn Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
```

```
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670
```

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 1623
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1623

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Arg Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
```

```
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525
```

```
Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1624

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1624

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro

```
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ser Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Met Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1625
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1625

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Gly Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
```

```
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1626
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1626
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tgcatccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc caaaaagaga ctcaatttcg gtcagactgg cggcacagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg atacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1627
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1627
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1628
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1628
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttggaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacaggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

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cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1629
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1629

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc cgccgttccc agcggacgtt ttcatgattc ctcagtacgg ctacctaaca 1140

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgattttcg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 1630
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1630
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagaaaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctg 2208

<210> 1631
<211> 2211
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1631
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc ttcaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaaccg cttccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caaccatcca 960

ggtcaaggag gtcacgcaga atgaaggcac caagaccatc gccaataacc tcaccagcac 1020

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt gggtaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1632
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1632
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaaca tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccaacggga cttcgggagg aagcaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca acttcaaact cttcaacatc 960

caagtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctccgcccac 1080

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atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg atccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1633
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1633
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggcgccgac 660

ggagtgggta attcctcggg aaattggcat tgcgattcca catggatggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caagtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

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atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacac aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1634
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (676)..(676)
<223> n is a, c, g, or t

<400> 1634
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagaaaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcangaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgcca cctataacaa ccacctctac aagcaaatct 780

ccagtgcttc aacgggggcg cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

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gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtttg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacacagt actccacggg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actactacaa atctacaaat gtggactttg ctgttaacac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1635
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (715)..(715)
<223> n is a, c, g, or t

<400> 1635
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc ttcaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagantcatc 720

accaccagca cccgaacctg ggccctgccc acctataaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact ttcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1636
<211> 2211
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1636
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccctac ctcaagtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1637
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1637
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc ttcaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaaccg cttccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

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ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1638
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1638
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg ggacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacttcggg aggaagcacc aacgacaaca cctacttcgg ctgcgtcacg 840

ccctgggggt attttgactt taacaaattc cactgccact tttcaccgga tgactggcaa 900

cgactcatca acaacggctg gggattccgg actaagcgac tcaacttcaa gctcttcagc 960

atgaaagtca aaaagggtac ggacaacact ggaatcaaga ccatcgcgaa taaccttacc 1020

aacacggtcc atgtcttcgc ggactcggag taccagttgc cgtacgtcct cggctctgcg 1080

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ttcccatcgc agatgctgag aacgggcaac aactttacct tcagctacac ctttgaggac 1260

gttcctttcc acagcagcta cgctcacagc cagagtctgg accgtctcat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

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aatcctggca tcgctatggc aacacacaaa gacgacaagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggaaaaca gcaagcgctg gaacccggag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaacccca ccccattggc acccgttacc tcacccgtcc cctgtaa 2217

<210> 1639
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1639
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgat 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg ggacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaaacaa 780

atttccagcg cttcaacggg agcctcgaac gacaatcact actttggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcggagtac cagttgccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcagta cggctaccta 1140

acgctcaaca atggcagcca ggcagtggga cggtcatcct tttactgcct ggaatatttc 1200

ccatcgcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggacgtt 1260

cctttccaca gcagctacgc tcacagccag agtctggacc gtctcatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acctgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ttcacacgga cggcaacttt cacccttctc cgctgatggg agggtttgga 1920

atgaagcacc cgcctcctcc gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgccgaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggt 2160

gtgtactatg aaccccaccc cattggcacc cgttacctca cccctcccct gtaa 2214

<210> 1640
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1640
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggca 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac atgggccttg cccacctata acaaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcacaa caattggggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcggagtac cagttgccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcagta cggctaccta 1140

acgctcaaca atggcagcca ggcagtggga cggtcatcct tttactgcct ggaatatttc 1200

ccatcgcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggacgtt 1260

cctttccaca gcagctacgc tcacagccag agtctggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1641
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1641
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagaaaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgatcc cccagtacgg ctacctaaca 1140

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tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg cttcggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1642
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1642
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctca gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgcccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattccc aatggctggg ggacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccactttt caccacgtga ctggcaaaga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cgggtacctg 1140

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atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacac agtactccac gggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactacta caaatctaca aatgtggact ttgctgttaa cacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1643
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1643

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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggatgggtga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacacagt actccacggg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actactacaa atctacaaat gtggactttg ctgttaacac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacttcaccc gtcccctgta a 2211

<210> 1644
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1644
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaaaaga ctcaattttg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtttg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacacagt actccacggg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actactacaa atctacaaat gtggactttg ctgttaacac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1645
<211> 2211
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1645
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcacca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctgact 1140

ctgaacaatg gcagtcaggc cgtgggccgt tcctccttct actgcctaga gtactttcct 1200

tctcaaatgc tgagaacggg caacaacttt gagttcagct accagtttga ggacgtgcct 1260

tttcacagca gctacgcgca cagccaaagc ctggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat atgaatggaa gaaattcatt ggttaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgttgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtattgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc atctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtcgccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1646
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1646

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

```
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Arg Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
```

```
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1647
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1647

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Ala Ser Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Gly Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
```

```
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590
```

```
Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1648
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1648

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30
```

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460
```

```
Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1649
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1649

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Glu Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
```

545 550 555 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
580 585 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1650
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1650

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
```

```
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1651
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1651

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
```

```
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
```

725 730 735

<210> 1652
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1652

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn His Pro
305                 310                 315                 320

Gly Gln Gly Gly His Ala Glu Arg His Gln Asp His Arg Gln Pro His
                325                 330                 335

Gln His Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val
            340                 345                 350

Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
        355                 360                 365

Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln
    370                 375                 380
```

```
Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
385                 390                 395                 400

Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe Glu Asp
                405                 410                 415

Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
            420                 425                 430

Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln
        435                 440                 445

Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser Gln Gly
    450                 455                 460

Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn Asn Asn
                485                 490                 495

Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn Gly Arg
            500                 505                 510

Asn Ser Leu Gly Asn Pro Gly Ile Ala Met Ala Thr His Lys Asp Asp
        515                 520                 525

Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly Lys Gln
    530                 535                 540

Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu Thr Ser
545                 550                 555                 560

Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly
                565                 570                 575

Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln Ile Gly
            580                 585                 590

Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg
```

595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
610 615 620

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro
645 650 655

Pro Thr Ala Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr
690 695 700

Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr Ser
705 710 715 720

Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 1653
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1653

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys His Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
```

```
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685
```

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Asp Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 1654
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1654

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
```

```
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540
```

```
Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 1655

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (226)..(226)
<223> Xaa can be any naturally occurring amino acid

<400> 1655

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Xaa Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Pro Ile Thr Thr Thr Ser
                245                 250                 255

Thr Ser Lys Ser Pro Val Leu Gln Arg Gly Arg Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
```

```
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590
```

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1656
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (239)..(239)
<223> Xaa can be any naturally occurring amino acid

<400> 1656

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Xaa Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
```

```
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Phe Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1657
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1657

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
```

```
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525
```

```
Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1658

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1658

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro

```
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1659
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1659

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270
```

```
Asn Thr Tyr Phe Gly Cys Val Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Lys Phe His Cys His Phe Ser Pro Asp Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Gly Trp Gly Phe Arg Thr Lys Arg Leu Asn Phe Lys Leu Phe Ser
305                 310                 315                 320

Met Lys Val Lys Lys Gly Thr Asp Asn Thr Gly Ile Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Asn Thr Val His Val Phe Ala Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
```

```
               485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
               565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
               645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Pro Leu

<210> 1660
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1660

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
```

```
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560
```

```
Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Leu
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Met Lys His Pro Pro Pro Pro Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Pro Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Tyr Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Pro Pro
                725                 730                 735

Leu
```

<210> 1661
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1661

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180   185   190

Pro Ala Ala Pro Ser Gly Val Ala Pro Asn Thr Met Ala Ala Gly Gly

```
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Thr Thr
    290                 295                 300

Ile Gly Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415
```

```
Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
```

625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 1662
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1662

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn His Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
```

```
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1663
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1663

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Gln Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
```

```
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Ala Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575
```

```
Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 1664
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1664

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

```
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Phe Thr Arg Pro Leu
                725                 730                 735
```

<210> 1665
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1665

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
```

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
```

```
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1666
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1666

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

```
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Met Asn
            500                 505                 510

Gly Arg Asn Ser Leu Val Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Val Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1667
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1667
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtttggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 1668
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1668

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
```

```
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575
```

```
Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 1669
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1669

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
```

```
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430
```

```
Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
```

```
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1670
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1670

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
```

```
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300
```

```
Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Leu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Arg Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
```

```
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Phe Arg Asp Leu Ser Ser Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Ser Thr Pro Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1671
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1671

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145 150 155 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
165 170 175

```
Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
```

```
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Tyr Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Leu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605
```

```
Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1672
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1672

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
```

```
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480
```

```
Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Gly Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Ile Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Leu Tyr Asp Ala Ser Ser Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Leu Thr Leu Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
```

690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1673
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1673

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350
```

```
Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Thr Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Thr Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Gly Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
```

565 570 575

Gly Asn Leu Pro Arg Val Asp Thr Ser Ala Ser Asn Leu Pro Thr Val
580 585 590

Asp Arg Tyr Thr Asn Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
595 600 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1674
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1674

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
1               5                   10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220
```

```
Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
```

```
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Ser Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Phe Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Asp Tyr Asp Ser Ser Leu Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Asp Thr Thr Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655
```

```
Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1675
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1675

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
```

```
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Ser Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Trp Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Cys Ala Thr Ala Gly
        515                 520                 525
```

```
Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gln Gly Asp Ser Ser Leu Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Met Thr Val Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1676

<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1676

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145 150 155 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
165 170 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met

```
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400
```

```
Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Cys Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Arg Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Leu Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Tyr Lys Asp Ser Ser Arg Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Glu Thr Ser Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
```

610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1677
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1677

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270
```

```
Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Ile Ile Pro Ala
```

```
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Tyr Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Arg Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Trp Ile Asp Asn Ser Arg Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Pro Thr Ser Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Lys Asn Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Thr Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700
```

```
Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720


Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735


<210>  1678
<211>  735
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1678

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
```

```
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Gly Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Ile Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Arg Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575
```

```
Gly Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1679
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1679

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
```

```
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445
```

```
Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Val Ile Pro Ala
                485                 490                 495

Thr Glu Ser Asp Ser Leu Ile Tyr Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Tyr Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Pro Arg Asp Asp Ser Thr Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Lys Thr Tyr Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
```

660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1680
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1680

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320
```

```
Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Tyr Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Ile Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Ile Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
```

```
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ser Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Thr Asp Asp Asp Ser Arg Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Met Thr Leu Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735

<210>  1681
<211>  735
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1681

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175


Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190
```

```
Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
```

```
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr His Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Tyr Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Ser Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Arg Arg Asp Ser Ser Val Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Tyr Thr Asp Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

```
Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685


Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700


Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720


Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1682
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1682

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
```

```
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Ser Ile Pro Ala
                485                 490                 495
```

```
Thr Gly Ser Asp Ser Leu Ile Ser Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Arg Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Arg His Asp Ser Ser Leu Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Asn Thr Gly Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
```

705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1683
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1683

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly

```
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365
```

```
Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Phe Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Arg Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Leu Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Val Ile Asp Phe Ser Lys Ser Asn Leu Pro Thr Val
```

580 585 590

Asp Arg Leu Thr His Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
595 600 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1684
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1684

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240
```

```
Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
```

```
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Val Arg Asp Phe Ser Leu Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Thr Thr Lys Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670
```

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1685
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1685

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
```

```
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Phe Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Gln Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540
```

```
Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1686
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1686

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175


Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190


Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
```

```
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415
```

```
Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Met Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Ile Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Phe Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Val Trp
                565                 570                 575

Gly Asn Leu Pro Ser Gly Asp His Ser Gln Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Pro Thr Met Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
```

625 630 635 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Ile Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val His Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asp Tyr
690 695 700

Gly Gln His Ser Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Thr Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1687
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1687

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285
```

```
Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Asp Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
```

```
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720
```

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730

<210> 1688
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1688

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145 150 155 160

```
Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
```

```
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Ile Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Thr Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Val Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Phe Asn Asp Asp Ser Ser Ser Asn Leu Pro Thr Val
            580                 585                 590
```

```
Asp Arg Ser Thr Phe Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1689
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1689

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
```

```
               245                 250                 255

Thr Ser Ser Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460
```

```
Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
```

675 680 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
690 695 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 1690
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1690

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Ala Thr Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Lys Thr Pro Asn Arg Pro Thr Asn Pro Asp Ser Gly Lys
145                 150                 155                 160

Ala Pro Ala Lys Lys Lys Gln Lys Asp Gly Glu Pro Ala Asp Ser Ala
                165                 170                 175

Arg Arg Thr Leu Asp Phe Glu Asp Ser Gly Ala Gly Asp Gly Pro Pro
            180                 185                 190

Glu Gly Ser Ser Ser Gly Glu Met Ser His Asp Ala Glu Met Arg Ala
        195                 200                 205

Ala Pro Gly Gly Asn Ala Val Glu Ala Gly Gln Gly Ala Asp Gly Val
    210                 215                 220

Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Ser Glu Gly
225                 230                 235                 240

Arg Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Thr Tyr Asn
                245                 250                 255

Asn His Leu Tyr Leu Arg Ile Gly Thr Thr Ala Asn Ser Asn Thr Tyr
            260                 265                 270

Asn Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Leu Arg Pro Lys Ser Met Arg Val Lys Ile Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ala Asn Asn Leu
                325                 330                 335
```

```
Thr Ser Thr Val Gln Ile Phe Ala Asp Ser Thr Tyr Glu Leu Pro Tyr
            340                 345                 350

Val Met Asp Ala Gly Gln Glu Gly Ser Phe Pro Pro Phe Pro Asn Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Val Val Thr Gly Lys
    370                 375                 380

Asn Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Val Ser Tyr Gln
                405                 410                 415

Phe Glu Lys Val Pro Phe His Ser Met Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Met Met Asn Pro Leu Leu Asp Gln Tyr Leu Trp His Leu Gln
        435                 440                 445

Ser Thr Thr Thr Gly Asn Ser Leu Asn Gln Gly Thr Ala Thr Thr Thr
    450                 455                 460

Tyr Gly Lys Ile Thr Thr Gly Asp Phe Ala Tyr Tyr Arg Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Ala Cys Ile Lys Gln Gln Lys Phe Ser Lys Asn Ala Asn
                485                 490                 495

Gln Asn Tyr Lys Ile Pro Ala Ser Gly Gly Asp Ala Leu Leu Lys Tyr
            500                 505                 510

Asp Thr His Thr Thr Leu Asn Gly Arg Trp Ser Asn Met Ala Pro Gly
        515                 520                 525

Pro Pro Met Ala Thr Ala Gly Ala Gly Asp Ser Asp Phe Ser Asn Ser
    530                 535                 540

Gln Leu Ile Phe Ala Gly Pro Asn Pro Ser Gly Asn Thr Thr Thr Ser
```

545 550 555 560

Ser Asn Asn Leu Leu Phe Thr Ser Glu Glu Glu Ile Ala Thr Thr Asn
565 570 575

Pro Arg Asp Thr Asp Met Phe Gly Gln Ile Ala Asp Asn Asn Gln Asn
580 585 590

Ala Thr Thr Ala Pro His Ile Ala Asn Leu Asp Ala Met Gly Ile Val
595 600 605

Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile
610 615 620

Trp Ala Lys Val Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
625 630 635 640

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Phe Ile Lys
645 650 655

Asn Thr Pro Val Pro Ala Asn Pro Asn Thr Thr Phe Ser Ala Ala Arg
660 665 670

Ile Asn Ser Phe Leu Thr Gln Tyr Ser Thr Gly Gln Val Ala Val Gln
675 680 685

Ile Asp Trp Glu Ile Gln Lys Glu His Ser Lys Arg Trp Asn Pro Glu
690 695 700

Val Gln Phe Thr Ser Asn Tyr Gly Thr Gln Asn Ser Met Leu Trp Ala
705 710 715 720

Pro Asp Asn Ala Gly Asn Tyr His Glu Leu Arg Ala Ile Gly Ser Arg
725 730 735

Phe Leu Thr His His Leu
740

<210> 1691
<211> 733
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1691

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160


Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175


Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190
```

```
Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Ser Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Gly Lys Val Pro Phe His Ser Met
```

```
               405                 410                 415

Tyr Ala Tyr Ser Gln Ser Pro Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
               485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
               565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620
```

```
His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640


Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655


Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670


Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685


Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
    690                 695                 700


Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705                 710                 715                 720


Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730
```

<210> 1692
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1692

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Leu
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe His Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
```

```
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495
```

```
Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Gly Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685

Ser Lys Arg Arg Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
    690                 695                 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
```

705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 1693
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1693

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Glu Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys

```
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365
```

```
Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Thr Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Gly Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
```

```
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Tyr Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Cys Gly Asn
    690                 695                 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705                 710                 715                 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730


<210>  1694
<211>  735
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1694

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
```

```
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240
```

```
Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
```

```
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Glu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Ser Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670
```

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1695
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1695

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
```

```
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Glu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540
```

```
Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Ser Ser Asn Leu Pro Val Val
            580                 585                 590

Arg Gly Leu Arg Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1696
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1696

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145   150   155   160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165   170   175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180   185   190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu

```
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415
```

```
Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Glu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Ser Ser Asn Leu Pro Val Val
            580                 585                 590

Asn Arg Leu Ser Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
```

625 630 635 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1697
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1697

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285
```

```
Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Glu Tyr Glu Thr His Ser Thr Leu Asp
```

```
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Ser Ser Asn Leu Pro Pro Val
            580                 585                 590

Met Gly Leu Gly Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720
```

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1698
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1698

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145 150 155 160

```
Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
```

```
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Glu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Arg Val Asp Arg Leu Pro Thr
            580                 585                 590
```

```
Val Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln
        675                 680                 685

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
    690                 695                 700

Tyr Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys
705                 710                 715                 720

Tyr Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1699
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1699

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
```

```
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460
```

```
Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Glu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Arg Ala Leu Arg Leu Pro Thr
            580                 585                 590

Val Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln
```

675 680 685

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
690 695 700

Tyr Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys
705 710 715 720

Tyr Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1700
<211> 1172
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1700
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ggcgaccttt ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gagtggccaa 120

ctccatcact aggggttcct tgtagttaat gattaacccg ccatgctact tatctaccag 180

ggtaatgggg atcctctaga actatagcta gtcgacattg attattgact agttattaat 240

agtaatcaat tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac 300

ttacggtaaa tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa 360

tgacgtatgt tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggact 420

atttacggta aactgcccac ttggcagtac atcaagtgta tcatatgcca agtacgcccc 480

ctattgacgt caatgacggt aaatggcccg cctggcatta tgcccagtac atgaccttat 540

gggactttcc tacttggcag tacatctacg tattagtcat cgctattacc atgtcgaggc 600

cacgttctgc ttcactctcc ccatctcccc cccctcccca cccccaattt tgtatttatt 660

tatttttaa ttattttgtg cagcgatggg ggcgggggggg gggggcgcgc gccaggcggg 720

gcggggcggg gcgaggggcg gggcggggcg aggcggagag gtgcggcggc agccaatcag 780

agcggcgcgc tccgaaagtt tccttttatg gcgaggcggc ggcggcggcg gccctataaa 840

aagcgaagcg cgcggcgggc gggagcaagc tttattgcgg tagtttatca cagttaaatt 900

gctaacgcag tcagtgcttc tgacacaaca gtctcgaact taagctgcag aagttggtcg 960

tgaggcactg ggcaggtaag tatcaaggtt acaagacagg tttaaggaga ccaatagaaa 1020

ctgggcttgt cgagacagag aagactcttg cgtttctgat aggcacctat tggtcttact 1080

gacatccact ttgcctttct ctccacaggt gtccactccc agttcaatta cagctcttaa 1140

ggctagagta cttaatacga ctcsactata gg 1172

<210> 1701
<211> 3231
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1701
taagaattca cgcgtggtac ctctagagtc gacccgggcg gcctcgagga cggggtgaac 60

tacgcctgag gatccgatct ttttccctct gccaaaaatt atggggacat catgaagccc 120

cttgagcatc tgacttctgg ctaataaagg aaatttattt tcattgcaat agtgtgttgg 180

aatttttgt gtctctcact cggaagcaat tcgttgatct gaatttcgac cacccataat 240

acccattacc ctggtagata agtagcatgg cgggttaatc attaactaca aggaacccct 300

agtgatggag ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc 360

aaaggtcgcc cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag 420

ccttaattaa cctaattcac tggccgtcgt tttacaacgt cgtgactggg aaaaccctgg 480

cgttacccaa cttaatcgcc ttgcagcaca tccccctttc gccagctggc gtaatagcga 540

agaggcccgc accgatcgcc cttcccaaca gttgcgcagc ctgaatggcg aatgggacgc 600

gccctgtagc ggcgcattaa gcgcggcggg tgtggtggtt acgcgcagcg tgaccgctac 660

acttgccagc gccctagcgc ccgctccttt cgctttcttc ccttcctttc tcgccacgtt 720

cgccggcttt ccccgtcaag ctctaaatcg ggggctccct ttagggttcc gatttagtgc 780

tttacggcac ctcgacccca aaaaacttga ttagggtgat ggttcacgta gtgggccatc 840

gccctgatag acggtttttc gccctttgac gttggagtcc acgttcttta atagtggact 900

cttgttccaa actggaacaa cactcaaccc tatctcggtc tattcttttg atttataagg 960

gattttgccg atttcggcct attggttaaa aaatgagctg atttaacaaa aatttaacgc 1020

gaattttaac aaaatattaa cgcttacaat ttaggtggca cttttcgggg aaatgtgcgc 1080

ggaaccccta tttgtttatt tttctaaata cattcaaata tgtatccgct catgagacaa 1140

taaccctgat aaatgcttca ataatattga aaaaggaaga gtatgagtat tcaacatttc 1200

cgtgtcgccc ttattccctt ttttgcggca ttttgccttc ctgtttttgc tcacccagaa 1260

acgctggtga aagtaaaaga tgctgaagat cagttgggtg cacgagtggg ttacatcgaa 1320

ctggatctca acagcggtaa gatccttgag agttttcgcc ccgaagaacg ttttccaatg 1380

atgagcactt ttaaagttct gctatgtggc gcggtattat cccgtattga cgccgggcaa 1440

gagcaactcg gtcgccgcat acactattct cagaatgact tggttgagta ctcaccagtc 1500

acagaaaagc atcttacgga tggcatgaca gtaagagaat tatgcagtgc tgccataacc 1560

atgagtgata acactgcggc caacttactt ctgacaacga tcggaggacc gaaggagcta 1620

accgcttttt tgcacaacat gggggatcat gtaactcgcc ttgatcgttg ggaaccggag 1680

ctgaatgaag ccataccaaa cgacgagcgt gacaccacga tgcctgtagc aatggcaaca 1740

acgttgcgca aactattaac tggcgaacta cttactctag cttcccggca acaattaata 1800

gactggatgg aggcggataa agttgcagga ccacttctgc gctcggccct tccggctggc 1860

tggtttattg ctgataaatc tggagccggt gagcgtgggt ctcgcggtat cattgcagca 1920

ctggggccag atggtaagcc ctcccgtatc gtagttatct acacgacggg gagtcaggca 1980

actatggatg aacgaaatag acagatcgct gagataggtg cctcactgat taagcattgg 2040

taactgtcag accaagttta ctcatatata ctttagattg atttaaaact tcatttttaa 2100

tttaaaagga tctaggtgaa gatccttttt gataatctca tgaccaaaat cccttaacgt 2160

gagttttcgt tccactgagc gtcagacccc gtagaaaaga tcaaaggatc ttcttgagat 2220

cctttttttc tgcgcgtaat ctgctgcttg caaacaaaaa aaccaccgct accagcggtg 2280

gtttgtttgc cggatcaaga gctaccaact ctttttccga aggtaactgg cttcagcaga 2340

gcgcagatac caaatactgt tcttctagtg tagccgtagt taggccacca cttcaagaac 2400

tctgtagcac cgcctacata cctcgctctg ctaatcctgt taccagtggc tgctgccagt 2460

ggcgataagt cgtgtcttac cgggttggac tcaagacgat agttaccgga taaggcgcag 2520

cggtcgggct gaacgggggg ttcgtgcaca cagcccagct tggagcgaac gacctacacc 2580

gaactgagat acctacagcg tgagctatga gaaagcgcca cgcttcccga agggagaaag 2640

gcggacaggt atccggtaag cggcagggtc ggaacaggag agcgcacgag ggagcttcca 2700

gggggaaacg cctggtatct ttatagtcct gtcgggtttc gccacctctg acttgagcgt 2760

cgatttttgt gatgctcgtc agggggggcgg agcctatgga aaaacgccag caacgcggcc 2820

tttttacggt tcctggcctt ttgctggcct tttgctcaca tgttctttcc tgcgttatcc 2880

cctgattctg tggataaccg tattaccgcc tttgagtgag ctgataccgc tcgccgcagc 2940

cgaacgaccg agcgcagcga gtcagtgagc gaggaagcgg aagagcgccc aatacgcaaa 3000

ccgcctctcc ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac 3060

tggaaagcgg gcagtgagcg caacgcaatt aatgtgagtt agctcactca ttaggcaccc 3120

caggctttac actttatgct tccggctcgt atgttgtgtg gaattgtgag cggataacaa 3180

tttcacacag gaaacagcta tgaccatgat tacgccagat ttaattaagg c 3231

<210> 1702
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (264)..(264)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (266)..(266)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (268)..(268)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (448)..(448)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (459)..(460)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (467)..(467)
<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (474)..(474)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (495)..(495)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (516)..(516)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (533)..(533)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (547)..(547)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (551)..(551)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (555)..(555)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (557)..(557)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (561)..(561)

<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (563)..(563)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (577)..(577)
<223> Xaa can be any naturally occurring amino acid

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<222> (583)..(583)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (593)..(593)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (596)..(596)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (661)..(662)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (664)..(665)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (710)..(710)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (717)..(719)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (723)..(723)
<223> Xaa can be any naturally occurring amino acid

<400> 1702

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220
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```
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Xaa Ser Xaa Gly Xaa Thr Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Xaa
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Xaa Xaa Glu Leu Leu Phe
    450                 455                 460

Ser Gln Xaa Gly Pro Xaa Xaa Met Ser Xaa Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Xaa Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Xaa Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Xaa Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Xaa Gly Ala Gly Xaa Asn Asn Thr Xaa Leu Xaa Asn Val Met
545                 550                 555                 560

Xaa Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Xaa Tyr Gly Val Val Ala Xaa Asn Leu Gln Ser Ser Asn Thr Ala Pro
            580                 585                 590

Xaa Thr Gly Xaa Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655
```

Ala Asn Pro Pro Xaa Xaa Phe Xaa Xaa Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Xaa Asn Val Asp Phe Ala Val Xaa Xaa Xaa Gly
705 710 715 720

Val Tyr Xaa Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 1703
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1703

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
               85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
               165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
               245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Ser Gly Ser Thr Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Asn Arg Glu Leu Leu Phe
    450                 455                 460

Ser Gln Gly Gly Pro Ser Asn Met Ser Ala Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Ala Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510
```

```
Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Glu Gly Ala Gly Ala Asn Asn Thr Ala Leu Glu Asn Val Met
545                 550                 555                 560

Leu Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Val Val Ala Ser Asn Leu Gln Ser Ser Asn Thr Ala Pro
            580                 585                 590

Ala Thr Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Thr Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Ala Lys Ser Thr Asn Val Asp Phe Ala Val Asn Asn Glu Gly
705                 710                 715                 720
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Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 1704
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1704

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ser Gly Ser Thr Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
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Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Asn Arg Glu Leu Leu Phe
    450                 455                 460

Ser Gln Gly Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Ser Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ala Gly Ala Asn Asn Thr Thr Leu Asp Asn Val Met
545                 550                 555                 560

Met Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575
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Gln Tyr Gly Val Val Ala Ser Asn Leu Gln Ser Ser Asn Thr Ala Pro
            580                 585                 590

Gln Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Val Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Ala Lys Ser Thr Asn Val Asp Phe Ala Val Asn Ser Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
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<210> 1705
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1705

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220
```

```
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Ser Gly Ser Thr Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
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```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Arg Glu Leu Leu Phe
    450                 455                 460

Ser Gln Gly Gly Pro Ser Asn Met Ser Ala Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Thr Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ala Gly Ala Asn Asn Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Val Val Ala Ser Asn Leu Gln Ser Ser Asn Thr Ala Pro
            580                 585                 590

Ala Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655
```

Ala Asn Pro Pro Thr Val Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Thr Asn Val Asp Phe Ala Val Asn Ser Glu Gly
705 710 715 720

Val Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 1706
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (264)..(264)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (448)..(448)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (459)..(459)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (470)..(470)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (495)..(495)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (533)..(533)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (547)..(547)
<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<220>
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<223> Xaa can be any naturally occurring amino acid

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<222> (563)..(563)
<223> Xaa can be any naturally occurring amino acid

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<222> (593)..(593)
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<220>
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<222> (596)..(596)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (661)..(662)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (664)..(664)

<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (718)..(718)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (723)..(723)
<223> Xaa can be any naturally occurring amino acid

<400> 1706

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

```
Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Xaa Ser Ser Gly Ser Thr Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Xaa
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Xaa Arg Glu Leu Leu Phe
    450                 455                 460

Ser Gln Gly Gly Pro Xaa Asn Met Ser Ala Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Xaa Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Xaa Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Xaa Gly Ala Gly Ala Asn Asn Thr Xaa Leu Xaa Asn Val Met
545                 550                 555                 560

Xaa Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Val Val Ala Ser Asn Leu Gln Ser Ser Asn Thr Ala Pro
            580                 585                 590
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```
Xaa Thr Gly Xaa Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Xaa Xaa Phe Xaa Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Ala Lys Ser Thr Asn Val Asp Phe Ala Val Asn Xaa Glu Gly
705                 710                 715                 720


Val Tyr Xaa Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu
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<210> 1707
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

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<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (448)..(448)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (470)..(470)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (533)..(533)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (547)..(547)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (555)..(555)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (557)..(557)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (561)..(561)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (563)..(563)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (593)..(593)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (596)..(596)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (662)..(662)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (664)..(664)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (718)..(718)
<223> Xaa can be any naturally occurring amino acid

<400> 1707

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln

```
               165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Xaa Ser Ser Gly Ser Thr Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Xaa
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Asn Arg Glu Leu Leu Phe
    450                 455                 460

Ser Gln Gly Gly Pro Xaa Asn Met Ser Ala Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Ser Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Xaa Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Xaa Gly Ala Gly Ala Asn Asn Thr Xaa Leu Xaa Asn Val Met
545                 550                 555                 560

Xaa Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Val Val Ala Ser Asn Leu Gln Ser Ser Asn Thr Ala Pro
            580                 585                 590

Xaa Thr Gly Xaa Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
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595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Ala Xaa Phe Xaa Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Thr Asn Val Asp Phe Ala Val Asn Xaa Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 1708
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1708
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 1709
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1709

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu

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        115                 120                 125

Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Val Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr Gly
                165                 170                 175

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro Ala
            180                 185                 190

Ala Pro Ser Gly Val Gly Ser Thr Thr Met Ala Ser Gly Gly Gly Ala
        195                 200                 205

Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser
    210                 215                 220

Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255

Lys Gln Ile Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Tyr Phe
            260                 265                 270

Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
        275                 280                 285

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
    290                 295                 300

Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys
305                 310                 315                 320

Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu Thr
                325                 330                 335
```

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Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val
            340                 345                 350

Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
        355                 360                 365

Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln
    370                 375                 380

Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
385                 390                 395                 400

Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp
                405                 410                 415

Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
            420                 425                 430

Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln
        435                 440                 445

Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460

Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480

Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn Ser
                485                 490                 495

Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp Lys
        515                 520                 525

Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu Gly
    530                 535                 540

Thr Asn Ala Asn Asn Ala Asp Leu Glu Asn Val Met Ile Thr Asp Glu
```

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545                 550                 555                 560

Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Thr
                565                 570                 575

Val Ser Asn Asn Leu Gln Asn Ser Asn Ala Gly Pro Thr Thr Gly Thr
            580                 585                 590

Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg Asp
        595                 600                 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro
                645                 650                 655

Thr Asn Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys
    690                 695                 700

Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu
705                 710                 715                 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730
```

<210> 1710
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1710
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcaggtggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1711
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1711

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp

```
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300
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Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
```

```
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Val Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 1712
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1712
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cggtcaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1713
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1713

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val

```
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270
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Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
```

```
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Val Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700
```

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 1714
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1714
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacac ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1715
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1715

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys

```
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240
```

```
Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
```

```
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Thr Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670
```

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 1716
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1716
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cggtcaacac ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1717
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1717

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                  10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205
```

```
Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
```

```
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Val Asn Thr Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640
```

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 1718
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1718
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggccgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1719
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1719

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

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Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
```

```
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605
```

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Ala Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 1720
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1720
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1721
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1721

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

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Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Met Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
```

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        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575
```

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 1722
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1722
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtcgatgtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1723
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1723

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

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Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Asp Val Phe Thr Asp
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                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540
```

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Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 1724
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1724
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggacccag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1725
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1725

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

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Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
```

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    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Gln Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510
```

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Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 1726
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1726
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagtcgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1727
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1727

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

```
Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
```

```
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480
```

```
Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Ser Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
```

690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 1728
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1728
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccaggggg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1729
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1729

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

```
Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
```

```
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445
```

```
Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Gly Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
```

660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 1730
<211> 2194
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1730
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcggg aagcaaggct cagagaaaac aaatgtggac 1620

attgaaaagg tcatgatcac cagcgagagc gagacgcagc cggtgaaccg cgtggcgtac 1680

aacgtcggcg ggcagatggc caccaacaac cagagctcca ccactgcccc cgcgaccggc 1740

acgtacaacc tccaggaaat cgtgcccggc agcgtgtgga tggagaggga cgtgtacctc 1800

caaggaccca tctgggccaa gatcccagag acgggggcgc actttcaccc ctctccggcc 1860

atgggcggat tcggactcaa acacccaccg cccatgatgc tcatcaagaa cacgcctgtg 1920

cccggaaata tcaccagctt ctcggacgtg cccgtcagca gcttcatcac ccagtacagc 1980

accgggcagg tcaccgtgga gatggagtgg gagctcaaga aggaaaactc caagaggtgg 2040

aacccagaga tccagtacac aaacaactac aacgaccccc agtttgtgga ctttgccccg 2100

gacagcaccg gggaatacag aaccaccaga cctatcggaa cccgatacct tacccgaccc 2160

ctttaaccca ttcatgtcgc ataccctcaa taaa 2194

<210> 1731
<211> 721
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1731

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1   5   10   15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20   25   30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50   55   60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65   70   75   80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100   105   110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115   120   125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130   135   140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145   150   155   160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165   170   175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180   185   190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala

```
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415
```

```
Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val
    530                 535                 540

Met Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr
545                 550                 555                 560

Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala
                565                 570                 575

Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val
            580                 585                 590

Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
        595                 600                 605

Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe
    610                 615                 620

Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val
```

625 630 635 640

Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile
645 650 655

Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu
660 665 670

Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn
675 680 685

Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly
690 695 700

Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
705 710 715 720

Leu

<210> 1732
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1732

Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp
1 5 10 15

Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro
20 25 30

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly
35 40 45

Gly Ala Thr Asn Asp Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
50 55 60

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp

```
65                  70                  75                  80

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser
                85                  90                  95

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly
            100                 105                 110

Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr
        115                 120                 125

Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly
    130                 135                 140

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly
145                 150                 155                 160

Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe
                165                 170                 175

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn
            180                 185                 190

Phe Gln Phe Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr
        195                 200                 205

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln
    210                 215                 220

Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn
225                 230                 235                 240

Thr Gln Thr Leu Gly Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn
                245                 250                 255

Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val
            260                 265                 270

Ser Thr Thr Thr Gly Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala
        275                 280                 285
```

```
Gly Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly
    290                 295                 300

Ile Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser
305                 310                 315                 320

Asn Gly Ile Leu Ile Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala
                325                 330                 335

Asp Tyr Ser Asp Val Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr
            340                 345                 350

Asn Pro Val Ala Thr Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln
        355                 360                 365

Gln Gln Asn Thr Ala Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala
    370                 375                 380

Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro
385                 390                 395                 400

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
                405                 410                 415

Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile
            420                 425                 430

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser
        435                 440                 445

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
    450                 455                 460

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
465                 470                 475                 480

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe
                485                 490                 495

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
```

```
            500                 505                 510


Arg Tyr Leu Thr Arg Asn Leu
        515


<210>  1733
<211>  738
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1733

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
```

```
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
```

```
Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
```

```
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 1734
<211> 725
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1734

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
```

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Thr Gly Lys Arg
    130                 135                 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145                 150                 155                 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
                165                 170                 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
            180                 185                 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
        195                 200                 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
    210                 215                 220
```

```
Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225                 230                 235                 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
                245                 250                 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305                 310                 315                 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
                325                 330                 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
            340                 345                 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
        355                 360                 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
    370                 375                 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
                405                 410                 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
            420                 425                 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
```

```
        435                 440                 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
    450                 455                 460

Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465                 470                 475                 480

Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met
                485                 490                 495

Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met
            500                 505                 510

Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met
        515                 520                 525

Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu
    530                 535                 540

Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn
545                 550                 555                 560

Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser
                565                 570                 575

Ser Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val
            580                 585                 590

Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile
        595                 600                 605

Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala
    610                 615                 620

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys
625                 630                 635                 640

Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val
                645                 650                 655
```

Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met
660 665 670

Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
675 680 685

Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro
690 695 700

Asp Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr
705 710 715 720

Leu Thr Arg Pro Leu
725

<210> 1735
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1735

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
```

```
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1736

<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1736

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro
130 135 140

Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly Lys
145 150 155 160

Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr Gly
165 170 175

Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala

```
            180                 185                 190

Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly Ala
        195                 200                 205

Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser
    210                 215                 220

Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255

Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr Phe
            260                 265                 270

Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
        275                 280                 285

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
    290                 295                 300

Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val Lys
305                 310                 315                 320

Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu Thr
                325                 330                 335

Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val
            340                 345                 350

Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
        355                 360                 365

Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln
    370                 375                 380

Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
385                 390                 395                 400
```

```
Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp
                405                 410                 415

Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
            420                 425                 430

Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln
        435                 440                 445

Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr Thr
            580                 585                 590

Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
```

610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1737
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1737

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
```

```
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1738
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1738

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
```

```
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575
```

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
580 585 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1739
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1739

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
```

```
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445
```

```
Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Ser Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
```

660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1740
<211> 3695
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1740
ctctttgcgc ttgcgttttc ccttgtccag atagcccagt agctgacatt catccggggt 60

cagcaccgtt tctgcggact ggctttctac gtgaaaagga tctaggtgaa gatccttttt 120

gataatctca tgcctgacat ttatattccc cagaacatca ggttaatggc gtttttgatg 180

tcattttcgc ggtggctgag atcagccact tcttccccga taacggagac cggcacactg 240

gccatatcgg tggtcatcat gcgccagctt tcatccccga tatgcaccac cgggtaaagt 300

tcacgggaga ctttatctga cagcagacgt gcactggcca gggggatcac catccgtcgc 360

cccggcgtgt caataatatc actctgtaca tccacaaaca gacgataacg gctctctctt 420

ttataggtgt aaaccttaaa ctgccgtacg tataggctgc gcaactgttg ggaagggcga 480

tcggtgcggg cctcttcgct attacgccag ctggcgaaag ggggatgtgc tgcaaggcga 540

ttaagttggg taacgccagg gttttcccag tcacgacgtt gtaaaacgac ggccagtgaa 600

ttgtaatacg actcactata gggcgaattg aatttagcgg ccgcgaattc gcccttatga 660

tatctggtgg gaggagggca agatgacggc caaggtcgtg gagtccgcca aggccattct 720

cggcggcagc aaagtgcgcg tggaccaaaa gtgcaagtcg tccgcccaga tcgatcccac 780

tcccgtcatt gtcacctcca acaccaacat gtgcgccgtg attgacggga acagcaccac 840

cttcgagcac cagcagccgt tgcaggaccg gatgttcaaa tttgaactta cccgccgtct 900

ggagcatgac tttggcaagg tgacaaagca ggaagtcaaa gagttcttcc gctgggcgca 960

ggatcacgtg accgaggtgg cgcatgagtt ccacgtcaga aagggtggag ccaacaagag 1020

acccgccccc gatgacgctg ataaaagcga gcccaagcgg gcctgcccct cagtcgcaga 1080

tccatcgacg tcagacgcgg aaggagctcc ggtggacttt gccgacaggt accaaaacaa 1140

atgttctcgt cacgcgggca tgcttcagat gctgtttccc tgcaagacat gcgagagaat 1200

gaatcagaat ttcaacattt gcttcacgca cgggaccagg gactgttcgg agtgcttccc 1260

cggcgtgtca gaatctcaac cggtcgtcag aaaaaggacg tatcggaaac tctgtgccat 1320

tcatcatctg ctggggaggg ctcccgagat tgcttgctcg gcctgcgatc tggtcaacgt 1380

ggacctggat gactgtgtct ctgagcaata aatgacttaa accaggtatg gctgccgatg 1440

gttatcttcc agattggctc gaggacaacc tctctgaggg cattcgcgag tggtgggact 1500

tgaaacctgg agccccgaaa cccaaagcca accagcaaaa gcaggacgac ggccggggtc 1560

tggtgcttcc tggctacaag tacctcggac ccttcaacgg actcgacaag ggggagcccg 1620

tcaacgcggc ggacgcagcg gccctcgagc acgacaaggc ctacgaccag cagctcaaag 1680

cgggtgacaa tccgtacctg cggtataacc acgccgacgc cgagtttcag gagcgtctgc 1740

aagaagatac gtcttttggg ggcaacctcg ggcgagcagt cttccaggcc aagaagcggg 1800

ttctcgaacc tctcggtctg gttgaggaag gcgctaagac ggctcctgga aagaagagac 1860

cggtagagca gtcaccccaa gaaccagact cctcatcggg catcggcaag acaggccagc 1920

agcccgctaa aaagagactc aattttggtc agactggcga cacagagtca gtccccgacc 1980

cacaacctct cggagaacct ccagcagccc cctcaggtct gggacctaat acaatggctt 2040

caggcggtgg cgctccaatg gcagacaata acgaaggcgc cgacggagtg ggtaattcct 2100

cgggaaattg gcattgcgat tccacatggc tgggggacag agtcatcacc accagcaccc 2160

gaacctgggc cctgcccacc tacaacaacc acctctacaa gcaaatctcc aacggcacct 2220

cgggaggaag caccaacgac aacacctact ttggctacag cacccctgg gggtattttg 2280

acttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc atcaacaaca 2340

attggggatt ccggcccaag agactcaact tcaagctctt caacatccag gtcaaggaag 2400

tcacgacgaa cgaaggcacc aagaccatcg ccaataatct caccagcacc gtgcaggtct 2460

ttacggactc ggagtaccag ctaccgtacg tgctaggatc agctcaccag ggatgtctgc 2520

ctccgttccc ggcggacgtc ttcatggttc ctcagtacgg ttatctaact ctgaacaatg 2580

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aagcaggccc tagctcaatg gccagccagg ctagaaactg ggtgcccgga ccgagctacc 2880

ggcagcagcg cgtctccacg acaaccaacc agaacaacaa cagcaacttt gcctggacgg 2940

gagctgccaa atttaaactg aacggccgag actctctaat gaaccccggc gtggccatgg 3000

cttcacacaa ggatgacgag gaccgcttct tcccttctag cggggtcctg attttcggca 3060

agcaaggagc cgggaatgat ggagtggatt acagccaagt gctgattaca gatgaggaag 3120

aaatcaaggc taccaacccc gtggcaacag aggaatatgg agcagtggcc atcaacaacc 3180

aggccgctaa tacgcaggcg cagaccggac tcgtgcacaa ccaggggggtg attcccggca 3240

tggtgtggca gaacagagac gtgtacctgc agggtcccat ctgggccaaa attcctcaca 3300

cggacggcaa ctttcacccg tctcccctga tgggcggctt tggactgaag cacccgcctc 3360

ctcaaattct catcaagaac acaccggttc cagcggaccc gccgcttacc ttcaaccagg 3420

ccaagctgaa ctctttcatc acgcagtaca gcaccggaca ggtcagcgtg gaaatcgagt 3480

gggagctgca gaaagaaaac agcaaacgct ggaatccaga gattcagtac acttccaact 3540

actacaaatc tacaaatgtg gactttgctg tcaacacgga aggagtgtat agcgagcctc 3600

gccccattgg cacccgttac ctcacccgca acctgtaatt gcctgttaat caataaaccg 3660

gttaattcgt ttcagtaagg aagaattcgt ttaaa 3695

<210> 1741
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1741

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

```
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  1742
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  1742

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
```

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Asn Met Ala Ser Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
```

```
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1743
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1743

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Ser Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
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385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

```
Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 1744
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1744

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460
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```
Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1745
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1745

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
```

```
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Val Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
```

545 550 555 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
565 570 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
580 585 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Val Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1746
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
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<222> (168)..(168)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (204)..(204)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (266)..(266)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (311)..(311)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (411)..(411)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (460)..(460)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (493)..(493)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (562)..(562)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (576)..(576)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (587)..(587)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature

<222> (609)..(609)
<223> Xaa can be any naturally occurring amino acid

<400> 1746

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Xaa Ala Gly Gly Gly
```

```
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Xaa Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Xaa Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Xaa Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Xaa Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Xaa Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Xaa
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Xaa Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Xaa Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
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625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1747
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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<222> (502)..(504)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (610)..(612)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (796)..(798)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (931)..(933)

<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1231)..(1233)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1378)..(1380)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1477)..(1479)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1684)..(1686)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1726)..(1728)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1759)..(1761)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1825)..(1827)
<223> n is a, c, g, or t

<400> 1747
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcaatcaccc caggaaccag actcctcttc gggcatcggc 480

aagaaaggcc agcagcccgc gnnnaagaga ctcaactttg ggcagacagg cgactcagag 540

tcagtgcccg accctcaacc actcggagaa ccccccgcag ccccctctgg tgtgggatct 600

aatacaatgn nngcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaacg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctcccc acctacaaca accacctcta caagcaaatc 780

tccagccaat cgggannnag caccaacgac aacacctact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag nnnctcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgacgaa tgatggcacc acgaccatcg ccaataacct taccagcacg 1020

gttcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctgc ctccgttccc ggcggacgtc ttcatgattc ctcagtacgg gtacctgact 1140

ctgaacaatg gcagtcaggc cgtgggccgt tcctccttct actgcctgga gtactttcct 1200

tctcaaatgc tgagaacggg caacaacttt nnnttcagct acacgtttga ggacgtgcct 1260

tttcacagca gctacgcgca cagccaaagc ctggaccggc tgatgaaccc cctcatcgac 1320

cagtacctgt actacctgtc tcggactcag accacgagtg gtaccgcagg aaatcggnnn 1380

ttgcaatttt ctcaggccgg gcctagtagc atggcgaatc aggccaaaaa ctggctaccc 1440

gggccctgct accggcagca acgcgtctcc aagacannna atcaaaataa caacagcaac 1500

tttgcctgga ccggtgccac caagtatcat ctgaatggca gagactctct ggtaaatccc 1560

ggtcccgcta tggcaaccca caaggacgac gaagacaaat tttttccgat gagcggagtc 1620

ttaatatttg ggaaacaggg agctggaaat agcaacgtgg accttgacaa cgttatgata 1680

accnnngagg aagaaattaa aaccaccaac ccagtggcca cagaannnta cggcacggtg 1740

gccactaacc tgcaatcgnn naacaccgct cctgctacag ggaccgtcaa cagtcaagga 1800

gccttacctg gcatggtctg gcagnnncgg gacgtgtacc tgcagggtcc tatctgggcc 1860

aagattcctc acacggacgg acactttcat ccctcgccgc tgatgggagg ctttggactg 1920

aaacacccgc ctcctcagat cctgattaag aatacacctg ttcccgcgaa tcctccaact 1980

accttcagtc cagctaagtt tgcgtcgttc atcacgcagt acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc agagattcaa 2100

tacacttcca actacaacaa atctacaaat gtggactttg ctgttgacac aaatggcgtt 2160

tattctgagc ctcgccccat cggcacccgt tacctcaccc gtaatctg 2208

<210> 1748
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

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<221> misc_feature
<222> (157)..(157)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (168)..(168)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (262)..(263)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (312)..(312)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (412)..(412)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (460)..(461)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (552)..(552)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (556)..(557)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (563)..(563)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (580)..(580)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (588)..(588)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (664)..(664)
<223> Xaa can be any naturally occurring amino acid

<400> 1748

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Xaa Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Xaa Xaa Gln Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Xaa Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350
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Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Xaa Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Gly Asn Xaa Xaa Leu Gln Phe
    450                 455                 460

Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ala Gly Asn Xaa Asn Val Asp Xaa Xaa Asn Val Met
545                 550                 555                 560
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Ile Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Xaa Val Ala Thr Asn Leu Gln Ser Xaa Asn Thr Ala Pro
            580                 585                 590

Gln Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Thr Thr Phe Xaa Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
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<210> 1749
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
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<222> (469)..(471)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (502)..(504)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (784)..(789)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (934)..(936)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1234)..(1236)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1378)..(1383)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1654)..(1656)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1666)..(1671)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1687)..(1689)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1738)..(1740)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (1762)..(1764)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1990)..(1992)
<223> n is a, c, g, or t

<400> 1749
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcaatcaccc caggaaccag actcctctnn nggcatcggc 480

aagaaaggcc agcagcccgc gnnnaagaga ctcaactttg ggcagactgg cgactcagag 540

tcagtgcccg accctcaacc actcggagaa ccccccgcag ccccctctgg tgtgggatct 600

aatacaatgg ctgcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctcccc acctacaaca accacctcta caagcaaatc 780

tccnnnnnnc aatcgggagg aagcaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagnnnctca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgac gaatgatggc accacgacca tcgccaataa ccttaccagc 1020

acggttcagg tctttacgga ctcggaatac cagctcccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cgggtacctg 1140

actctgaaca atggcagtca ggccgtgggc cgttcctcct tctactgcct ggagtacttt 1200

ccttctcaaa tgctgagaac gggcaacaac tttnnnnttca gctacacgtt tgaggacgtg 1260

ccttttcaca gcagctacgc gcacagccaa agcctggacc ggctgatgaa ccccctcatc 1320

gaccagtacc tgtactacct gtctcggact cagaccacgg gaggtaccgc aggaaatnnn 1380

nnnttgcaat tttctcaggc cgggcctagt agcatggcga atcaggccaa aaactggcta 1440

cccgggccct gctaccggca gcaacgcgtc tccaagacaa cgaatcaaaa taacaacagc 1500

aactttgcct ggaccggtgc caccaagtat catctgaatg gcagagactc tctggtaaat 1560

cccggtgtcg ctatggcaac ccacaaggac gacgaagacc gatttttttcc gtccagcgga 1620

gtcttaatat ttgggaaaca gggagctgga aatnnnaacg tggacnnnnn naacgttatg 1680

ataaccnnng aggaagaaat taaaaccacc aacccagtgg ccacagaaga gtacggcnnn 1740

gtggccacta acctgcaatc gnnnaacacc gctcctcaaa cagggaccgt caacagtcaa 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcctatctgg 1860

gccaagattc ctcacacgga cggaaacttt catccctcgc cgctgatggg aggctttgga 1920

ctgaaacacc cgcctcctca gatcctgatt aagaatacac ctgttcccgc gaatcctcca 1980

actaccttcn nnccagctaa gtttgcgtcg ttcatcacgc agtacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaaa gaaaacagca aacgctggaa cccagagatt 2100

caatacactt ccaactacaa caaatctaca aatgtggact ttgctgttga cacagaaggc 2160

gtttattctg agcctcgccc catcggcacc cgttacctca cccgtaatct g 2211

<210> 1750
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (158)..(158)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (169)..(169)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (564)..(564)
<223> Xaa can be any naturally occurring amino acid

<400> 1750

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Arg Glu Pro Asp Ser Ser Xaa Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly
        195                 200                 205
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Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
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            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Gly Thr Gln Thr Leu Gln
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Asn Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Ile Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Val Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala
            580                 585                 590

Pro Gln Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
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Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 1751
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (472)..(474)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (505)..(507)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1690)..(1692)
<223> n is a, c, g, or t

<400> 1751

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gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcagtcacca cagcgtgagc ccgactcctc cnnnggcatc 480

ggcaagaaag gccagcagcc cgccnnnaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

tctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aagaggtcac gacgaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccgtcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aactttcaat tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagacta cgggaggcac agcgggaacc 1380

cagacgttgc agttttctca ggccgggcct agcagcatgg cgaatcaggc caaaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga caacgaatca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagg accgcttctt cccatccagc 1620

ggcgtcctca tatttggcaa gcagggagct ggaaatgaca acgtggacta tagcaacgtg 1680

atgataaccn nngaggaaga aatcaagacc accaaccccg tggccacaga agagtatggc 1740

gtggtggcta ctaacctaca gtcggcaaac accgctcctc aaacggggac cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacaacgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctg 2214

<210> 1752
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (158)..(158)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (169)..(169)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (315)..(315)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (413)..(413)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (472)..(472)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (534)..(534)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (542)..(542)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (595)..(595)
<223> Xaa can be any naturally occurring amino acid

<400> 1752

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

```
Pro Val Glu Gln Ser Pro Gln Arg Glu Pro Asp Ser Ser Xaa Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Xaa Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
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Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Xaa Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Gly Thr Gln Thr Leu Gln
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Xaa Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Xaa Arg Phe Phe Pro Ser Ser Gly Xaa Leu Ile
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575
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Glu Glu Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Xaa Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 1753
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<221> misc_feature
<222> (472)..(474)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (505)..(507)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (943)..(945)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1237)..(1239)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1414)..(1416)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1600)..(1602)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1624)..(1626)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1783)..(1785)
<223> n is a, c, g, or t

<400> 1753
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gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcagtcacca cagcgtgagc ccgactcctc cnnnggcatc 480

ggcaagaaag gccagcagcc cgccnnnaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

tctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcnnnttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aactttnnnt tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagacta cgggaggcac agcgggaacc 1380

cagacgttgc agttttctca ggccgggcct agcnnnatgg cgaatcaggc caaaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga caacgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagn nncgcttctt cccatccagc 1620

ggcnnnctca tatttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga agagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctcctc aannngggac cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacaacgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctg 2214

<210> 1754
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (169)..(169)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (315)..(315)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (534)..(534)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (542)..(542)
<223> Xaa can be any naturally occurring amino acid

<400> 1754

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

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Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
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Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Xaa Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495
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Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Xaa Arg Phe Phe Pro Ser Ser Gly Xaa Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720
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Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 1755
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (505)..(507)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (943)..(945)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1600)..(1602)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1624)..(1626)
<223> n is a, c, g, or t

<400> 1755
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gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccnnnaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tggtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcnnnttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aactttgagt tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc caaaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagn nncgcttctt cccatccagc 1620

ggcnnnctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacaacgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctg 2214

<210> 1756
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (471)..(471)
<223> Xaa can be any naturally occurring amino acid

<400> 1756

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
```

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            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Xaa Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560
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Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 1757
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (1411)..(1413)
<223> n is a, c, g, or t

<400> 1757
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctc cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacttcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtcct cggctctgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggccgtg ggccgttcct ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgagt tcagctacac gtttgaggac 1260

gtgcctttc acagcagcta cgcgcacagc caaagcctgg accggctgat gaacccctc 1320

atcgaccagt acctgtacta cctgtctcgg actcagtcca cgggaggtac cgcaggaact 1380

cagcagttgc tattttctca ggccgggcct nnnaacatgt cggctcaggc caaaaactgg 1440

ctacccgggc cctgctaccg gcagcaacgc gtctccacga cactgtcgca aaataacaac 1500

agcaactttg cctggaccgg tgccaccaag tatcatctga atggcagaga ctctctggta 1560

aatcccggtg tcgctatggc aacccacaag gacgacgaag agcgattttt tccgtccagc 1620

ggagtcttaa tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtt 1680

atgctaacca gtgaggaaga aattaaaacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac accgctccta ttgtaggggc cgtcaacagt 1800

caaggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatc 1860

tgggccaaga ttcctcacac ggacggaaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaaac acccgcctcc tcagatcctg attaagaata cacctgttcc cgcggatcct 1980

ccaactacct tcagtcaagc taagctggcg tcgttcatca cgcagtacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaagaaaaca gcaaacgctg gaacccagag 2100

attcaataca cttccaacta ctacaaatct acaaatgtgg actttgctgt taacacagaa 2160

ggcacttatt ctgagcctcg ccccatcggc acccgttacc tcacccgtaa tctg 2214

<210> 1758
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (148)..(148)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (169)..(169)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (314)..(314)
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<220>
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<223> Xaa can be any naturally occurring amino acid

<400> 1758

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            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Xaa Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Xaa Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
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            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Thr Thr Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Xaa Gln Ala Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560
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Met Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
565 570 575

Glu Tyr Gly Xaa Val Ser Ser Asn Leu Gln Ser Xaa Asn Thr Ala Pro
580 585 590

Gln Thr Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Asp Lys Ser Thr Asn Val Asp Phe Ala Val Asp Ser Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 1759
<211> 2211
<212> DNA
<213> Artificial Sequence

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<223> n is a, c, g, or t

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<222> (940)..(942)
<223> n is a, c, g, or t

<220>
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<222> (1396)..(1398)
<223> n is a, c, g, or t

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<222> (1687)..(1689)
<223> n is a, c, g, or t

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<222> (1738)..(1740)
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<223> n is a, c, g, or t

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gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtcattt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gnnntcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccnnnaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

attaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc aaagtgcagg tagtaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagaagctgn nnttcaagct cttcaacatc 960

caggtcaagg aggtcacgac gaatgacggc gttacgacca tcgctaataa ccttaccagc 1020

acggttcagg tattctcgga ctcggaatac cagctgccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg 1140

actctcaaca atggcagtca gtctgtggga cgttcctcct tctactgcct ggagtacttc 1200

ccctctcaga tgctgagaac gggcaacaac tttgagttca gctacacctt cgaggacgtg 1260

cctttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcccctcatc 1320

gaccagtact tgtactacct ggccagaaca cagagtacca caggaggcac agctggcaat 1380

cgggaactgc agtttnnnca ggccgggcct tcaactatgg ccgaacaagc caagaattgg 1440

ttacctggac cttgctaccg gcaacaaaga gtctccaaaa cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggcagaaa ctcgttggtt 1560

aatcccggcg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc 1620

ggagtcctga tttttggaaa aactggagca gctaacaaaa ctacattgga aaatgtgtta 1680

atgacannng aagaagaaat taaaactact aatcctgtag ccacggaaga atacgggnnn 1740

gtcagcagca acttacaatc gnnnaatact gcaccccaga cacaaactgt caacagccag 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga tggcaacttt cacccgtctc ctttgatggg cggctttgga 1920

cttaaacatc cgcctcctca gatcctgatc aagaacactc ccgttcccgc taatcctccg 1980

gaggtgttta ctcctgccaa gtttgcttcg ttcatcacac agtacagcac cggacaagtc 2040

agcgtggaaa tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatt 2100

cagtacacct ccaactatga taagtcgact aatgtggact ttgccgttga cagcgagggt 2160

gtttactctg agcctcgccc tattggcact cgttacctca cccgtaatct g 2211

<210> 1760
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
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<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
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<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (224)..(224)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (310)..(310)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (410)..(410)
<223> Xaa can be any naturally occurring amino acid

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<222> (446)..(446)
<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

<400> 1760

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Xaa Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
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            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Xaa
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Xaa Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
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Gln Met Leu Arg Thr Gly Asn Asn Phe Xaa Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Xaa Arg Thr
        435                 440                 445

Gln Thr Thr Ser Gly Thr Ala Gln Asn Arg Glu Leu Xaa Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Xaa Asn Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ala Gly Ala Ser Asn Val Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala Thr
            580                 585                 590

Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
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610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Xaa Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1761
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<222> (1336)..(1338)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1381)..(1383)
<223> n is a, c, g, or t

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctcttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagnnnggcc agcagcccgc tnnnaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcag ccccctctgg tgtgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatn nntcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

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caagtcttca cggactcgga gtaccagttg ccgtacgtcc tcggctctgc gcaccagggc 1080

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tacctgtatt acctgnnnag aactcagact acgtccggaa ctgcccaaaa cagggagttg 1380

nnntttagcc aggcgggtcc atctagcatg nnnaatcagg ccaaaaactg gctacctgga 1440

ccctgttacc ggcagcagcg cgtttctaaa acagcaaatg acaacaacaa cagcaacttt 1500

gcctggactg gtgctacaaa atatcacctt aatgggcgtg attctttagt caaccctggc 1560

cctgctatgg cctcacacaa agacgacgaa gacaagttct ttcccatgag cggtgtcttg 1620

atttttggaa agcagggcgc cggagcttca aacgttgatt tggacaatgt catgatcaca 1680

gacgaagagg aaatcaaaac cactaacccc gtggccaccg aacaatatgg gactgtggca 1740

accaatctcc agagcagcaa cacagcccct gcgaccggaa ctgtgaattc tcagggagcc 1800

ttacctggaa tggtgtggca agacagagac gtatacctgc agggtcctat ttgggccaaa 1860

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ttttcgcctg caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg 2040

gagattgaat gggagctgca gaaagaaaac agcaaacgct ggaatcccga aatacagtat 2100

acatctaact ataataaatc tnnnaacgtt gatttcactg tggacaccaa tggagtttat 2160

agtgagcctc gccccattgg cacccgttac ctcacccgta acctg 2205

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<211> 735
<212> PRT
<213> Artificial Sequence

<220>
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<222> (446)..(446)
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<222> (461)..(461)
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<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (504)..(504)
<223> Xaa can be any naturally occurring amino acid

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<222> (539)..(539)
<223> Xaa can be any naturally occurring amino acid

<400> 1762

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            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asp Xaa Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190
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Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Xaa Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Xaa Phe Ser Tyr Thr Phe Glu
                405                 410                 415
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Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Xaa Arg Thr
        435                 440                 445

Gln Thr Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Xaa Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Xaa Gln Gln Ala Xaa Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Ala Trp Thr Xaa Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Xaa Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Ala Ser Asn Val Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala Thr
            580                 585                 590

Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

```
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  1763
<211>  2205
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polynucleotide


<220>
<221>  misc_feature
<222>  (124)..(126)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (502)..(504)
<223>  n is a, c, g, or t

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<221>  misc_feature
<222>  (928)..(930)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
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<222> (1228)..(1230)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1336)..(1338)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1381)..(1383)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1411)..(1413)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1423)..(1425)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1510)..(1512)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1615)..(1617)
<223> n is a, c, g, or t

<400> 1763
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg atctgaaacc tggagcccct caacccaaag cgaaccaaca acaccaggac 120

gacnnncggg gtcttgtgct tccgggttac aaatacctcg gacccttaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga gggtccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga acagtctcct caggaaccgg actcatcatc tggtattggc 480

aaatcgggcc aacagcctgc cnnnaaaaga ctaaatttcg gtcagactgg agactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag ccccctcagg tgtgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagnnn ctcaacttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

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cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgnnnag aacgcaaaca acctctggaa caacccaaca atcacggctg 1380

nnntttagcc aggctgggcc ttcgtctatg nnncagcagg ccnnnaattg gctacctggg 1440

ccctgctacc ggcaacagag agtttcaaag actgctaacg acaacaacaa cagtaacttt 1500

gcttggacan nngccaccaa atatcatctc aatggccgcg actcgctggt gaatccagga 1560

ccagctatgg ccagtcacaa ggacgatgaa gaaaaatttt tccctatgca cggcnnncta 1620

atatttggca aacaagggac aggggcaagt aacgtagatt tagataatgt aatgattacg 1680

gatgaagaag agattcgtac caccaatcct gtggcaacag agcagtatgg aactgtggca 1740

actaacttgc agagctcaaa tacagctccc gcgactggaa ctgtcaatag tcaggggggcc 1800

ttacctggca tggtgtggca agatcgtgac gtgtaccttc aaggacctat ctgggcaaag 1860

attcctcaca cggatggaca ctttcatcct tctcctctga tgggaggctt tggactgaaa 1920

catccgcctc ctcaaatctt gatcaaaaat actccggtac cggcaaatcc tccgacgact 1980

ttcagcccgg ccaagtttgc ttcatttatc actcagtact ccactggaca ggtcagcgtg 2040

gaaattgagt gggagctaca gaaagaaaac agcaaacgtt ggaatccaga gattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tagacactaa tggtgtttat 2160

agtgaacctc gccctattgg aacccggtat ctcacacgaa acttg 2205

<210> 1764
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1764

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

```
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1765
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1765

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Thr Asn Asp Asn Thr
```

```
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
```

690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1766
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1766

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
```

565 570 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
580 585 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1767
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1767

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
```

```
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1768
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1768

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
```

```
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1769

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1769

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro

```
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1770
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1770

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270
```

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Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
```

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                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1771
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1771

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
```

```
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575
```

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
580 585 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1772
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1772
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcaatcaccc caggaaccag actcctcttc gggcatcggc 480

aagaaaggcc agcagcccgc gaaaaagaga ctcaactttg ggcagacagg cgactcagag 540

tcagtgcccg accctcaacc actcggagaa ccccccgcag ccccctctgg tgtgggatct 600

aatacaatgg ctgcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaacg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctcccc acctacaaca accacctcta caagcaaatc 780

tccagccaat cgggagcaag caccaacgac aacacctact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgacgaa tgatggcacc acgaccatcg ccaataacct taccagcacg 1020

gttcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctgc ctccgttccc ggcggacgtc ttcatgattc ctcagtacgg gtacctgact 1140

ctgaacaatg gcagtcaggc cgtgggccgt tcctccttct actgcctgga gtactttcct 1200

tctcaaatgc tgagaacggg caacaacttt gagttcagct acacgtttga ggacgtgcct 1260

tttcacagca gctacgcgca cagccaaagc ctggaccggc tgatgaaccc cctcatcgac 1320

cagtacctgt actacctgtc tcggactcag accacgagtg gtaccgcagg aaatcggacg 1380

ttgcaatttt ctcaggccgg gcctagtagc atggcgaatc aggccaaaaa ctggctaccc 1440

gggccctgct accggcagca acgcgtctcc aagacagcga atcaaaataa caacagcaac 1500

tttgcctgga ccggtgccac caagtatcat ctgaatggca gagactctct ggtaaatccc 1560

ggtcccgcta tggcaaccca caaggacgac gaagacaaat tttttccgat gagcggagtc 1620

ttaatatttg ggaaacaggg agctggaaat agcaacgtgg accttgacaa cgttatgata 1680

accagtgagg aagaaattaa aaccaccaac ccagtggcca cagaacagta cggcacggtg 1740

gccactaacc tgcaatcgtc aaacaccgct cctgctacag ggaccgtcaa cagtcaagga 1800

gccttacctg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc tatctgggcc 1860

aagattcctc acacggacgg acactttcat ccctcgccgc tgatgggagg ctttggactg 1920

aaacacccgc ctcctcagat cctgattaag aatacacctg ttcccgcgaa tcctccaact 1980

accttcagtc cagctaagtt tgcgtcgttc atcacgcagt acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc agagattcaa 2100

tacacttcca actacaacaa atctacaaat gtggactttg ctgttgacac aaatggcgtt 2160

tattctgagc ctcgccccat cggcacccgt tacctcaccc gtaatctgta a 2211

<210> 1773
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1773

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
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                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540
```

```
Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 1774

<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1774

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro

```
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
```

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
```

610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 1775
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (157)..(157)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (169)..(169)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (457)..(457)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (463)..(463)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (508)..(508)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (510)..(511)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (558)..(558)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (585)..(585)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (587)..(587)
<223> Xaa can be any naturally occurring amino acid

<400> 1775

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Xaa Leu Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
```

```
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Thr Xaa Gly Thr Gln Thr Leu Xaa Phe
    450                 455                 460

Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Xaa Lys Xaa Xaa Leu
```

```
            500                 505                 510

Asn Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ala Gly Asn Asp Asn Val Asp Tyr Ser Xaa Val Met
545                 550                 555                 560

Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ala Val Ala Thr Asn Xaa Gln Xaa Leu Ala Asn Thr Gln
            580                 585                 590

Ala Gln Thr Gly Leu Val His Asn Gln Gly Val Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720
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Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 1776
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (469)..(471)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (502)..(504)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1366)..(1368)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1384)..(1386)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1519)..(1521)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1525)..(1530)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1669)..(1671)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (1750)..(1752)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1756)..(1758)
<223> n is a, c, g, or t

<400> 1776
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa agcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga ggccggtaga gcagtcgcca caagagccag actcctccnn nggcatcggc 480

aagacaggcc agcagcccgc tnnnaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcag ccccctcagg tgtgggatct 600

aatacaatgg cttcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggca cctcgggagg aagcaccaac gacaacacct attttggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcactttt caccacgtga ctggcaacga 900

ctcatcaaca acaattgggg attccggccc aaaagactca acttcaagct gttcaacatc 960

caggtcaagg aagtcacgac gaacgaaggc accaagacca tcgccaataa tctcaccagc 1020

accgtgcagg tctttacgga ctcggagtac cagttaccgt acgtgctagg atccgctcac 1080

cagggatgtc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctattta 1140

actttaaaca atggaagcca agccgtggga cgttcctcct tctactgtct ggagtatttc 1200

ccatcgcaga tgctgagaac cggcaacaac tttcagttca gctacacctt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agcctggaca ggctgatgaa tcccctcatc 1320

gaccagtacc tgtactacct gtccagaacg caaacgactg gaactnnngg gacgcagact 1380

ctgnnnttca gccaagcggg tcctagctca atggccaacc aggctagaaa ttgggtgccc 1440

ggaccttgct accggcagca gcgcgtctcc acgacaacca accagaacaa caacagcaac 1500

tttgcctgga cgggagctnn naagnnnnnn ctgaacggcc gagactctct aatgaatccg 1560

ggcgtggcaa tggcttccca caaggatgac gaggaccgct tcttcccttc gagcggggtc 1620

ctgatttttg gcaagcaagg agccgggaac gataatgtgg attacagcnn ngtgatgatt 1680

acaaatgagg aagaaatcaa gactaccaac cccgtggcca cagaagaata tggagcagtg 1740

gccaccaacn nncagnnngc caatacgcag gcgcagaccg gactcgtgca caaccagggg 1800

gtgcttcccg gcatggtgtg gcagaataga gacgtgtacc tgcagggtcc catctgggcc 1860

aaaattcctc acacggacgg caactttcac ccgtctcccc tgatgggcgg ctttggactg 1920

aagcacccgc ctcctcaaat tctcatcaag aacacaccgg ttccagcgga cccgccgact 1980

accttcaacc aggccaagct gaactctttc atcacgcagt acagcaccgg acaggtcagc 2040

gtggaaatcg agtgggagct gcagaaagaa aacagcaaac gctggaatcc agagattcaa 2100

tacacttcca actactacaa atctacaaat gtggactttg ctgtcaacac ggagggggtt 2160

tatagcgagc ctcgccccat tggcacccgt tacctcaccc gcaacctgta a 2211

<210> 1777
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1777

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270
```

```
Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
```

```
               485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
               565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
               645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
    690                 695                 700
```

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 1778
<211> 4472
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1778
ctccatcact aggggtaacc gcgaagcgcc tcccacgctg ccgcgtcagc gctgacgtaa 60

attacgtcat aggggagtgg tcctgtatta gctgtcacgt gagtgctttt gcgacatttt 120

gcgacaccac gtggccattc atggtatata tggccgagtg agcgagcagg atctccattt 180

tgaccgcgaa atttgaacga gcagcagcca tgccgggctt ctacgagatc gtgcttaagg 240

tgccgagcga cctggacgag cacctgccgg gcatttctga ctcgtttgtg aactgggtgg 300

cagagaagga atgggagctg cccccggatt ctgacatgga tcggaatctg attgagcagg 360

caccctgac cgtggccgag aagctacagc gcgacttcct ggtccaatgg cgccgcgtga 420

gtaaggcccc ggaggccctc ttctttgttc agttcgagaa gggcgagtcc tacttccacc 480

tccatattct ggtagagacc acgggggtca aatccatggt gctgggccgc ttcctgagtc 540

agattcggga caagctggtg cagaccatct accgcgggat cgagccgacc ctgcccaact 600

ggttcgcggt gacaaagacg cgtaatggcg ccggaggggg gaacaaggtg gtggacgagt 660

gctacatccc caactacctg ctgcccaaga ctcagcccga gctgcagtgg gcgtggacta 720

acatggagga gtatataagc gcgtgcttga acctggccga gcgcaaacgg ctcgtggcgc 780

agcacctgac ccacgtcagc cagacccagg agcagaacaa ggagaatctg aacccgaatt 840

ctgacgcgcc tgtcatccgg tcaaaaacct ccgcgcgcta catggagctg gtcgggtggc 900

tggtggaccg gggcatcacc tccgagaagc agtggatcca ggaggaccag gcctcgtaca 960

tctccttcaa cgccgcctcc aactcgcggt ctcagatcaa ggccgcgctg gacaatgccg 1020

gcaagatcat ggcgctgacc aaatccgcgc ccgactacct ggtaggcccc gctctgcccg 1080

cggacattaa atccaaccgc atctaccgca tcctggagct gaatggctac gaccctgcct 1140

acgccggttc cgtctttctc ggctgggccc agaaaaagtt tggcaaaagg aacaccatct 1200

ggctgtttgg gccggccacc acgggcaaga ccaacatcgc ggaagccatc gcccacgccg 1260

tgcccttcta cggctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg 1320

acaagatggt gatctggtgg gaggagggca agatgacggc caaggtcgtg gagtccgcca 1380

aggccattct cggcggcagc aaggtgcgcg tggaccaaaa gtgcaagtcg tccgcccaga 1440

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<210> 1779
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

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acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 1780
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1780

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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Lys Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
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               245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
               325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
               405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
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Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
```

675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1781
<211> 8376
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat gtggtcacgc 180

tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga ggtttgaacg 240

cgcagccacc acgccggggt tttacgagat tgtgattaag gtccccagcg accttgacgg 300

gcatctgccc ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt 360

gccgccagat tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga 420

gaagctgcag cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct 480

tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac 540

caccggggtg aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat 600

tcagagaatt taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac 660

cagaaatggc gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt 720

gctccccaaa acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag 780

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taccgttcat cgattctctt gtttgctcca gactctcagg caatgacctg atagcctttg 5760

tagagacctc tcaaaaatag ctaccctctc cggcatgaat ttatcagcta gaacggttga 5820

atatcatatt gatggtgatt tgactgtctc cggcctttct cacccgtttg aatctttacc 5880

tacacattac tcaggcattg catttaaaat atatgagggt tctaaaaatt tttatccttg 5940

cgttgaaata aaggcttctc ccgcaaaagt attacagggt cataatgttt ttggtacaac 6000

cgatttagct ttatgctctg aggctttatt gcttaatttt gctaattctt tgccttgcct 6060

gtatgattta ttggatgttg gaattcctga tgcggtattt tctccttacg catctgtgcg 6120

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gccagccccg acacccgcca acacccgctg acgcgccctg acgggcttgt ctgctcccgg 6240

catccgctta cagacaagct gtgaccgtct ccgggagctg catgtgtcag aggttttcac 6300

cgtcatcacc gaaacgcgcg agacgaaagg gcctcgtgat acgcctattt ttataggtta 6360

atgtcatgat aataatggtt tcttagacgt caggtggcac ttttcgggga aatgtgcgcg 6420

gaacccctat ttgtttattt ttctaaatac attcaaatat gtatccgctc atgagacaat 6480

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cgctggtgaa agtaaaagat gctgaagatc agttgggtgc acgagtgggt tacatcgaac 6660

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tgagtgataa cactgcggcc aacttacttc tgacaacgat cggaggaccg aaggagctaa 6960

ccgctttttt gcacaacatg ggggatcatg taactcgcct tgatcgttgg gaaccggagc 7020

tgaatgaagc cataccaaac gacgagcgtg acaccacgat gcctgtagca atggcaacaa 7080

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gcgataagtc gtgtcttacc gggttggact caagacgata gttaccggat aaggcgcagc 7860

ggtcgggctg aacgggggt tcgtgcacac agcccagctt ggagcgaacg acctacaccg 7920

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cggacaggta tccggtaagc ggcagggtcg gaacaggaga gcgcacgagg gagcttccag 8040

ggggaaacgc ctggtatctt tatagtcctg tcgggtttcg ccacctctga cttgagcgtc 8100

gatttttgtg atgctcgtca gggggggcgga gcctatggaa aaacgccagc aacgcggcct 8160

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ctgattctgt ggataaccgt attaccgcct ttgagtgagc tgataccgct cgccgcagcc 8280

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<210> 1782
<211> 1085
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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<222> (611)..(611)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (640)..(640)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1039)..(1039)
<223> n is a, c, g, or t

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gccacttctc accacgtgac tggcagcgac tcattaacaa caactgggga ttccggccca 180

agaaactcag cttcaagctc ttcaacatcc aagttagagg ggtcacgcag aacgatggca 240

cgacgactat tgccaataac cttaccagca cggttcaagt gtttacggac tcggagtatc 300

agctcccgta cgtgctcggg tcggcgcacc aaggctgtct cccgccgttt ccagcggacg 360

tcttcatggt ccctcagtat ggatacctca ccctgaacaa cggaagtcaa gcggtgggac 420

gctcatcctt ttactgcctg gagtacttcc cttcgcagat gctaaggact ggaaataact 480

tccaattcag ctataccttc gaggatgtac cttttcacag cagctacgct cacagccaga 540

gtttggatcg cttgatgaat cctcttattg atcagtatct gtactacctg aacagaacgc 600

aargcamcvc nrgcggaaca rccrvcmhsm rsvvsctgvn gtttagccag gctgggcctc 660

agtctatgtc tttgcaggcc agaaattggc tacctgggcc ctgctaccgg caacagagac 720

tttcaamary cbmcrvcsrs aacaacaaca gtrastttcc ttggmcagcg gccagcamat 780

atcatctcaa tggccgcgac tcgctggtga atccaggacc agctatggcc agtcacrrgg 840

acgatrmsgr saratttttc cctatgcacg gcaatctaat atttggcaaa saarrcrscr 900

vsrvarvcra trycgmsdwc grsvrsgtaa tgattacgga tgaagaagag attcgtacca 960

ccaatcctgt ggcaacagag cagtatggaa ctgtggcaaa taacttgcag rvsvvsmrsr 1020

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atcgt 1085

<210> 1783
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

<220>
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<223> Xaa can be any naturally occurring amino acid

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<222> (462)..(462)
<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<222> (597)..(597)
<223> Xaa can be any naturally occurring amino acid

<400> 1783

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130                 135                 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Xaa Xaa Gly Ala Xaa Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
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            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Xaa Xaa Xaa Xaa Gly Thr Xaa Xaa Xaa Xaa Xaa Leu Xaa Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Xaa Xaa Xaa Xaa Xaa Asn
                485                 490                 495

Asn Asn Ser Xaa Phe Pro Trp Xaa Ala Ala Ser Xaa Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Xaa
        515                 520                 525

Asp Asp Xaa Xaa Xaa Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Met Ile
545                 550                 555                 560
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Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
565 570 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Xaa Xaa Xaa Xaa Xaa Pro Thr
580 585 590

Xaa Xaa Xaa Val Xaa His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
610 615 620

<210> 1784
<211> 1491
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1784
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tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 120

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 180

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 240

agaggggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 300

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 360

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 420

aacaacggaa gtcaagcggt gggacgctca tcctttact gcctggagta cttcccttcg 480

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 540

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 600

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 660

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 720

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 780

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 840

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 900

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 960

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1020

gcaaataact tgcagagctc aaatacagct cccacgactg gaactgtcaa tcatcagggg 1080

gccttacctg gcatggtgtg gcaagatcgt gacgtctacc ttcaaggacc tatctgggca 1140

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1200

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1260

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 1320

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 1380

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 1440

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgtg a 1491

<210> 1785
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1785

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
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Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
20 25 30

Phe Gly Tyr Ser Thr Pro Trp Tyr Phe Asp Phe Asn Arg Phe His Cys
35 40 45

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Asn Asn Asn Trp Gly Phe
50 55 60

Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Arg Gly Val
65 70 75 80

Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr

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                85                  90                  95

Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            100                 105                 110

Ala His Gln Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro
        115                 120                 125

Gln Tyr Gly Tyr Leu Thr Asn Asn Gly Ser Gln Ala Val Gly Arg Ser
    130                 135                 140

Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Gln Met Leu Arg Thr Gly Asn
145                 150                 155                 160

Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp Val Pro His Ser Ser Tyr
                165                 170                 175

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Tyr
            180                 185                 190

Leu Tyr Tyr Leu Asn Arg Thr Gln Gly Thr Thr Ser Gly Thr Thr Asn
        195                 200                 205

Gln Ser Leu Leu Phe Ser Gln Ala Gly Pro Gln Ser Met Ser Leu Gln
    210                 215                 220

Ala Arg Asn Trp Leu Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys
225                 230                 235                 240

Thr Ala Asn Asp Asn Asn Asn Ser Phe Pro Trp Thr Ala Ala Ser Lys
                245                 250                 255

Tyr His Leu Asn Gly Arg Asp Ser Leu Val Asn Gly Pro Ala Met Ala
            260                 265                 270

Ser His Lys Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Leu Ile
        275                 280                 285

Phe Gly Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val
    290                 295                 300
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Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
305                 310                 315                 320

Glu Gln Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala
                325                 330                 335

Pro Thr Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val
            340                 345                 350

Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
        355                 360                 365

Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe
    370                 375                 380

Gly Leu Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val
385                 390                 395                 400

Pro Ala Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe
                405                 410                 415

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
            420                 425                 430

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
        435                 440                 445

Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn
    450                 455                 460

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
465                 470                 475                 480

Asn Leu
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<210> 1786
<211> 1140
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
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<222> (636)..(636)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (665)..(665)
<223> n is a, c, g, or t

<220>
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<222> (1064)..(1064)
<223> n is a, c, g, or t

<400> 1786
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tccagcvvmd caggagctas caacgacaac cactactttg gctacagcac cccttggggg 120

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 180

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 240

agaggggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 300

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 360

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 420

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 480

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 540

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 600

tatctgtact acctgaacag aacgcaargc amcvcnrgcg gaacarccrv cmhsmrsvvs 660

ctgvngttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 720

gggccctgct accggcaaca gagactttca amarycbmcr vcsrsaacaa caacagtras 780

tttccttggm cagcggccag camatatcat ctcaatggcc gcgactcgct ggtgaatcca 840

ggaccagcta tggccagtca crrggacgat rmsgrsarat ttttccctat gcacggcaat 900

ctaatatttg gcaaasaarr crscrvsrva rvcratrycg msdwcgrsvr sgtaatgatt 960

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1020

gcaaataact tgcagrvsvv smrsrvcvvs cccacgdhtv vsrnsgtcvm scatcagggg 1080

gccttacctg gcatggtgtg gcaagatcgt gacgtctacc ttcaaggacc tatctgggca 1140

<210> 1787
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (263)..(264)
<223> Xaa can be any naturally occurring amino acid

<220>
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<220>
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<222> (450)..(453)
<223> Xaa can be any naturally occurring amino acid

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<220>
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<220>
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<400> 1787

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

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65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130                 135                 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Xaa Xaa Gly Ala Xaa Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

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Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Xaa Xaa Xaa Xaa Gly Thr Xaa Xaa Xaa Xaa Xaa Leu Xaa Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Xaa Xaa Xaa Xaa Xaa Asn
                485                 490                 495

Asn Asn Ser Xaa Phe Pro Trp Xaa Ala Ala Ser Xaa Tyr His Leu Asn
```

500 505 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Xaa
515 520 525

Asp Asp Xaa Xaa Xaa Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
530 535 540

Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
565 570 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Xaa Xaa Xaa Xaa Xaa Pro Thr
580 585 590

Xaa Xaa Xaa Val Xaa His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
610 615 620

<210> 1788
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1788

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270
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Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
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                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 1789
<211> 2258
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1789
tcgaggacaa cctctctgag ggcattcgcg agtggtggga cttgaaacct ggagccccga 60

aacccaaagc caaccagcaa aagcaggacg acggccgggg tctggtgctt cctggctaca 120

agtacctcgg acccttcaac ggactcgaca agggggagcc cgtcaacgcg gcggacgcag 180

cggccctcga gcacgacaag gcctacgacc agcagctcaa agcgggtgac aatccgtacc 240

tgcggtataa ccacgccgac gccgagtttc aggagcgtct gcaagaagat acgtcttttg 300

ggggcaacct cgggcgagca gtcttccagg ccaagaagcg ggttctcgaa cctctcggtc 360

tggttgagga aggcgctaag acggctcctg gaaagaagag accggtagag ccatcacccc 420

agcgttctcc agactcctct acgggcatcg gcaagaaagg ccagcagccc gcgaaaaaga 480

gactcaactt tgggcagact ggcgactcag agtcagtgcc cgaccctcaa ccaatcggag 540

aacccccgc aggcccctct ggtctgggat ctggtacaat ggctgcaggc ggtggcgctc 600

caatggcaga caataacgaa ggcgccgacg gagtgggtag ttcctcagga aattggcatt 660

gcgattccac atggctgggc gacagagtca tcaccaccag cacccgaacc tgggccctcc 720

ccacctacaa caaccacctc tacaagcaaa tctccaacgg gacttcggga ggaagcacca 780

acgacaacac ctacttcggc tacagcaccc cctgggggta ttttgacttt aacagattcc 840

actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg ggattccggc 900

ccaagagact caacttcaag ctcttcaaca tccaggtcaa ggaggtcacg cagaatgaag 960

gcaccaagac catcgccaat aaccttacca gcacgattca ggtctttacg gactcggaat 1020

accagctccc gtacgtcctc ggctctgcgc accagggctg cctgcctccg ttcccggcgg 1080

acgtcttcat gattcctcag tacgggtacc tgactctgaa caatggcagt caggccgtgg 1140

gccgttcctc cttctactgc ctggagtact ttccttctca aatgctgaga acgggcaaca 1200

actttgagtt cagctaccag tttgaggacg tgccttttca cagcagctac gcgcacagcc 1260

aaagcctgga ccggctgatg aacccctca tcgaccagta cctgtactac ctgtctcgga 1320

ctcagtccac gggaggtacc gcaggaactc agcagttgct attttctcag gccgggccta 1380

ataacatgtc ggctcaggcc aaaaactggc tacccgggcc ctgctaccgg cagcaacgcg 1440

tctccacgac actgtcgcaa aataacaaca gcaactttgc ctggaccggt gccaccaagt 1500

atcatctgaa tggcagagac tctctggtaa atcccggtgt cgctatggca acccacaagg 1560

acgacgaaga gcgatttttt ccgtccagcg gagtcttaat gtttgggaaa cagggagctg 1620

gaaaagacaa cgtggactat agcagcgtta tgctaaccag tgaggaagaa attaaaacca 1680

ccaacccagt ggccacagaa cagtacggcg tggtggccga taacctgcaa cagcaaaacg 1740

ccgctcctat tgtaggggcc gtcaacagtc aaggagcctt acctggcatg gtctggcaga 1800

accgggacgt gtacctgcag ggtcctatct gggccaagat tcctcacacg gacggaaact 1860

ttcatccctc gccgctgatg ggaggctttg gactgaaaca cccgcctcct cagatcctga 1920

ttaagaatac acctgttccc gcggatcctc caactacctt cagtcaagct aagctggcgt 1980

cgttcatcac gcagtacagc accggacagg tcagcgtgga aattgaatgg gagctgcaga 2040

aagaaaacag caaacgctgg aacccagaga ttcaatacac ttccaactac tacaaatcta 2100

caaatgtgga ctttgctgtt aacacagatg gcacttattc tgagcctcgc cccatcggca 2160

cccgttacct cacccgtaat ctgtaattgc ttgttaatca ataaaccggt tgattcgttt 2220

cagttgaact ttggtctctg cgaagggcga attcgttt 2258

<210> 1790
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1790

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt tcttaagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaattc 1500

tcgtggaccg gtgctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg taccagattc ctgactcgta atctgtaa 2208

<210> 1791
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1791

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

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Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
```

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305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
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His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Trp Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro
            580                 585                 590

Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 1792
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1792
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagcgctt caacgggagc ctcgaacgac aatcactact ttggctacag cacccttgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt taacattcaa 960

gtcaaagagg tcacgcagaa tgacggtacg acgacgattg ccaataacct taccagcacg 1020

gttcaggtgt ttactgactc ggagtaccag ctcccgtacg tcctcggctc ggcgcatcaa 1080

ggatgcctcc cgccgttccc agcagacgtc ttcatggtgc cacagtatgg atacctcacc 1140

ctgaacaacg ggagtcaggc agtaggacgc tcttcatttt actgcctgga gtactttcct 1200

tctcagatgc tgcgtaccgg aaacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacttgag cagaacaaac actccaagtg gaaccaccac gcagtcaagg 1380

cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct 1440

ggaccctgtt accgccagca gcgagtatca aagacatctg cggataacaa caacagtgaa 1500

tactcgtgga ctggagctac caagtaccac ctcaatggca gagactctct ggtgaatccg 1560

ggcccggcca tggcaagcca caaggacgat gaagaaaagt tttttcctca gagcggggtt 1620

ctcatctttg ggaagcaagg ctcagagaaa acaaatgtgg acattgaaaa ggtcatgatt 1680

acagacgaag aggaaatcag gacaaccaat cccgtggcta cggagcagta tggttctgta 1740

tctaccaacc tccagagagg caacagacaa gcagctaccg cagatgtcaa cacacaaggc 1800

gttcttccag gcatggtctg gcaggacaga gatgtgtacc ttcaggggcc catctgggca 1860

aagattccac acacggacgg acattttcac ccctctcccc tcatgggtgg attcggactt 1920

aaacaccctc ctccacagat tctcatcaag aacaccccgg tacctgcgaa tccttcgacc 1980

accttcagtg cggcaaagtt tgcttccttc atcacacagt actccacggg acaggtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaaac gctggaatcc cgaaattcag 2100

tacacttcca actacgccaa gtctgtcaat gtggacttta ctgtggacaa taatggcgtg 2160

tattcagagc ctcgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 1793
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1793
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caggggccag caacgacaac cactacttcg gctacagcac cccctggggg 840

tattttgatt tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaatt ggggattccg gcccaagaga ctcaacttca aactcttcaa catccaagtc 960

aaggaggtca cgacgaatga tggcgtcaca accatcgcta ataaccttac cagcacggtt 1020

caagtcttct cggactcgga gtaccagctt ccgtacgtcc tcggctctgc gcaccagggc 1080

tgcctccctc cgttcccggc ggacgtgttc atgattccgc aatacggcta cctgacgctc 1140

aacaatggca gccaagccgt gggacgttca tccttttact gcctggaata tttcccttct 1200

cagatgctga gaacgggcaa caactttacc ttcagctaca cctttgagga agtgcctttc 1260

cacagcagct acgcgcacag ccagagcctg gaccggctga tgaatcctct catcgaccaa 1320

tacctgtatt acctgaacag aactcaaaat cagtccggaa gtgcccaaaa caaggacttg 1380

ctgtttagcc gtgggtctcc agctggcatg tctgttcagc ccaaaaactg gctacctgga 1440

ccctgttatc ggcagcagcg cgtttctaaa acaaaaacag acaacaacaa cagcaatttt 1500

acctggactg gtgcttcaaa atataacctc aatgggcgtg aatccatcat caaccctggc 1560

actgctatgg cctcacacaa agacgacgaa gacaagttct ttcccatgag cggtgtcatg 1620

atttttggaa aagagagcgc cggagcttca aacactgcat tggacaatgt catgattaca 1680

gacgaagagg aaattaaagc cactaaccct gtggccaccg aaagatttgg gaccgtggca 1740

gtcaatttcc agagcagcag cacagaccct gcgaccggag atgtgcatgc tatgggagca 1800

ttacctggca tggtgtggca agatagagac gtgtacctgc agggtcccat ttgggccaaa 1860

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aacccgcctc ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcggag 1980

ttttcagcta caaagtttgc ttcattcatc acccaatact ccacaggaca agtgagtgtg 2040

gaaattgaat gggagctgca gaaagaaaac agcaagcgct ggaatcccga agtgcagtac 2100

acatccaatt atgcaaaatc tgccaacgtt gattttactg tggacaacaa tggactttat 2160

actgagcctc gccccattgg cacccgttac cttacccgtc ccctgtaa 2208

<210> 1794
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1794
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agtggtggga cttgaaacct ggagccccga aacccaaagc caaccagcaa aagcaggacg 120

acggccgggg tdggtgcttc ctggctacaa gtacctcgga cccttcaacg gactcgacaa 180

gggggagccc gtcaacgcgg cggatgcagc ggccctcgag cacgacaagg cctacgacca 240

gcagctcaaa gcgggtgaca atccgtacct gcggtataac cacgccgacg ccgagtttca 300

ggagcgtctg caagaagata cgtcttttgg gggcaacctc gggcgagcag tcttccaggc 360

caagaagagg gttctcgaac cttttggtdg gttgaggaag gtgctaagac ggctcctgga 420

aagaaacgtc cggtagagca gtcgccacaa gagccagact cctcctcggg cattggcaag 480

acaggccagc agcccgctaa aaagagactc aattttggtc agactggcga ctcagagtca 540

gtccccgacc cacaacctct cggagaacct ccagcaaccc ccgctgctgt gggacctact 600

acaatggctt caggcggtgg cgcaccaatg gcagacaata acgaaggcgc cgacggagtg 660

ggtaatgcct caggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc 720

accagcaccc gaacatgggc cttgcccacc tataacaacc acctctacaa gcaaatctcc 780

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tttgatttca acagattcca ctgccatttc tcaccacgtg actggcagcg actcatcaac 900

aacaattggg gattccggcc caagagactc aacttcaagc tcttcaacat ccaagtcaag 960

gaggtcacga cgaatgatgg cgtcacgacc atcgctaata accttaccag cacggttcaa 1020

gtcttctcgg actcggagta ccagttgccg tacgtcctcg gctctgcgca ccagggctgc 1080

ctccctccgt tcccggcgga cgtgttcatg attccgcagt acggctacct aacgctcaac 1140

aatggcagcc aggcagtggg acggtcatcc ttttactgcc tggaatattt cccatcgcag 1200

atgctgagaa cgggcaataa ctttaccttc agctacacct tcgaggacgt gcctttccac 1260

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ctgtattacc tgaacagaac tcagaatcag tccggaagtg cccaaaacaa ggacttgctg 1380

tttagccggg ggtctccagc tggcatgtct gttcagccca aaaactggct acctggaccc 1440

tgttaccggc agcagcgcgt ttctaaaaca aaaacagaca acaacaacag caactttacc 1500

tggactggtg cttcaaaata taaccttaat gggcgtgaat ctataatcaa ccctggcact 1560

gctatggcct cacacaaaga cgacaaagac aagttctttc ccatgagcgg tgtcatgatt 1620

tttggaaagg agagcgccgg agcttcaaac actgcattgg acaatgtcat gatcacagac 1680

gaagaggaaa tcaaagccac taaccccgtg gccaccgaaa gatttgggac tgtggcagtc 1740

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tcggctacaa agtttgcttc attcatcacc cagtattcca caggacaagt gagcgtggag 2040

attgaatggg agctgcagaa agaaaacagc aaacgctgga atcccgaagt gcagtataca 2100

tctaactatg caaaatctgc caacgttgat ttcactgtgg acaacaatgg actttatact 2160

gagcctcgcc ccattggcac ccgttacctc acccgtcccc tgtaa 2205

<210> 1795
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1795
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

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gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

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cacagcagct acgcgcacag ccagagcctg gaccggctga tgaatcctct catcgaccag 1320

tacctgtatt acctgaacag aactcagaat cagtccggaa gtgcccaaaa caaggacttg 1380

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acctggactg gtgcttcaaa atataacctt aatgggcgtg aatctataat caaccctggc 1560

actgctatgg cctcacacaa agacgacgaa gacaagttct ttcccatgag cggtgtcatg 1620

atttttggaa aggagagcgc cggagcttca aacactgcat tggacaatgt catgatcaca 1680

gacgaagagg aaatcaaagc cactaacccc gtggccaccg aaagatttgg gactgtggca 1740

gtcaatctcc agagcagcag cacagaccct gcgaccggag atgtgcatgt tatgggagcc 1800

ttacctggaa tggtgtggca agacagagac gtatacctgc agggtcctat ttgggccaaa 1860

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cacccgcctc ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcagag 1980

ttttcggcta caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg 2040

gagattgaat gggagctgca gaaagaaaac agcaaacgct ggaatcccga agtgcagtat 2100

acatctaact atgcaaaatc tgccaacgtt gatttcactg tggacaacaa tggactttat 2160

actgagcctc gccccattgg cacccgttac ctcacccgtc ccctgtaa 2208

<210> 1796
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1796
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

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cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctg tggccggacc cagtaacatg gctgtccagg gaaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaattt 1500

gcttggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agcaacagaa cacagcacca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

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caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 1797
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1797

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
```

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    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
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Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Val
    450                 455                 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Gln Gln Asn Thr Ala Pro Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
```

645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1798
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1798
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aagtcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

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tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

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cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgat gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg ataacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtatt ttcctcagag cggggttctc 1620

atctttggga agcaagactc aggaaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

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acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 1799

<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1799
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aagtcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgat gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg ataacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtatt ttcctcagag cggggttctc 1620

atctttggga agcaagactc aggaaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 1800
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1800

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
```

```
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
```

705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1801
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1801

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly

```
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Phe Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
```

580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1802
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1802

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro

```
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
```

```
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Ala Ala Ala Gly Ser
            580                 585                 590

Thr Pro Pro Pro Met Ala Ala Arg Gln Ala Ala Thr Ala Asp Val Asn
        595                 600                 605

Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr
    610                 615                 620

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe
625                 630                 635                 640

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
                645                 650                 655

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr
            660                 665                 670
```

Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
675 680 685

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
690 695 700

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val
705 710 715 720

Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg
725 730 735

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
740 745

<210> 1803
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1803

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
```

```
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
```

```
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Ala Ala Ala Gly Glu
            580                 585                 590

Thr Arg Ala Pro Leu Ala Ala Arg Gln Ala Ala Thr Ala Asp Val Asn
        595                 600                 605

Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr
    610                 615                 620

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe
625                 630                 635                 640

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
                645                 650                 655

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr
            660                 665                 670

Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
        675                 680                 685

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
    690                 695                 700

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val
705                 710                 715                 720

Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg
                725                 730                 735

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

740 745

<210> 1804
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1804

Ala Gln Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1805
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1805

Ala Gln Ser Val Ser Lys Pro Phe Leu Ala Gln
1 5 10

<210> 1806
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1806

Ala Gln Phe Thr Leu Thr Thr Pro Lys Ala Gln
1 5 10

<210> 1807
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1807

Asp Gly Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1808
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1808

Glu Ser Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1809
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1809

Gly Gly Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1810
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1810

Ala Gln Thr Leu Ala Thr Pro Phe Lys Ala Gln
1 5 10

<210> 1811
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1811

Ala Thr Thr Leu Ala Thr Pro Phe Lys Ala Gln
1 5 10

<210> 1812
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1812

Asp Gly Thr Leu Ala Thr Pro Phe Lys Ala Gln
1 5 10

<210> 1813
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1813

Gly Gly Thr Leu Ala Thr Pro Phe Lys Ala Gln
1 5 10

<210> 1814
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1814

Ser Gly Ser Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1815
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1815

Ala Gln Thr Leu Ala Gln Pro Phe Lys Ala Gln
1   5   10

<210> 1816
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1816

Ala Gln Thr Leu Gln Gln Pro Phe Lys Ala Gln
1   5   10

<210> 1817
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1817

Ala Gln Thr Leu Ser Asn Pro Phe Lys Ala Gln
1   5   10

<210> 1818
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1818

Ala Gln Thr Leu Ala Val Pro Phe Ser Asn Pro
1   5   10

<210> 1819
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1819

Gln Gly Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1820
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1820

Asn Gln Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1821
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1821

Glu Gly Ser Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1822
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1822

Ser Gly Asn Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1823

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1823

Glu Gly Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1824
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1824

Asp Ser Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1825
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1825

Ala Val Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1826
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1826

Ala Gln Thr Leu Ser Thr Pro Phe Lys Ala Gln
1 5 10

<210> 1827
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1827

Ala Gln Thr Leu Pro Gln Pro Phe Lys Ala Gln
1   5   10

<210> 1828
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1828

Ala Gln Thr Leu Ser Gln Pro Phe Lys Ala Gln
1   5   10

<210> 1829
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1829

Ala Gln Thr Leu Gln Leu Pro Phe Lys Ala Gln
1   5   10

<210> 1830
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1830

Ala Gln Thr Leu Thr Met Pro Phe Lys Ala Gln

1 5 10

<210> 1831
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1831

Ala Gln Thr Leu Thr Thr Pro Phe Lys Ala Gln
1 5 10

<210> 1832
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1832

Ala Gln Tyr Thr Leu Ser Gln Gly Trp Ala Gln
1 5 10

<210> 1833
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1833

Ala Gln Met Asn Ala Thr Lys Asn Val Ala Gln
1 5 10

<210> 1834
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1834

Ala Gln Val Ser Gly Gly His His Ser Ala Gln
1 5 10

<210> 1835
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1835

Ala Gln Thr Leu Thr Ala Pro Phe Lys Ala Gln
1 5 10

<210> 1836
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1836

Ala Gln Thr Leu Ser Lys Pro Phe Lys Ala Gln
1 5 10

<210> 1837
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1837

Gln Ala Val Arg Thr Ser Leu
1 5

<210> 1838
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1838

Leu Ala Lys Glu Arg Leu Ser
1 5

<210> 1839
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1839

Met Asn Ser Thr Lys Asn Val
1 5

<210> 1840
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1840

Val Ser Gly Gly His His Ser
1 5

<210> 1841
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1841

Ser Ala Gln Thr Leu Ala Val Pro Phe Lys Ala Gln Ala Gln
1 5 10

<210> 1842
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (2)..(4)
<223> Xaa can be any naturally occurring amino acid

<400> 1842

Ser Xaa Xaa Xaa Leu Ala Val Pro Phe Lys Ala Gln Ala Gln
1   5   10

<210> 1843
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (4)..(6)
<223> Xaa can be any naturally occurring amino acid

<400> 1843

Ser Ala Gln Xaa Xaa Xaa Val Pro Phe Lys Ala Gln Ala Gln
1   5   10

<210> 1844
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (6)..(8)
<223> Xaa can be any naturally occurring amino acid

<400> 1844

Ser Ala Gln Thr Leu Xaa Xaa Xaa Phe Lys Ala Gln Ala Gln
1   5   10

<210> 1845
<211> 14
<212> PRT
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<220>
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<220>
<221> misc_feature
<222> (8)..(10)
<223> Xaa can be any naturally occurring amino acid

<400> 1845

Ser Ala Gln Thr Leu Ala Val Xaa Xaa Xaa Ala Gln Ala Gln
1 5 10

<210> 1846
<211> 14
<212> PRT
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<220>
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<220>
<221> misc_feature
<222> (10)..(12)
<223> Xaa can be any naturally occurring amino acid

<400> 1846

Ser Ala Gln Thr Leu Ala Val Pro Phe Xaa Xaa Xaa Ala Gln
1 5 10

<210> 1847
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1847

Thr Asn His Gln Ser Ala Gln
1 5

<210> 1848
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1848

Ala Gln Ala Gln Thr Gly Trp
1   5

<210> 1849
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1849

Asp Gly Thr Leu Ala Thr Pro Phe Lys
1   5

<210> 1850
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (10)..(11)
<223> Xaa can be any naturally occurring amino acid

<400> 1850

Asp Gly Thr Leu Ala Thr Pro Phe Lys Xaa Xaa
1   5   10

<210> 1851
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1851

Leu Ala Val Pro Phe Lys Ala Gln
1   5

<210> 1852
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1852

Val Pro Phe Lys Ala Gln
1   5

<210> 1853
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1853

Phe Lys Ala Gln
1

<210> 1854
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1854

Ala Gln Thr Leu Ala Val
1   5

<210> 1855
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1855

Ala Gln Thr Leu Ala Val Pro Phe
1 5

<210> 1856
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1856

Gln Ala Val Arg
1

<210> 1857
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1857

Ala Val Arg Thr
1

<210> 1858
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1858

Val Arg Thr Ser
1

<210> 1859

<211> 4
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1859

Arg Thr Ser Leu
1

<210> 1860
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1860

Gln Ala Val Arg Thr
1 5

<210> 1861
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1861

Ala Val Arg Thr Ser
1 5

<210> 1862
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1862

Val Arg Thr Ser Leu
1 5

<210> 1863
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1863

Gln Ala Val Arg Thr Ser
1 5

<210> 1864
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1864

Ala Val Arg Thr Ser Leu
1 5

<210> 1865
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1865
gatgggactt tggcggtgcc ttttaaggca cag 33

<210> 1866
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1866
gatgggacgt tggcggtgcc ttttaaggca cag 33

<210> 1867

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1867
caggcggtta ggacgtcttt g 21

<210> 1868
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1868
caggtcttca cggactcaga ctatcag 27

<210> 1869
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1869
caagtaaaac ctctacaaat gtggtaaaat cg 32

<210> 1870
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1870
actcatcgac caatacttgt actatctctc tagaac 36

<210> 1871
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1871
ggaagtattc cttggttttg aaccca 26

<210> 1872
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1872
ggtcgcggtt cttgtttgtg gat 23

<210> 1873
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1873
cgaccttgaa gcgcatgaac tcct 24

<210> 1874
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> misc_feature
<222> (42)..(43)
<223> n is a, c, g, or t

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<222> (45)..(46)
<223> n is a, c, g, or t

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<221> misc_feature
<222> (48)..(49)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (51)..(52)
<223> n is a, c, g, or t

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<222> (54)..(55)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (57)..(58)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (60)..(61)
<223> n is a, c, g, or t

<400> 1874
gtattccttg gttttgaacc caaccggtct gcgcctgtgc mnnmnnmnnm nnmnnmnnmn 60

nttgggcact ctggtggttt gtc 83

<210> 1875
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
<222> (36)..(37)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (39)..(40)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (42)..(43)
<223> n is a, c, g, or t

<400> 1875
gtattccttg gttttgaacc caaccggtct gcgcmnnmnn mnnaaaaggc accgccaaag 60

tttg 64

<210> 1876
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
<222> (42)..(43)
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<220>
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<222> (45)..(46)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (48)..(49)
<223> n is a, c, g, or t

<400> 1876
gtattccttg gttttgaacc caaccggtct gcgcctgtgc mnnmnnmnnc accgccaaag 60

tttgggcact 70

<210> 1877
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (48)..(49)
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<223> n is a, c, g, or t

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<222> (54)..(55)
<223> n is a, c, g, or t

<400> 1877
gtattccttg gttttgaacc caaccggtct gcgcctgtgc cttaaamnnm nnmnncaaag 60

tttgggcact ctggtgg 77

<210> 1878
<211> 83
<212> DNA
<213> Artificial Sequence

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<221> misc_feature
<222> (60)..(61)
<223> n is a, c, g, or t

<400> 1878
gtattccttg gttttgaacc caaccggtct gcgcctgtgc cttaaaaggc acmnnmnnmn 60

nttgggcact ctggtggttt gtg 83

<210> 1879
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1879
cttgcgaagg agcggctttc g 21

<210> 1880
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1880

Val Asn Leu Thr Trp Ser Arg Ala Ser Gly
1   5   10

<210> 1881
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1881

Glu Phe Cys Ile Asn His Arg Gly Tyr Trp Val Cys Gly Asp
1   5   10

<210> 1882
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1882

Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser
1   5   10

<210> 1883
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1883

Glu Lys Gln Arg Asn Gly Thr Leu Thr
1   5

<210> 1884
<211> 17
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1884

Thr Tyr Gln Cys Arg Val Thr His Pro His Leu Pro Arg Ala Leu Met
1 5 10 15

Arg

<210> 1885
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1885

Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly
1 5 10

<210> 1886
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1886

Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg
1 5 10

<210> 1887
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1887

Thr Ile Thr Cys Leu Trp Asp Leu Ala Pro Ser Lys

1 5 10

<210> 1888
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1888

Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
1 5 10

<210> 1889
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1889

Thr His Pro His Leu Pro Arg Ala Leu Met Arg Ser
1 5 10

<210> 1890
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1890

Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His Leu Pro Arg Ala
1 5 10 15

Leu Met Arg Ser Thr Thr Lys
20

<210> 1891
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1891

Leu Pro Arg Ala Leu Met Arg Ser
1   5

<210> 1892
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1892

Ile Asn His Arg Gly Tyr Trp Val
1   5

<210> 1893
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1893

Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp
1   5   10

<210> 1894
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1894

Ala Lys Ala Val Ser Asn Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln
1   5   10   15

Ser

<210> 1895
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1895

Ser Leu Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr
1   5   10

<210> 1896
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1896

Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp
1   5   10

<210> 1897
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1897

Ile Asn Pro Glu Ile Ile Thr Leu Asp Gly
1   5   10

<210> 1898
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1898

Asp Ile Ser Val Thr Gly Ala Pro Val Ile Thr Ala Thr Tyr Leu

1 5 10 15

<210> 1899
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1899

Asp Ile Ser Val Thr Gly Ala Pro Val Ile Thr Ala
1 5 10

<210> 1900
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1900

Pro Lys Thr Val Ser Asn Leu Thr Glu Ser Ser Ser Glu Ser Val Gln
1 5 10 15

Ser

<210> 1901
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1901

Ser Leu Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr
1 5 10

<210> 1902
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1902

Gln His Ser Val Ala Tyr Thr Phe Glu Glu Asp
1   5   10

<210> 1903
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1903

Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly
1   5   10

<210> 1904
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1904

Asp Ile Ser Leu Thr Gly Asp Pro Val Ile Thr Ala Ser Tyr Leu
1   5   10   15

<210> 1905
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1905

Asp Ile Ser Leu Thr Gly Asp Pro Val Ile Thr Ala
1   5   10

<210> 1906
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1906

Asp Gln Ser Ile Asp Phe Glu Ile Asp Ser Ala
1 5 10

<210> 1907
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1907

Lys Asn Val Ser Glu Asp Leu Pro Leu Pro Thr Phe Ser Pro Thr Leu
1 5 10 15

Leu Gly Asp Ser
20

<210> 1908
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1908

Lys Asn Val Ser Glu Asp Leu Pro Leu Pro Thr
1 5 10

<210> 1909
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1909

Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp

1 5 10

<210> 1910
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1910

Phe Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
1 5 10

<210> 1911
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1911

Asp Ala Glu Phe Arg His Asp Ser Gly
1 5

<210> 1912
<211> 16
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1912

His Tyr Ala Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu
1 5 10 15

<210> 1913
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1913

Tyr Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln
1 5 10

<210> 1914
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1914

Arg Ser Gln Lys Glu Gly Leu His Tyr Thr
1 5 10

<210> 1915
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1915

Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Trp Ala Asn Pro
1 5 10 15

Gln Ala Glu

<210> 1916
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1916

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Trp Ala Asn Pro
1 5 10 15

<210> 1917
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1917

Ser Ser Arg Thr Pro Ser Asp Lys Pro
1 5

<210> 1918
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1918

Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro
1 5 10

<210> 1919
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1919

Asp Gly Asn Val Asp Tyr His Met Asn Ser Val
1 5 10

<210> 1920
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1920

Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln
1 5 10 15

<210> 1921

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1921

Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala
1 5 10

<210> 1922
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1922

Gln Met Trp Ala Pro Gln Trp Gly Pro Asp
1 5 10

<210> 1923
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1923

Arg Gly Asn Arg Gln Ala
1 5

<210> 1924
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1924

Ser Ser Ser Thr Asp Pro
1 5

<210> 1925
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1925

Ser Ser Asn Thr Ala Pro
1   5

<210> 1926
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1926

Ser Asn Ser Asn Leu Pro
1   5

<210> 1927
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1927

Ser Ser Thr Thr Ala Pro
1   5

<210> 1928
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1928

Ala Ala Asn Thr Ala Ala

1 5

<210> 1929
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1929

Gln Gln Asn Thr Ala Pro
1 5

<210> 1930
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1930

Ser Ala Gln Ala Gln Ala
1 5

<210> 1931
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1931

Gln Ala Asn Thr Gly Pro
1 5

<210> 1932
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1932

Asn Ala Thr Thr Ala Pro
1 5

<210> 1933
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1933

Ser Ser Thr Ala Gly Pro
1 5

<210> 1934
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1934

Gln Gln Asn Thr Ala Ala
1 5

<210> 1935
<211> 6
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1935

Pro Ser Thr Ala Gly Pro
1 5

<210> 1936
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1936

Asn Gln Asn Thr Ala Pro
1 5

<210> 1937
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<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1937

Gln Ala Ala Asn Ala Pro
1 5

<210> 1938
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1938

Ser Ile Val Gly Leu Pro
1 5

<210> 1939
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1939

Ala Ala Ser Thr Ala Ala
1 5

<210> 1940
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1940

Ser Gln Asn Thr Thr Ala
1   5

<210> 1941
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1941

Gln Gln Asp Thr Ala Pro
1   5

<210> 1942
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1942

Gln Thr Asn Thr Gly Pro
1   5

<210> 1943
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1943

Gln Thr Asn Gly Ala Pro
1   5

<210> 1944
<211> 6
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1944

Gln Gln Asn Ala Ala Pro
1 5

<210> 1945
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1945

Ala Ala Asn Thr Gln Ala
1 5

<210> 1946
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1946

Asn Gly Arg Ala His Ala
1 5

<210> 1947
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1947

Gln Pro Glu His Ser Ser Thr
1 5

<210> 1948

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1948

Val Asn Thr Ala Asn Ser Thr
1 5

<210> 1949
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1949

His Gly Pro Met Gln Lys Ser
1 5

<210> 1950
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1950

Pro His Lys Pro Pro Leu Ala
1 5

<210> 1951
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1951

Ile Lys Asn Asn Glu Met Trp
1 5

<210> 1952
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1952

Arg Asn Leu Asp Thr Pro Met
1   5

<210> 1953
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1953

Val Asp Ser His Arg Gln Ser
1   5

<210> 1954
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1954

Tyr Asp Ser Lys Thr Lys Thr
1   5

<210> 1955
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1955

Ser Gln Leu Pro His Gln Lys

1 5

<210> 1956
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1956

Ser Thr Met Gln Gln Asn Thr
1 5

<210> 1957
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1957

Thr Glu Arg Tyr Met Thr Gln
1 5

<210> 1958
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1958

Asp Ala Ser Leu Ser Thr Ser
1 5

<210> 1959
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1959

Asp Leu Pro Asn Lys Lys Thr
1   5

<210> 1960
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1960

Asp Leu Thr Ala Ala Arg Leu
1   5

<210> 1961
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1961

Glu Pro His Gln Phe Asn Tyr
1   5

<210> 1962
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1962

Glu Pro Gln Ser Asn His Thr
1   5

<210> 1963
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1963

Met Ser Ser Trp Pro Ser Gln
1 5

<210> 1964
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1964

Asn Pro Lys His Asn Ala Thr
1 5

<210> 1965
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1965

Pro Asp Gly Met Arg Thr Thr
1 5

<210> 1966
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1966

Pro Asn Asn Asn Lys Thr Thr
1 5

<210> 1967
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1967

Gln Ser Thr Thr His Asp Ser
1   5

<210> 1968
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1968

Thr Gly Ser Lys Gln Lys Gln
1   5

<210> 1969
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1969

Ser Leu Lys His Gln Ala Leu
1   5

<210> 1970
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1970

Ser Pro Ile Asp Gly Glu Gln
1   5

<210> 1971
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
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<400> 1971

Trp Ile Phe Pro Trp Ile Gln Leu
1 5

<210> 1972
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1972

Cys Asp Cys Arg Gly Asp Cys Phe Cys
1 5

<210> 1973
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1973

Cys Asn Gly Arg Cys
1 5

<210> 1974
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1974

Cys Pro Arg Glu Cys Glu Ser
1 5

<210> 1975

<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1975

Cys Thr Thr His Trp Gly Phe Thr Leu Cys
1 5 10

<210> 1976
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1976

Cys Gly Arg Arg Ala Gly Gly Ser Cys
1 5

<210> 1977
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1977

Cys Lys Gly Gly Arg Ala Lys Asp Cys
1 5

<210> 1978
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1978

Cys Val Pro Glu Leu Gly His Glu Cys
1 5

<210> 1979
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1979

Cys Arg Arg Glu Thr Ala Trp Ala Lys
1   5

<210> 1980
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1980

Val Ser Trp Phe Ser His Arg Tyr Ser Pro Phe Ala Val Ser
1   5   10

<210> 1981
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1981

Gly Tyr Arg Asp Gly Tyr Ala Gly Pro Ile Leu Tyr Asn
1   5   10

<210> 1982
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature

<222> (1)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (5)..(7)
<223> Xaa can be any naturally occurring amino acid

<400> 1982

Xaa Xaa Xaa Tyr Xaa Xaa Xaa
1 5

<210> 1983
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa is Glu or Met

<400> 1983

Tyr Xaa Asn Trp
1

<210> 1984
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1984

Arg Pro Leu Pro Pro Leu Pro
1 5

<210> 1985
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1985

Ala Pro Pro Leu Pro Pro Arg
1   5

<210> 1986
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1986

Asp Val Phe Tyr Pro Tyr Pro Tyr Ala Ser Gly Ser
1   5   10

<210> 1987
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1987

Met Tyr Trp Tyr Pro Tyr
1   5

<210> 1988
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1988

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys
1   5   10

<210> 1989
<211> 8
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa is Gly or Leu

<400> 1989

Cys Trp Asp Asp Xaa Trp Leu Cys
1   5

<210> 1990
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1990

Glu Trp Cys Glu Tyr Leu Gly Gly Tyr Leu Arg Cys Tyr Ala
1   5   10

<210> 1991
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (4)..(5)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (8)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (11)..(11)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (13)..(13)
<223> Xaa can be any naturally occurring amino acid

<400> 1991

Tyr Xaa Cys Xaa Xaa Gly Pro Xaa Thr Trp Xaa Cys Xaa Pro
1   5   10

<210> 1992
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1992

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1   5   10

<210> 1993
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (3)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa is Tyr, Trp, Phe, or His

<400> 1993

Leu Trp Xaa Xaa Xaa
1   5

<210> 1994
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (3)..(4)
<223> Xaa can be any naturally occurring amino acid

<400> 1994

Xaa Phe Xaa Xaa Tyr Leu Trp
1   5

<210> 1995
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1995

Ser Ser Ile Ile Ser His Phe Arg Trp Gly Leu Cys Asp
1   5   10

<210> 1996
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1996

Met Ser Arg Pro Ala Cys Pro Pro Asn Asp Lys Tyr Glu
1   5   10

<210> 1997
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1997

Cys Leu Arg Ser Gly Arg Gly Cys
1 5

<210> 1998
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1998

Cys His Trp Met Phe Ser Pro Trp Cys
1 5

<210> 1999
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (2)..(3)
<223> Xaa can be any naturally occurring amino acid

<400> 1999

Trp Xaa Xaa Phe
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<210> 2000
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2000

Cys Ser Ser Arg Leu Asp Ala Cys
1   5

<210> 2001
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2001

Cys Leu Pro Val Ala Ser Cys
1   5

<210> 2002
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2002

Cys Gly Phe Glu Cys Val Arg Gln Cys Pro Glu Arg Cys
1   5   10

<210> 2003
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2003

Cys Val Ala Leu Cys Arg Glu Ala Cys Gly Glu Gly Cys
1   5   10

<210> 2004
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2004

Ser Trp Cys Glu Pro Gly Trp Cys Arg
1   5

<210> 2005
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2005

Tyr Ser Gly Lys Trp Gly Trp
1   5

<210> 2006
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2006

Gly Leu Ser Gly Gly Arg Ser
1   5

<210> 2007
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2007

Leu Met Leu Pro Arg Ala Asp
1   5

<210> 2008
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2008

Cys Ser Cys Phe Arg Asp Val Cys Cys
1 5

<210> 2009
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2009

Cys Arg Asp Val Val Ser Val Ile Cys
1 5

<210> 2010
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2010

Met Ala Arg Ser Gly Leu
1 5

<210> 2011
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2011

Met Ala Arg Ala Lys Glu
1 5

<210> 2012
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2012

Met Ser Arg Thr Met Ser
1 5

<210> 2013
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2013

Lys Cys Cys Tyr Ser Leu
1 5

<210> 2014
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2014

Met Tyr Trp Gly Asp Ser His Trp Leu Gln Tyr Trp Tyr Glu
1 5 10

<210> 2015
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2015

Met Gln Leu Pro Leu Ala Thr
1 5

<210> 2016
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2016

Glu Trp Leu Ser
1

<210> 2017
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2017

Ser Asn Glu Trp
1

<210> 2018
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2018

Thr Asn Tyr Leu
1

<210> 2019
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2019

Trp Asp Leu Ala Trp Met Phe Arg Leu Pro Val Gly
1   5   10

<210> 2020
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2020

Cys Thr Val Ala Leu Pro Gly Gly Tyr Val Arg Val Cys
1   5   10

<210> 2021
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2021

Cys Val Ala Tyr Cys Ile Glu His His Cys Trp Thr Cys
1   5   10

<210> 2022
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2022

Cys Val Phe Ala His Asn Tyr Asp Tyr Leu Val Cys
1   5   10

<210> 2023
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2023

Cys Val Phe Thr Ser Asn Tyr Ala Phe Cys
1 5 10

<210> 2024
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2024

Val His Ser Pro Asn Lys Lys
1 5

<210> 2025
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2025

Cys Arg Gly Asp Gly Trp Cys
1 5

<210> 2026
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
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<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<400> 2026

Xaa Arg Gly Cys Asp Xaa
1 5

<210> 2027
<211> 4
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (2)..(4)
<223> Xaa can be any naturally occurring amino acid

<400> 2027

Pro Xaa Xaa Xaa
1

<210> 2028
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2028

Ser Gly Lys Gly Pro Arg Gln Ile Thr Ala Leu
1 5 10

<210> 2029
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa is Ala or Gln

<220>

<221> misc_feature
<222> (11)..(11)
<223> Xaa is Asn or Ala

<220>
<221> misc_feature
<222> (12)..(14)
<223> Xaa can be any naturally occurring amino acid

<400> 2029

Ala Ala Ala Ala Ala Ala Ala Ala Ala Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 2030
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2030

Val Tyr Met Ser Pro Phe
1 5

<210> 2031
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2031

Ala Thr Trp Leu Pro Pro Arg
1 5

<210> 2032
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2032

His Thr Met Tyr Tyr His His Tyr Gln His His Leu

1 5 10

<210> 2033
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2033

Ser Glu Val Gly Cys Arg Ala Gly Pro Leu Gln Trp Leu Cys Glu Lys
1 5 10 15

Tyr Phe Gly

<210> 2034
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2034

Cys Gly Leu Leu Pro Val Gly Arg Pro Asp Arg Asn Val Trp Arg Trp
1 5 10 15

Leu Cys

<210> 2035
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2035

Cys Lys Gly Gln Cys Asp Arg Phe Lys Gly Leu Pro Trp Glu Cys
1 5 10 15

<210> 2036

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2036

Ser Gly Arg Ser Ala
1 5

<210> 2037
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2037

Trp Gly Phe Pro
1

<210> 2038
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2038

Ala Glu Pro Met Pro His Ser Leu Asn Phe Ser Gln Tyr Leu Trp Tyr
1 5 10 15

Thr

<210> 2039
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
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<222> (4)..(4)
<223> Xaa is Trp or Phe

<400> 2039

Trp Ala Tyr Xaa Ser Pro
1 5

<210> 2040
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2040

Ile Glu Leu Leu Gln Ala Arg
1 5

<210> 2041
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2041

Ala Tyr Thr Lys Cys Ser Arg Gln Trp Arg Thr Cys Met Thr Thr His
1 5 10 15

<210> 2042
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2042

Pro Gln Asn Ser Lys Ile Pro Gly Pro Thr Phe Leu Asp Pro His
1 5 10 15

<210> 2043

<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2043

Ser Met Glu Pro Ala Leu Pro Asp Trp Trp Trp Lys Met Phe Lys
1 5 10 15

<210> 2044
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2044

Ala Asn Thr Pro Cys Gly Pro Tyr Thr His Asp Cys Pro Val Lys Arg
1 5 10 15

<210> 2045
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2045

Thr Ala Cys His Gln His Val Arg Met Val Arg Pro
1 5 10

<210> 2046
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2046

Val Pro Trp Met Glu Pro Ala Tyr Gln Arg Phe Leu
1 5 10

<210> 2047
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2047

Asp Pro Arg Ala Thr Pro Gly Ser
1 5

<210> 2048
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2048

Phe Arg Pro Asn Arg Ala Gln Asp Tyr Asn Thr Asn
1 5 10

<210> 2049
<211> 9
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2049

Cys Thr Lys Asn Ser Tyr Leu Met Cys
1 5

<210> 2050
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
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<222> (2)..(2)
<223> Xaa is Gln or Arg

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa is Leu or Arg

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa is Gly or Asn

<220>
<221> misc_feature
<222> (6)..(7)
<223> Xaa is any amino acid residue

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa iis Ala or Val

<400> 2050

Cys Xaa Xaa Thr Xaa Xaa Xaa Gly Xaa Gly Cys
1 5 10

<210> 2051
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2051

Cys Pro Ile Glu Asp Arg Pro Met Cys
1 5

<210> 2052
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2052

His Glu Trp Ser Tyr Leu Ala Pro Tyr Pro Trp Phe

1 5 10

<210> 2053
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2053

Met Cys Pro Lys His Pro Leu Gly Cys
1 5

<210> 2054
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2054

Arg Met Trp Pro Ser Ser Thr Val Asn Leu Ser Ala Gly Arg Arg
1 5 10 15

<210> 2055
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2055

Ser Ala Lys Thr Ala Val Ser Gln Arg Val Trp Leu Pro Ser His Arg
1 5 10 15

Gly Gly Glu Pro
20

<210> 2056
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2056

Lys Ser Arg Glu His Val Asn Asn Ser Ala Cys Pro Ser Lys Arg Ile
1   5   10   15

Thr Ala Ala Leu
            20

<210> 2057
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2057

Glu Gly Phe Arg
1

<210> 2058
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2058

Ala Gly Leu Gly Val Arg
1   5

<210> 2059
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2059

Gly Thr Arg Gln Gly His Thr Met Arg Leu Gly Val Ser Asp Gly
1   5   10   15

<210> 2060
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2060

Ile Ala Gly Leu Ala Thr Pro Gly Trp Ser His Trp Leu Ala Leu
1   5   10   15

<210> 2061
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2061

Ser Met Ser Ile Ala Arg Leu
1   5

<210> 2062
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2062

His Thr Phe Glu Pro Gly Val
1   5

<210> 2063
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2063

Asn Thr Ser Leu Lys Arg Ile Ser Asn Lys Arg Ile Arg Arg Lys

1 5 10 15

<210> 2064
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2064

Leu Arg Ile Lys Arg Lys Arg Arg Lys Arg Lys Lys Thr Arg Lys
1 5 10 15

<210> 2065
<211> 21
<212> DNA
<213> adeno-associated virus 2

<220>
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<222> (3)..(3)
<223> n is a, c, g, or t

<220>
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<222> (4)..(5)
<223> n is a, c or g

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a or c

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, g, or t

<220>
<221> misc_feature
<222> (13)..(13)
<223> n is a or g

<220>
<221> misc_feature
<222> (14)..(14)
<223> n is g or c

<220>

<221> misc_feature
<222> (17)..(17)
<223> n is g or c

<400> 2065
agnnnnncag ganncancaa c 21

<210> 2066
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2066

Ser Asp Ser Gly Ala Ser Asn
1 5

<210> 2067
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2067

Ser Pro Ser Gly Ala Ser Asn
1 5

<210> 2068
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2068

Ser His Ser Gly Ala Ser Asn
1 5

<210> 2069
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2069

Ser Arg Ser Gly Ala Ser Asn
1   5

<210> 2070
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2070

Ser Lys Ser Gly Ala Ser Asn
1   5

<210> 2071
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2071

Ser Asn Ser Gly Ala Ser Asn
1   5

<210> 2072
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2072

Ser Gly Ser Gly Ala Ser Asn
1   5

<210> 2073
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2073

Ser Ala Ser Gly Ala Ser Asn
1   5

<210> 2074
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2074

Ser Glu Ser Gly Thr Ser Asn
1   5

<210> 2075
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2075

Ser Thr Thr Gly Gly Ser Asn
1   5

<210> 2076
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2076

Ser Ser Ala Gly Ser Thr Asn
1   5

<210> 2077
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2077

Asn Asn Asp Ser Gln Ala
1 5

<210> 2078
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2078

Asn Asn Arg Asn Gln Ala
1 5

<210> 2079
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2079

Asn Asn Asn Lys Gln Ala
1 5

<210> 2080
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2080

Asn Ala Lys Arg Gln Ala
1 5

<210> 2081
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2081

Asn Asp Glu His Gln Ala
1 5

<210> 2082
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2082

Asn Thr Ser Gln Lys Ala
1 5

<210> 2083
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2083

Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Asp Thr Gln Ser
1 5 10 15

Arg Leu Val Phe Ser Gln Ala Gly Ala
20 25

<210> 2084
<211> 25
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2084

Tyr Tyr Leu Ser Arg Thr Asn Thr Asp Ser Gly Thr Glu Thr Gln Ser
1 5 10 15

Gly Leu Asp Phe Ser Gln Ala Gly Ala
20 25

<210> 2085
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2085

Tyr Tyr Leu Ser Arg Thr Asn Thr Glu Ser Gly Thr Pro Thr Gln Ser
1 5 10 15

Ala Leu Glu Phe Ser Gln Ala Gly Ala
20 25

<210> 2086
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2086

Tyr Tyr Leu Ser Arg Thr Asn Thr His Ser Gly Thr His Thr Gln Ser
1 5 10 15

Pro Leu His Phe Ser Gln Ala Gly Ala
20 25

<210> 2087
<211> 25
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2087

Tyr Tyr Leu Ser Arg Thr Asn Thr Ser Ser Gly Thr Ile Thr Ile Ser
1 5 10 15

His Leu Ile Phe Ser Gln Ala Gly Ala
20 25

<210> 2088
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2088

Tyr Tyr Leu Ser Arg Thr Asn Thr Arg Ser Gly Ile Met Thr Lys Ser
1 5 10 15

Ser Leu Met Phe Ser Gln Ala Gly Ala
20 25

<210> 2089
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2089

Tyr Tyr Leu Ser Arg Thr Asn Thr Lys Ser Gly Arg Lys Thr Leu Ser
1 5 10 15

Asn Leu Ser Phe Ser Gln Ala Gly Ala
20 25

<210> 2090
<211> 25
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2090

Tyr Tyr Leu Ser Arg Thr Asn Asp Gly Ser Gly Pro Val Thr Pro Ser
1   5   10   15

Lys Leu Arg Phe Ser Gln Arg Gly Ala
            20   25

<210> 2091
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2091

Tyr Tyr Leu Ser Arg Thr Asn Ala Ala Ser Gly His Ala Thr His Ser
1   5   10   15

Asp Leu Lys Phe Ser Gln Pro Gly Ala
            20   25

<210> 2092
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2092

Tyr Tyr Leu Ser Arg Thr Asn Gly Gln Ala Gly Ser Leu Thr Met Ser
1   5   10   15

Glu Leu Gly Phe Ser Gln Val Gly Ala
            20   25

<210> 2093
<211> 25
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2093

Tyr Tyr Leu Ser Arg Thr Asn Ser Thr Gly Gly Asn Gln Thr Thr Ser
1   5   10   15

Gln Leu Leu Phe Ser Gln Leu Ser Ala
            20   25

<210> 2094
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2094

Tyr Phe Leu Ser Arg Thr Asn Asn Asn Thr Gly Leu Asn Thr Asn Ser
1   5   10   15

Thr Leu Asn Phe Ser Gln Gly Arg Ala
            20   25

<210> 2095
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2095

Ser Lys Thr Gly Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1   5   10   15

<210> 2096
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2096

Ser Lys Thr Asp Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 2097
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2097

Ser Lys Thr Glu Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 2098
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2098

Ser Lys Thr Pro Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 2099
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2099

Ser Lys Thr His Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 2100
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2100

Ser Lys Thr Gln Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 2101
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2101

Ser Lys Thr Ile Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 2102
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2102

Ser Lys Thr Met Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 2103
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2103

Ser Lys Thr Arg Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 2104
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2104

Ser Lys Thr Asn Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 2105
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2105

Ser Lys Thr Val Gly Arg Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 2106
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2106

Ser Lys Thr Ala Asp Arg Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 2107
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2107

Ser Lys Lys Leu Ser Gln Asn Asn Asn Ser Lys Tyr Ser Trp Gln Gly
1 5 10 15

<210> 2108
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2108

Ser Lys Pro Thr Thr Gly Asn Asn Asn Ser Asp Tyr Ser Trp Pro Gly
1   5   10   15

<210> 2109
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2109

Ser Thr Gln Lys Asn Glu Asn Asn Asn Ser Asn Tyr Ser Trp Pro Gly
1   5   10   15

<210> 2110
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2110

His Lys Asp Asp Glu Gly Lys Phe
1   5

<210> 2111
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2111

His Lys Asp Asp Asn Arg Lys Phe
1   5

<210> 2112
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2112

His Lys Asp Asp Thr Asn Lys Phe
1 5

<210> 2113
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2113

His Glu Asp Ser Asp Lys Asn Phe
1 5

<210> 2114
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2114

His Arg Asp Gly Ala Asp Ser Phe
1 5

<210> 2115
<211> 8
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2115

His Gly Asp Asn Lys Ser Arg Phe
1 5

<210> 2116
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2116

Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Phe Glu Glu Val
1   5   10

<210> 2117
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2117

Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ser Glu Glu Val
1   5   10

<210> 2118
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2118

Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Val Glu Glu Val
1   5   10

<210> 2119
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2119

Lys Gln Gly Ser Asp Lys Thr Asn Val Asp Asp Ala Gly Val
1   5   10

<210> 2120
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2120

Lys Gln Gly Ser Ser Lys Thr Asn Val Asp Pro Arg Glu Val
1 5 10

<210> 2121
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2121

Lys Gln Gly Ser Arg Lys Thr Asn Val Asp His Lys Gln Val
1 5 10

<210> 2122
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2122

Lys Gln Gly Ser Lys Gly Gly Asn Val Asp Thr Asn Arg Val
1 5 10

<210> 2123
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2123

Lys Gln Gly Ser Gly Glu Ala Asn Val Asp Asn Gly Asp Val
1 5 10

<210> 2124
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2124

Lys Gln Asp Ala Ala Ala Asp Asn Ile Asp Tyr Asp His Val
1 5 10

<210> 2125
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2125

Lys Gln Ser Gly Thr Arg Ser Asn Ala Ala Ala Ser Ser Val
1 5 10

<210> 2126
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2126

Lys Glu Asn Thr Asn Thr Asn Asp Thr Glu Leu Thr Asn Val
1 5 10

<210> 2127
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2127

Gln Arg Gly Asn Asn Val Ala Ala Thr Ala Asp Val Asn Thr
1 5 10

<210> 2128
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2128

Gln Arg Gly Asn Asn Glu Ala Ala Thr Ala Asp Val Asn Thr
1 5 10

<210> 2129
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2129

Gln Arg Gly Asn Asn Pro Ala Ala Thr Ala Asp Val Asn Thr
1 5 10

<210> 2130
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2130

Gln Arg Gly Asn Asn His Ala Ala Thr Ala Asp Val Asn Thr
1 5 10

<210> 2131
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2131

Gln Glu Glu Asn Asn Ile Ala Ala Thr Pro Gly Val Asn Thr
1   5   10

<210> 2132
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2132

Gln Pro Pro Asn Asn Met Ala Ala Thr His Glu Val Asn Thr
1   5   10

<210> 2133
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2133

Gln His His Asn Asn Ser Ala Ala Thr Thr Ile Val Asn Thr
1   5   10

<210> 2134
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2134

Gln Thr Thr Asn Asn Arg Ala Ala Phe Asn Met Val Glu Thr
1   5   10

<210> 2135
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2135

Gln Lys Lys Asn Asn Asn Ala Ala Ser Lys Lys Val Ala Thr
1   5   10

<210> 2136
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2136

Gln Gly Gly Asn Asn Lys Ala Ala Asp Asp Ala Val Lys Thr
1   5   10

<210> 2137
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2137

Gln Ala Ala Lys Gly Gly Ala Ala Asp Asp Ala Val Lys Thr
1   5   10

<210> 2138
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2138

Gln Asp Asp Arg Ala Ala Ala Ala Asn Glu Ser Val Asp Thr
1   5   10

<210> 2139
<211> 14

<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2139

Gln Gln Gln His Asp Asp Ala Ala Tyr Gln Arg Val His Thr
1 5 10

<210> 2140
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2140

Gln Ser Ser Ser Ser Leu Ala Ala Val Ser Thr Val Gln Thr
1 5 10

<210> 2141
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2141

Gln Asn Asn Gln Thr Thr Ala Ala Ile Arg Asn Val Thr Thr
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<210> 2142
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2142

Asn Tyr Asn Lys Lys Ser Asp Asn Val Asp Phe Thr
1 5 10

<210> 2143
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<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2143

Asn Tyr Asn Lys Lys Ser Glu Asn Val Asp Phe Thr
1 5 10

<210> 2144
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2144

Asn Tyr Asn Lys Lys Ser Leu Asn Val Asp Phe Thr
1 5 10

<210> 2145
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2145

Asn Tyr Asn Lys Lys Ser Pro Asn Val Asp Phe Thr
1 5 10

<210> 2146
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2146

Asn Tyr Ser Lys Lys Ser His Cys Val Asp Phe Thr
1 5 10

<210> 2147
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2147

Asn Tyr Arg Lys Thr Ile Tyr Val Asp Phe Thr
1   5   10

<210> 2148
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2148

Asn Tyr Lys Glu Lys Lys Asp Val His Phe Thr
1   5   10

<210> 2149
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2149

Asn Tyr Gly His Arg Ala Ile Val Gln Phe Thr
1   5   10

<210> 2150
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2150

Asn Tyr Ala Asn His Gln Phe Val Val Cys Thr
1 5 10

<210> 2151
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2151

Asn Tyr Asp Asp Asp Pro Thr Gly Val Leu Leu Thr
1 5 10

<210> 2152
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2152

Asn Tyr Asp Asp Pro Thr Gly Val Leu Leu Thr
1 5 10

<210> 2153
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2153

Asn Phe Glu Gln Gln Asn Ser Val Glu Trp Thr
1 5 10

<210> 2154
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2154

Ser Gln Ser Gly Ala Ser Asn
1 5

<210> 2155
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2155

Asn Asn Gly Ser Gln Ala
1 5

<210> 2156
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2156

Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Thr Thr Trp Ser
1 5 10 15

Arg Leu Gln Phe Ser Gln Ala Gly Ala
20 25

<210> 2157
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2157

Ser Lys Thr Ser Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 2158
<211> 8

<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2158

His Lys Asp Asp Glu Glu Lys Phe
1 5

<210> 2159
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2159

Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Glu Val
1 5 10

<210> 2160
<211> 14
<212> PRT
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<220>
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<400> 2160

Gln Arg Gly Asn Asn Gln Ala Ala Thr Ala Asp Val Asn Thr
1 5 10

<210> 2161
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2161

Asn Tyr Asn Lys Lys Ser Val Asn Val Asp Phe Thr
1 5 10

<210> 2162
<211> 42
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2162

Ser Gln Ser Gly Ala Ser Asn Tyr Asn Thr Pro Ser Gly Thr Thr Thr
1   5   10   15

Gln Ser Arg Leu Gln Phe Ser Thr Ser Ala Asp Asn Asn Asn Ser Glu
            20   25   30

Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His
        35   40

<210> 2163
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2163

Ser Ala Ser Gly Ala Ser Asn Phe Asn Ser Glu Gly Gly Ser Leu Thr
1   5   10   15

Gln Ser Ser Leu Gly Phe Ser Thr Asp Gly Glu Asn Asn Asn Ser Asp
            20   25   30

Phe Ser Trp Thr Gly Ala Thr Lys Tyr His
        35   40

<210> 2164
<211> 42
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2164

Ser Gln Ser Gly Ala Ser Asn Tyr Asn Thr Pro Ser Gly Thr Thr Thr
1 5 10 15

Gln Ser Arg Leu Gln Phe Ser Thr Asp Gly Glu Asn Asn Asn Ser Asp
20 25 30

Phe Ser Trp Thr Gly Ala Thr Lys Tyr His
35 40

<210> 2165
<211> 42
<212> PRT
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<400> 2165

Ser Ala Ser Gly Ala Ser Asn Tyr Asn Thr Pro Ser Gly Thr Thr Thr
1 5 10 15

Gln Ser Arg Leu Gln Phe Ser Thr Ser Ala Asp Asn Asn Asn Ser Glu
20 25 30

Phe Ser Trp Pro Gly Ala Thr Thr Tyr His
35 40

<210> 2166
<211> 42
<212> PRT
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<400> 2166

Ser Gln Ser Gly Ala Ser Asn Phe Asn Ser Glu Gly Gly Ser Leu Thr
1 5 10 15

Gln Ser Ser Leu Gly Phe Ser Thr Asp Gly Glu Asn Asn Asn Ser Asp
20 25 30

Phe Ser Trp Thr Gly Ala Thr Lys Tyr His
35 40

<210> 2167
<211> 42
<212> PRT
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<220>
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<400> 2167

Ser Ala Ser Gly Ala Ser Asn Tyr Asn Thr Pro Ser Gly Ser Leu Thr
1 5 10 15

Gln Ser Ser Leu Gly Phe Ser Thr Asp Gly Glu Asn Asn Asn Ser Asp
20 25 30

Phe Ser Trp Thr Gly Ala Thr Lys Tyr His
35 40

<210> 2168
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<400> 2168

Ser Gln Ser Gly Ala Ser Asn Tyr Asn Thr Pro Ser Gly Thr Thr Thr
1 5 10 15

Gln Ser Arg Leu Gln Phe Ser Thr Ser Ala Asp Asn Asn Asn Ser Asp
20 25 30

Phe Ser Trp Thr Gly Ala Thr Lys Tyr His
35 40

<210> 2169
<211> 42
<212> PRT
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<400> 2169

Ser Gly Ala Gly Ala Ser Asn Phe Asn Ser Glu Gly Gly Ser Leu Thr
1 5 10 15

Gln Ser Ser Leu Gly Phe Ser Thr Asp Gly Glu Asn Asn Asn Ser Asp
20 25 30

Phe Ser Trp Thr Gly Ala Thr Lys Tyr His
35 40

<210> 2170
<211> 7
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2170

Ser Gly Ala Gly Ala Ser Asn
1 5

<210> 2171
<211> 15
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2171

Asn Ser Glu Gly Gly Ser Leu Thr Gln Ser Ser Leu Gly Phe Ser
1 5 10 15

<210> 2172
<211> 11
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2172

Thr Asp Gly Glu Asn Asn Asn Ser Asp Phe Ser
1 5 10

<210> 2173
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<212> PRT
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<220>
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<400> 2173

Ser Glu Phe Ser Trp Pro Gly Ala Thr Thr
1 5 10

<210> 2174
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<220>
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<400> 2174

Thr Ser Ala Asp Asn Asn Asn Ser Asp Phe Ser Trp Thr
1 5 10

<210> 2175
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<212> PRT
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<220>
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<400> 2175

Ser Gln Ser Gly Ala Ser Asn Tyr
1 5

<210> 2176
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<400> 2176

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
1 5 10 15

<210> 2177
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<220>
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<400> 2177

Thr Ser Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr
1 5 10 15

Lys Tyr His

<210> 2178
<211> 8
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<400> 2178

Ser Ala Ser Gly Ala Ser Asn Phe
1 5

<210> 2179
<211> 19
<212> PRT
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<220>
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<400> 2179

Thr Asp Gly Glu Asn Asn Asn Ser Asp Phe Ser Trp Thr Gly Ala Thr
1 5 10 15

Lys Tyr His

<210> 2180
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<220>
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<400> 2180

Ser Ala Ser Gly Ala Ser Asn Tyr
1   5

<210> 2181
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2181

Thr Ser Ala Asp Asn Asn Asn Ser Glu Phe Ser Trp Pro Gly Ala Thr
1   5   10   15

Thr Tyr His

<210> 2182
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<212> PRT
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<220>
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<400> 2182

Asn Thr Pro Ser Gly Ser Leu Thr Gln Ser Ser Leu Gly Phe Ser
1   5   10   15

<210> 2183
<211> 19
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<400> 2183

Thr Ser Ala Asp Asn Asn Asn Ser Asp Phe Ser Trp Thr Gly Ala Thr
1 5 10 15

Lys Tyr His

<210> 2184
<211> 8
<212> PRT
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<220>
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<400> 2184

Ser Gly Ala Gly Ala Ser Asn Phe
1 5

<210> 2185
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<400> 2185

Cys Thr Cys Cys Ala Gly Val Val Ser Val Val Ser Met Arg Ser Arg
1 5 10 15

Val Cys Val Asn Ser Gly Cys Ala Gly Cys Thr Asp His Cys Val Val
20 25 30

Ser Arg Asn Ser Gly Thr Cys Val Met Ser Ala Cys Ala Cys Ala Ala
35 40 45

<210> 2186
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<400> 2186

Cys Thr Cys Cys Ala Gly Ala Gly Ala Gly Gly Cys Ala Ala Cys Ala
1 5 10 15

Gly Ala Cys Ala Ala Gly Cys Ala Gly Cys Thr Ala Cys Cys Gly Cys
20 25 30

Ala Gly Ala Thr Gly Thr Cys Ala Ala Cys Ala Cys Ala Cys Ala Ala
35 40 45

<210> 2187
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<220>
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<400> 2187

Ser Ala Ala Gly Ala Ser Asn
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<212> PRT
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<220>
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<400> 2188

Tyr Phe Leu Ser Arg Thr Asn Thr Glu Ser Gly Ser Thr Thr Gln Ser
1 5 10 15

Thr Leu Arg Phe Ser Gln Ala Gly
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<210> 2189
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<400> 2189

Ser Lys Thr Ser Ala Asp Asn Asn Asn Ser Asp Phe Ser
1 5 10

<210> 2190
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<400> 2190

Lys Gln Gly Ser Glu Lys Thr Asp Val Asp Ile Asp Lys Val
1 5 10

<210> 2191
<211> 7
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<400> 2191

Ser Thr Ala Gly Ala Ser Asn
1 5

<210> 2192
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<400> 2192

Tyr Phe Leu Ser Arg Thr Asn Thr Thr Ser Gly Ile Glu Thr Gln Ser
1 5 10 15

Thr Leu Arg Phe Ser Gln Ala Gly
20

<210> 2193
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<212> PRT
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<400> 2193

Ser Lys Thr Asp Gly Glu Asn Asn Asn Ser Asp Phe Ser
1   5   10

<210> 2194
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<400> 2194

Lys Gln Gly Ala Ala Ala Asp Asp Val Glu Ile Asp Gly Val
1   5   10

<210> 2195
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<400> 2195

Ser Glu Ala Gly Ala Ser Asn
1   5

<210> 2196
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2196

Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser
1   5   10   15

Arg Leu Gln Phe Ser Gln Ala Gly
            20

<210> 2197
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2197

Ser Lys Thr Ser Ala Asp Asn Asn Asn Ser Glu Tyr Ser
1   5   10

<210> 2198
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2198

Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val
1   5   10

<210> 2199
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2199

Tyr Phe Leu Ser Arg Thr Asn Asp Ala Ser Gly Ser Asp Thr Lys Ser
1   5   10   15

Thr Leu Leu Phe Ser Gln Ala Gly
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<210> 2200
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<400> 2200

Ser Thr Thr Pro Ser Glu Asn Asn Asn Ser Glu Tyr Ser
1   5   10

<210> 2201
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<220>
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<400> 2201

Ser Ala Ala Gly Ala Thr Asn
1   5

<210> 2202
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<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2202

Tyr Phe Leu Ser Arg Thr Asn Gly Glu Ala Gly Ser Ala Thr Leu Ser
1   5   10   15

Glu Leu Arg Phe Ser Gln Ala Gly
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<210> 2203
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<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2203

His Gly Asp Asp Ala Asp Arg Phe
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<210> 2204
<211> 14
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2204

Lys Gln Gly Ala Glu Lys Ser Asp Val Glu Val Asp Arg Val
1 5 10

<210> 2205
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2205

Lys Gln Asp Ser Gly Gly Asp Asn Ile Asp Ile Asp Gln Val
1 5 10

<210> 2206
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<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2206

Ser Asp Ala Gly Ala Ser Asn
1 5

<210> 2207
<211> 24
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2207

Tyr Phe Leu Ser Arg Thr Asn Thr Glu Gly Gly His Asp Thr Gln Ser
1   5   10   15

Thr Leu Arg Phe Ser Gln Ala Gly
            20

<210> 2208
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2208

Lys Glu Asp Gly Gly Gly Ser Asp Val Ala Ile Asp Glu Val
1   5   10

<210> 2209
<211> 7
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2209

Ser Asn Ala Gly Ala Ser Asn
1   5

<210> 2210
<211> 24
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2210

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1   5   10   15

Glu Leu Arg Phe Ser Gln Pro Gly
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<210> 2211
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<220>
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tctcagnncn gngcg 75

<210> 2215
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<210> 2216
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<210> 2218
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<210> 2219
<211> 30
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ttgttgaaca tcaccacgtg acgcacgttc 30

<210> 2220
<211> 30
<212> DNA
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<400> 2220
tccccgtggt tctactacat aatgtggccg 30

<210> 2221

<211> 30
<212> DNA
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ttccacactc cgttttggat aatgttgaac 30

<210> 2222
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<400> 2222
agggacatcc ccagctccat gctgtggtcg 30

<210> 2223
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<400> 2223
agggacaacc cctccgactc gccctaatcc 30

<210> 2224
<211> 30
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<400> 2224
tcctagtaga agacaccctc tcactgcccg 30

<210> 2225
<211> 30
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agtaccatgt acacccactc tcccagtgcc 30

<210> 2226
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<400> 2226
atatggacgt tcatgctgat caccataccg 30

<210> 2227
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<220>
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agcaggagct ccttggcctc agcgtgcgag 30

<210> 2228
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<220>
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acaagcagct tcactatgac aaccactgac 30

<210> 2229
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rvcsrsaaca acaacagtra sttctcctgg mmaggagcta ccaagtacca cctcaatggc 120

agagactctc tggtgaatcc cggaccagct atggcaagcc acrrggacrr crmsrrsars 180

ttttttcctc agagcggggt tctcatcttt gggaagsaar rcrscrvsrv arvcratryc 240

gmsnhcrvmv rsgtcatgat tacagacgaa gaggagatct ggac 284

<210> 2230
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<400> 2230
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<210> 2231
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<210> 2232
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<220>
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ccacttaggg cctggtcgat accgttcggt g 31

<210> 2233
<211> 32
<212> DNA
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tctcgcccca agagtagaaa cccttcstty yg 32

<210> 2234
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<212> PRT
<213> Adeno-associated virus 2

<400> 2234

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
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        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575
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Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
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<213> Adeno-associated virus 9

<400> 2235

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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
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Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
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Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
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Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
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Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
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<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  2236

Gly Ser Thr Pro Pro Pro Met
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<210>  2237
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<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

<400>  2237

Gly Glu Thr Arg Ala Pro Leu
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<210>  2238
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<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence: Synthetic polypeptide

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Ser Pro Ala Lys Phe Ala
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<210> 2239
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Asn Lys Asp Lys Leu Asn
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actccatcac taggggttcc ttgtagttaa tgattaaccc gccatgctac ttatctacgt 180

agccatgcgt cgacataacg cgtgtttaca acatttgctg cccacttttc ctaggtttct 240

tgagacctct acaagagttg gagttgacac ttggggtact ttcttggtgt aacgaactaa 300

tagcctgaaa aaaagaagtc atgtgttttc agcaaggcaa gaaactgtct aacatagtag 360

ataaaacaga gaacacttgg ccggaatcaa ctaagatgtt gctatgttcc attcatcata 420

ttatctccat ctgcagagta gtgggttagt ggagggtaga aaacattctc ctgaacaact 480

agttaaactt ggctttgagt tccacctgta ccacttgcat aatcttggga aagtgagttg 540

cctaattcag tgacattaat aaatttatta atttcttctt tcaataaaac ctggagagag 600

cttcatatgt atcagcatat gctaaacttg aaagatacaa gtagaaaatg gaaggaaata 660

tatctgactc aatagggata gttcaagggt taaattaaaa gtagtaaagt attataatta 720

atctgacatg gtacctaata tataataatc atgtattaag aatgccagtc accctctagc 780

ggccgcaatt cgaacgctga cgtcatcaac ccgctccaag gaatcgcggg cccagtgtca 840

ctaggcggga acacccagcg cgcgtgcgcc ctggcaggaa gatggctgtg agggacaggg 900

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caatatcaca catacacaca catgcatgca cacacacatg cacacaaaca tgcacacaca 1980

cacattactt ccttctgctt atgaaagcta gcattatcaa tatctaaagg taaaattttt 2040

tcattattaa tttattatat ttttttaaag actcacatag tcttctgcac agggcattct 2100

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<212> DNA
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<220>
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aagatcaatt caattcacgc gtccatggct tagaaggcaa gaatcctggc tgtggaaaga 180

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acgacctgga tggagtggga cagagaaatt aacaattaca caagcttaat acactcctta 360

attgaagaat cgcaaaacca gcaagaaaag aatgaacaag aattattgga attagataaa 420

tgggcaagtt tgtggaattg gtttaacata acaaattggc tgtggtatat aaaattattc 480

ataatgatag taggaggctt ggtaggttta agaatagttt ttgctgtact ttctatagtg 540

aatagagtta ggcagggata ttcaccatta tcgtttcaga cccacctccc aaccccgagg 600

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attcgattag tgaacggatc tcgacggtat cgatcacgag actagcctcg agcggccgca 720

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ttggatttgg gaatcttata agttctgtat gagaccacac cggtgaagca aagaaggggc 960

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